GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 9, 2004, 16:09:10 ; Search time 1392 Seconds (without alignments) 3.908 Million cell updates/sec Run on:

us-10-664-775-2 3572 1 gtcaggaagggcagtga......gcaacaacagcagaaagctt 3572 Title: Perfect score: Sequence:

1612 ségs, 761539 residues IDENTITY NUC Gapoxt 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

Searched:

3224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00% Maximum Match 100% Listing first 250 summaries

rngdb:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Oligonucleotide for detecting cytosine methylation SEQ ID NO 34560. ABQ47969 standard; DNA; 612 BP (first entry) 12-JUL-2002 ABQ47969; RESULT 1 ABQ47969/c

Human; cytosine methylation; S'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG

Berlin K, Guetig D; Piepenbrock C, olek A,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons diagnosis and prognosis, com from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-0pG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-RPC sections are of cytosine methylation described in the disclosure of the invention

Sequence 612 BP; 232 A; 219 C; 72 G; 89 T; 0 U; 0 Other;

0; Gaps DB 1; Length 612; 37; Indels O.8%; Score 28.8; DE Local Similarity 58.0%; Pred. No. 1.6; tes 51; Conservative 0; Mismatches Query Match Best Loc Matches

280 TITITIGAAGAITITITICGGGTITITITICGAAGGAGTAITIGTITITITITITITITITIT 221

3267 AAGAATGTCATTCTTTGTGAAGTTTTGA 3294

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220 AGGGAGTTCGGTCGTAGTTTTTTAGGA 193

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RESULT 2

ABQ47968 standard; DNA; 612

ABQ47968;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 34559.

Human, cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826 05-SEP-2000; 2000DE-01044543

(EPIG-) EPIGENOMICS AG.

Berlin K, Guetig D; Olek A, Piepenbrock C,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons diagnosis and prognosis, com from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated Chemically to convert cytosine (C) but not methylated C, to uradil, then part of the genomic cample of DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the rwo classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs not of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations of single nucleotide polymorphisms (SNP'8); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ19410-ABQ24121 represent genomic DNA sequences used to illustrate the method of the contract investigating cell differentiation. The method allows the methylation abcorder of the contract of the co disclosure of the invention

Sequence 612 BP; 89 A; 72 C; 219 G; 232 T; 0 U; 0 Other;

0; Gaps 0.8%; Score 28.8; DB 1; Length 612; 58.0%; Pred. No. 1.6; tive 0; Mismatches 37; Indels C 51; Conservative Similarity Query Match Local Matches

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AAK19599 standard; DNA; 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                              Human bone marrow expressed single exon probe SEQ ID NO: 20161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other;
3267 AAGAATGTCATTCTTTGTGAAGTTTTGA 3294
                    393 AGGGAGTICGGICGIAGITTTTITAGGA 420
                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK, Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                     2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                             AAK45604 standard; DNA; 267 BP
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RESULT 4 AAK19599/c

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2661 TGGCATCÁCTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAG 2720
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                                                                                                                        Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhaimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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                                                            Human brain expressed single exon probe SEQ ID NO: 19590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other;
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30-JUN-2000; 2000US-0207456P.
03-MUG-2000; 2000US-023468P.
27-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification for complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproceinaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences 261 TGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAG 2720 Human genome-derived single exon nucleic acid probes useful for analyzing 1; Gaps Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss. Similarity 56.8%; Score 28.7; DB 1; Length 267; Similarity 56.8%; Pred. No. 1.3; 1.7; Conservative 0; Mismatches 53; Indels 1 Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other; Human liver single exon probe, SEQ ID No 20284. Claim 4; SEQ ID NO 20284; 658pp; English. Penn SG, Hanzel DK, Chen W, Rank DR; gene expression in human adult liver. 26-MXY - 2000; 2000US-0207456P. 30-JUN - 2000; 2000US-00608408. 03-AXG-2000; 2000US-06532366. 21-SEP-2000; 2000US-0236359P. 27-SEP-2000; 2000US-0236359P. 04-CCT-2000; 2000GB-00024563. ABS19876 standard; DNA; 267 BP. (MOLE-) MOLECULAR DYNAMICS INC. 30-JAN-2001; 2001WO-US000664. 04-FEB-2000; 2000US-0180312P 71; Conservative WPI; 2001-488898/53. 2721 GGAGG 2725 WO200157273-A2. Homo sapiens. ABS19876; Query Match Local ABS19876/c Matches RESULT 6 Вb à

19-AUG-2002 (first entry)

Human genome-derived single exon probe ORF from lung SEQ ID No 19867

Human, ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tubercous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocyctosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.

Homo sapiens.

WC200186003-A2.

15-NOV-2001

30-JAN-2001; 2001WO-US000665.

04-FEB-2000; 2000US-0180312P. 26-MX-2000; 2000US-0207456P. 30-UIX-2000; 2000US-00608408. 03-AUG-2000; 2000US-00533366. 21-SEP-2000; 2000US-023468PP. 27-SEP-2000; 2000US-023468PP.

(MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 4; SEQ ID NO 19867; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuran lung comprising single exon nucleic acid probes having one of 12014 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the movel set of probes which hybridise at high stringency to a nucleic probes. Also included are a microarray comprising the array with a carry man unua, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung conjection of detectably labeled nucleic acids derived from human lung conjection of detectably labeled nucleic acids derived from human lung array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (b) detectably labeled nucleic acids from entaryote lung mRNA, to a single exon probe, labeled nucleic acids from entaryote lung mRNA, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several criscus and/or cell types using hybridisation to a single exon to a single exon to microarrays having a probe with the exon, where a common pattern of expression of the exons should be assigned to a single gene, a pertial comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human cannor, chronic obstructive pulmonary disease (ORP), interestitial lung diseases (ILD), familial idiopathic pulmonary diseases such a sating. Created because with the exons such for elected pulmonary percent cuberous sc

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2601 GATGCTGGGAGGATTGGGGGCAGGAGAAGGGGACAACAGAGGATGAGATGGCTGGA 2660
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histiccytosis, lymphangiclelomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polymucleotide (III) having a cDNA sequence (SI) from the 10912 nucleotide sequences as given in ABL/7023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (SI) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 28.7; DB 1; Length 267; Best Local Similarity 56.8%; Pred. No. 1.3; Matches 71; Conservative 0; Mismatches 53; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian cancer related cDNA clone SEQ ID NO:3694.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 267 BP; 3 A; 151 C; 4 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3694; 489pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL80716 standard; cDNA; 373 BP.
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value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerses chain reaction (PCR). (I) comprising (III) and/or [II] is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells, and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques
                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepler WT, Jiang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pancreas; cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss.
                                                                                                                                                                          0.8%; Score 28.6; DB 1; Length 373; 38.6%; Pred. No. 1.5;
                                                                                                                                                                                                       4; Indels
                                                                                                                                                 Sequence 373 BP; 91 A; 94 C; 105 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human pancreatic cancer expressed cDNA SEQ ID NO 4051.
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                                                                                                                                                                                                                                                                                                                                   ABV98643 standard; cDNA; 517 BP
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31-JAN-2001, 2001US-026568P.
21-YAR-2001, 2001US-0267568P.
28-APR-2001, 2001US-0278651P.
28-APR-2001, 2001US-02113P.
16-MAY-2001, 2001US-03113P.
12-JUL-2001, 2001US-031369P.
20-AUG-2001; 2001US-0313999P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2002; 2002WO-US002781
                                                                                                                                                                                        88.68;
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                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benson DR, Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-627435/67.
                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200260317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2002.
                                                                                                                                                                            Query Match
                                                                                                                                                                                             Best Local
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                          ABV98643
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New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic

Claim 1; SEQ ID NO 4051; 300pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (a) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-

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Human; ss; gene; G-protein-coupled protease; gene therapy; transgenic;
protease mediated disorder; proliferative disorder;
differentiative disorder; developmental disorder;
haematoppietic disorder.
              Human G-protein-coupled protease #41.
                                                                               99US-00280116.
                                                                                        99US-00280116.
                                                                                                  (MILL-) MILLENNIUM PHARM INC.
    23-APR-2002 (first entry)
                                                 Homo sapiens.
                                                                               26-MAR-1999;
                                                           JS6331427-B1
                                                                                        26-MAR-1999;
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Robison KE;

WPI; 2002-129545/17.

New polynuclectides encoding protease homologs of the G-protein-coupled protease family, useful in identifying agonists and antagonists for diagnosis and treatment of protease mediated disorders.

Disclosure; Col 95-96; 246pp; English.

The invention relates to an isolated human protease mucleic acid molecule comprising a nucleotide sequence of 546 base pairs, one of 268 fully defined in the specification. Also discolsed are production of an isolated polypeptide encoded by the nucleic acid, use of an antibody to detect the mucleic acid, use of an antibody to detect the express the protein from the nucleic acid, use of an antibody to detect the encoded protein in a sample and to modulate its in vivo activity, identifying agents that bind to the protein and identification of a polymucleotide agent that modulates the expression or activity of the nucleic acid, and can be used to identify an agent that modulates the expression or activity of the nucleic acid, and can be used to isolate the protein. The nucleic acid and can be used to isolate the protein. The nucleic acid as well as activity in the context of a biological sample (e.g., blood, as well as activity in the context of a biological sample (e.g., blood, as well as activity in the context of a biological sample caid expression or activity of the nucleic acid. The nucleic as disorder, or is at risk of developing a disease or disorder, associated with aberrant expression or activity of the nucleic acid can be used a subsect of actect naturally-occurring genetic mutations in a protease gene. The nucleic acid can be used to detect naturally-occurring genetic mutations in a protease gene mediated disorders e.g., proliferative, differentiative, deen protease mediated disorders e.g., proliferative, differentiative, developmental or haematopolitic disorders. The nucleic acid can be used a can be used to design ribody as probes, primers, in biological assays, to determine patterns of gene expression, to design ribodyments represents one of the 268 disclosed human G-protein-

Seguence 387 BP; 80 A; 130 C; 103 G; 67 T; 0 U; 7 Other; coupled protease cDNA sequences

RESULT 13

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Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                        DNA encoding novel human diagnostic protein #4731.
      AAS68927 standard; cDNA; 237 BP.
                                                                                                                                                                                                                Tang YT,
                                                                                                                                                    30-MAR-2001; 2001WO-US008631
                                                                                                                                                                     31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                        13-FEB-2002 (first entry)
                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                 WPI; 2001-639362/73
                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                          P-PSDB; ABG04740.
                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                    Homo sapiens
                                                                                                                                    11-OCT-2001.
                         AAS68927;
AAS68927
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGF) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) the polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in game therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypurcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIDO at the printed sequences.

Claim 1; SEQ ID NO 4731; 103pp; English.

968 ACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTG 1027 0; Gaps 1028 GAATACGGAATGAAGCAGGGCAAAAGACTAATAGAGTTTTGCCAAGAAATG 1078 'Match 0.7%; Score 26.2; DB 1; Length 237; Local Similarity 52.3%; Pred. No. 5.9; onservative 0; Mismatches 53; Indels 0 Sequence 237 BP; 97 A; 34 C; 82 G; 24 T; 0 U; 0 Other; Query Match Matches

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Gaps ·,

13; Indels

0; Mismatches

ch 1 Similarity 72.9%; 35; Conservative (

Best Local Similarity

Matches

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Score 27.2; DB 1; Length 387; Pred. No. 3.7;

inactive zymogen; ss

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 TCCAAGTCCATCGTGCACCCGTCCTACAACTCCAACACTGTGAATGACATGACATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vectors for bovine trypsin and bovine trypsinogen - for cleavage of zymogens into active drugs, e.g. pro-insulin conversion into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant trypsin; trypsinogen analogue; mutated bovine trypsinogen; leader sequence; trypsin activity; recombinant protein production;
                                                                                                                                                                                                                                                                                        Cattle; cow; trypsin; enzyme; protease; proinsulin; insulin; hormone; plasmid pRWG4; ds.
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ttive 0; Mismatches 48; Indels
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4. .675
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                                                     AAQ63794 standard; DNA; 683 BP.
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                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greaney MG, Rosteck PR;
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                                                                                                                                                         (revised)
                                                                                                                                                                                                                                        Bovine trypsin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1993;
                                                                                                                                                         25-MAR-2003
01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP597681-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-1994.
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                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                        AAQ63794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA08526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin,
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RESULT 14
                            AAQ63794
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AAA08526
ID AAA0
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8 g

%XCCCCX8XFFFFX8XFXBXBXBXBXFFFFX8XXXXXBXBXBXBX8X

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This sequence encodes a claimed recombinant trypsin. The trypsin is produced by cleavage of a trypsinogen analogue (AAY91925). A wild type broduced by cleavage of a trypsinogen analogue (AAY91925). A wild type broduce trypsinogen was mutated to destroy the trypsin cleavage site. The lys residue present in the leader Sequence of the native bovine trypsinogen protein was mutated to an Asp residue. The vector was constructed such that DNA encoding a (Glu-Nal2) peptide was inserted between the C-terminus of the alpha factor signal and the N-terminus of the trypsinogen analogue leader sequence to improve the yield of the secreted protein. The specification claims an isolated trypsinogen some analogue leader sequence to improve the yield of the sequence having at least two amino acids which are not Lys or Arg. The captured from the recombinant trypsinogen is useful for the characterization of other proteins, and in the manufacture of other recombinant bioproducts, for example to cleave leader sequences from formal recombinant proteins appreciately as fusion proteins. The present method provides for expression of an inactive zymogen form that is soluble and properly folded yet is not activated until after the present from fermentation broth or cell extracts. This is analogue where the leader sequence is modified such that it lacks a trypsin-lake enzyme cleavage site. Specifically the trypsinogen analogues to the present invention lack a lysine or arginine in the N-terminal leader sequence of the prevent auto-activation or activation or activation by endougenous host cell enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 ricciaigracia regres de confecta ca a confecta de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New trypsinogen analog useful for the production of recombinant trypsin has a modified leader sequence not cleavable by trypsin or trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosteck PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.7%; Score 26.2; DB 1; Length 699; I Similarity 53.4%; Pred. No. 8; 55; Conservative 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 699 BP; 139 A; 221 C; 178 G; 161 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desplancg D, Larson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   881 AAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCT 923
                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "leader sequence"
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                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                            *tag= a
product= "trypsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/product= "trypsin"
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-283565/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2000.
                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                       Bos taurus
                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzymes.
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AAQ63795 standard; DNA; 701 BP.

(first entry)

(revised)

25-MAR-2003 01-DEC-1994

AAQ63795;

Bovine trypsinogen gene.

Cattle; cow; trypsinogen; enzyme; protease; proinsulin; insulin; hormone; plasmid pRMG4; ss.

Location/Qualifiers

Bos taurus.

/*tag= a

EP597681-A1 18-MAY-1994

. 694

92US-00977703. 93EP-00308959.

10-NOV-1993; 13-NOV-1992;

Greaney MG, Rosteck PR;

WPI; 1994-160671/20.

(ELIL) LILLY & CO ELI.

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New chymotrypsin-free trypsin and trypsinogen useful for manufacturing recombinant protein pharmaceuticals and pure trypsin.
                                                                                                                                                                                                                              Hanguier JM, Hershberger CL, Larson JL, Rosteck PR;
                                                                      Trypsinogen; bovine; trypsin; serine protease; ds.
                                                       Bovine met-phe-trypsinogen coding sequence.
                                                                                                                       /*tag= a
/product= "Trypsinogen"
                                                                                                      Location/Qualifiers
       AAF81479 standard; DNA; 699 BP
                                                                                                                                                                                                                                                                                              Claim 20; Fig 1; 55pp; English
                                                                                                                                                                             05-SEP-2000; 2000WO-US020813.
                                                                                                                                                                                              15-SEP-1999; 99US-0154019P.
                                      06-JUN-2001 (first entry)
                                                                                                               669.
                                                                                                                                                                                                             (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                                                                                      P-PSDB; AAB80953.
                                                                                                                                              WO200119970-A2
                                                                                                                                                              22-MAR-2001.
                                                                                       Bos sp.
AAF8147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 TCCAAGTCCATCGTGCACCCGTCCTACAACTCCAACACTCTGAACAATGACATCATGCTG 288
The present sequence is the coding sequence for bovine met-phetrypsinogen. Trypsin is a serine protease which cleaves the peptide bond on the carboxy-terminus of basic amino acid residues. Trypsin is synthesised in a slightly longer catalytically inactive form: trypsinogen, which itself is cleaved (leader sequence removed) to give trypsin. The leader sequence of the protein encoded by the present sequence consists of (Asp)4-Lys) and is present at the amino-terminus. The protein encoded by the present sequence has two additional residues at the amino terminus: Net and Phe. Bovine met-phe-trypsinogen is useful for the manufacture of recombinant protein pharmaceuticals. High purity trypsin products are produced by expressing trypsinogen inside a prokaryotic cell which is then isolated and activated to form trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 0.7%; Score 26.2; DB 1; Length 699; Local Similarity 53.4%; Pred. No. 8; es 55; Conservative 0; Mismatches 48; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 699 BP; 139 A; 221 C; 178 G; 161 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          881 AAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 Arcaagcicaagiccgccgcarcccigaacrcccgcgrgccr 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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RESULT 17 AAQ63795

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226 TCCAAGTCCATCGTGCACCCGTCCTACAACTCCCAACACTCTGAACAATGACATGACATGGCTG 285
                                                                                                                                                                                                                                                              Trypsinogen analogue, mutated bovine trypsinogen, leader seguence, trypsin activity, recombinant protein production, inactive zymogen, ss.
                              881 AAGAAGCIGAAGIIGAACGGICCIAIGAAGACCIACAAGACCI 923
                                                            286 ATCAAGTCCACCGCATCCCTGAACTCCCGCGTGGCCT 328
                                                                                                                                                                                                                                 DNA encoding a trypsinogen analogue.
                                                                                                                                       AAA08525 standard; DNA; 702 BP
                                                                                                                                                                                                 19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                           Synthetic.
Bos taurus.
                                                                                                                                                                     AAA08525;
                                                                                                          RESULT 18
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0; Gaps

821 TCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCCAACCAGTAATGCTG 880

Query Match 0.7%; Score 26.2; DB 1; Length 701; Sest Local Similarity 53.4%; Pred. No. 8; datches 55; Conservative 0; Mismatches 48; Indels 0 Sequence 701 BP; 141 A; 222 C; 180 G; 158 T; 0 U; 0 Other;

Query Match

Matches

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This gene is expressed in a recombinant host, e.g. E. coli, using plasmid pRMGY. The encoded bowine trypshinogen gene may be expressed recombinantly and is able to cleave zymogens into active drugs, e.g. pro-insulin conversion into insulin. (Updated on 25-MAR-2003 to correct PN field.)

Expression vectors for bovine trypsin and bovine trypsinogen - for cleavage of zymogens into active drugs, e.g. pro-insulin conversion into insulin.

Disclosure; Page 27; 35pp; English.

Protease, pig, virus activator, inhibitor identification; influenza;

Pig lung protease coding sequence

viral infection; ss.

WO200011193-A1.

Sus scrofa.

(first entry)

16-JUN-2000

AAA07168;

AAA07168 standard; DNA; 828

AAA07168

```
This sequence encodes a trypsinogen analogue. The wild type bovine trypsinogen was mutated to destroy the trypsin cleavage site. The lys residue present in the leader sequence of the native bovine trypsinogen protein was mutated to an Asp residue. The vector was constructed such that DNA encoding a (Glu-Ala)2 peptide was inserted between the C-cerminus of the alpha factor signal and the N-terminus of the trypsinogen analogue leader sequence to improve the yield of the secreted protein. The specification claims an isolated trypsinogen analogue comprising a protein having trypsin activity and a leader sequence having at least two amino acids which are not bys or Arg. A recombinantly produced trypsinogen is also claimed. The trypsin derived from the recombinant trypsinogen is useful for the characterization of other proteins, and in the manufacture of other recombinant bioproducts, for example to cleave the manufacture of other recombinant bioproducts, for example to cleave fusion proteins. The present method provides for expression of an initially as fusion proteins. The present method provides for expression of an initially as clusion proteins. This is accomplished through the expression of a single chain trypsinogen analogue where the leader sequence is modified such that it extracts. This is accomplished through the expression of a single chain analogues of the present invention lack a lyshe or arithin in the N-terminal leader sequence of the protein to prevent auto-activation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New trypsinogen analog useful for the production of recombinant trypsin has a modified leader sequence not cleavable by trypsin or trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larson JL, Rosteck PR;
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                                                                                                                                                                                    /*tag= .b
/note= "leader sequence"
30. .699
                                                                               a
"linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 45-47; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                /product= "trypsin"
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanquier JM, Hershberger CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US021047
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                                                                                                                                                       .29
                                                                       *tag=
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                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                           WO200017332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-1998;
                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000
                                     misc_RNA
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New pig lung protease with virus activation activity is used for screening potential inhibitors of virus infection, especially of influenza virus.

Yamashita M, Iida K, Kido H;

WPI; 2000-224708/19.

P-PSDB; AAY81826

(SANY) SANKYO CO LID.

99WO-JP004529. 98JP-00237240.

23-AUG-1999; 24-AUG-1998;

02-MAR-2000.

Claim 9; Page 54-56; 65pp; Japanese.

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2534 TGCTAAAGCTGAAACTCCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAA 2593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2594 AGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGAAAGGGGACGACAGAGGATGAGAŢ 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the protease of the invention, and was derived from pig lung. The protease has virus activation activity. The protease can be used for the identification of potential inhibitors of infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 AGGCCCTGGAGCGAGCACCGTGGGCGGAAAGGAAGCCCCTGGGCACAAGTGGCCCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein-encoding gene 4 cDNA clone HWHIH10, SEQ ID NO: 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TGCTGGTGCTGGCGCCTCCTCCTGGTGAGCCTGGTCCACACGGCCCCGGCCCCAGGCC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 26.2; DB 1; Length 828; 49.6%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 828 BP; 147 A; 280 C; 266 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD08286 standard; cDNA; 1151 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2654 GGCTGGATGGCATCA 2668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 GGCAGGTGAGCCTGA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viruses such as influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2001
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Best Local S
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RESULT 19

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0; Gaps

821 TCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCAACCAGTAATGCTG 880

psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy; ss.

TITITITIAAAGAATGICATICITIGIG 3285

3226 TICTAIGGCTIIAAIAAAGITIITITITII

셤 à 유

Ö

23;

Pred. No. 9.2; 0; Mismatches

Best Local Similarity 63.5%; Matches 40; Conservative

Homo sapiens.

Location/Qualifiers 42. .914

*tag= a product= "Human secreted protein precursor" /*tag= b 108. .911 . .107 sig_peptide mat_peptide

*tag= c product= "Mature human secreted protein"

WO200136440-A1

25-MAY-2001

15-NOV-2000; 2000WO-US031282.

Human, pancreas, cancer, gene therapy, vaccine, immunostimulant, cytostatic, tumour; gene; ss.

30-JAN-2002; 2002WO-US002781

WO200260317-A2. Homo sapiens

08-AUG-2002

Human pancreatic cancer expressed cDNA SEQ ID NO 3232.

(first entry)

14-JAN-2003

ABV97824;

ABV97824 standard; cDNA; 497 BP.

RESULT 21

19-NOV-1999; 99US-0166414P. 21-JUL-2000; 2000US-0219665P.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Komatsoulis GA, Birse CE, Moore PA;

WPI; 2001-343795/36 P-PSDB; AAE03821

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

Claim 1; Page 440-441; 553pp; English.

AAD08283-AAD08355 represent cDNAs corresponding to 23 human secreted protein genes, and AAE03818-AAE03870 represent the proteins they encode. AAE03818-AAE03818-AAE03870 represent the proteins they encode. AAE03818-AAE03818-AAE03870 represent thuman secreted proteins they encode. The secreted proteins and their genes are useful for preventing, treating to rameliorating medical conditions on be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 23 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haemactopicalic disorders, foetal and developmental abnormalities, haemactopicalic disorders (e.g., Alzhelmer's disease, Parkinson's disease), cognitive disorders (e.g., Alzhelmer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., angiogenic disorders, schizophrenia, asthma, skin disorders, (e.g., angiogenic disorders, kidney disorders, gastrointestinal disorders, angiogenic disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of prinding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties, Antibodies specific for a preservative to modify storage properties and in disorders mentioned above, and in diagnosit immunoassays e.g., and conting and above, and in disorders mentioned above, and in disorders mentyme lanked immunosoperic immunoassay or enzyme lanked immunosoperic immunoassay or enzyme lanked immunosoperic immunoassay or enzyme lanked immunosoperical and protein of the angele and enzyme lanked and protein and protein of the angele and and and present sequence represents a human secreted protein-encoding CDNA of the nvention

Sequence 1151 BP; 252 A; 370 C; 336 G; 193 T; 0 U; 0 Other;

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0.7%; Score 26.2; DB 1; Length 1151;
· Query Match
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The invention relates to an isolated polynuclectide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous trained and a sequences having at least 75¢ or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596 to (a) a patient and compositions comprising polypeptides (ABP68596 to an a patient and compositions comprising polypeptides, polynuclectides, and stimulating the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynuclectides can be used as preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour calls, in vaccines and for gene printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ, Persing DH, Hepler WT, Jiang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3232; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                         31-JAN-2001, 20010S-0265682P.

09-FEB-2001; 20010S-0267568P.

28-APR-2001; 20010S-0287112P.

16-MAY-2001; 20010S-029131P.

12-JUJ-2001; 20010S-039148P.

20-AUG-2001; 2001US-0313999P.

27-NOV-2001; 2001US-0313929P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-627435/67.
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                                                                                                                                                                                                                                                                                                                                                                                                      3233 GCTTTAATAAAGTTTTTTTTTTTTTTTTTTAAAGAATGTCATTCTTTGTGAA 3287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s ściritritritritritritritritritritri sa secesa secicani si secesa secicani secesa sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA construct used to transfect hosts - to produce protein which
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                                                                                                                           Query Match 0.7%; Score 25.8; DB 1; Length 497; Best Local Similarity 65.5%; Pred. No. 9.3; Matches 36; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hagen FS, Murry MJ, Berkner KL, Insley MY, Woodbury RG,
Sequence 497 BP; 113 A; 118 C; 122 G; 121 T; 0 U; 23 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2438 BP; 658 A; 670 C; 666 G; 444 T; 0 U; 0 Other;
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7. .1368
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor IX/Factor VII cDNA fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 7; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN60065 standard; DNA; 2438 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1986-326899/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
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The invention relates to human prostasin-like enzyme polypeptides and polymentides. The enzyme can be expressed by standard recombinant polymucleotides. The polypeptide, polymucleotide and modulators are useful for treating diseases like metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), angiogenesis, includemention, thronic obstructive pulmonary disease (COPD), particularly viral infection. The prostasin-like enzyme gene provides a therapeutic target of decreasing the enzyme activity, in particular for treating or preventing metastatic cancer. Neurodegenerative diseases include for e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrapie. The agonists and antagonists of the polypeptide may be useful to treat osteoproresis, antagonists of the polypeptide may be useful to treat osteoproresis, paget's disease, degradation of bone implants particularly dental implants. Altered levels of human prostasin-like enzyme activity inhibit the progression of restenosis and atherosclerosis. Anti-human prostasin-like enzyme activity inhibit the progression of restenosis and atherosclerosis. Anti-human prostasin-like enzyme activity in addinning diagnosis of micrometastases, autoimmune lesions and renal failure in blopsy specimens, plasma samples and body fluids. The present sequence represents a human prostasin-like enzyme polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2603 TGCTGGGAGGGATTGGGGGCAGGAGGAGAGAGACAACAAAGGGATGAGATGGCTGGATG 2662
                                                                                                                                                                                                                                                                                                Prostasin-like enzyme; human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; gene therapy; antisense therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human prostasin-like enzyme polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
Query Match 0.7%; Score 25.4; DB 1; Length 265; Best Local Similarity 63.3%; Pred. No. 9.9; Matches 38; Conservative 0; Mismatches 22; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 265 BP; 46 A; 99 C; 72 G; 45 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                      Human prostasin-like enzyme polynucleotide sequence.
                                                                                                               ABA94395 standard; cDNA; 265 BP
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22-MAR-2001; 2001US-0277612P.
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                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200198466-A2.
                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2001.
                                                                                                                                                              ABA94395;
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                                                                  RESULT 23
ABA94395/c
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138 TICAGGAAGGAAGGTGCTGGACACAGGAACTCCGAAGGCTGGAAGGTGCTGGGTG

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Gaps

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AAA61697/c ID AAA61697 standard; cDNA; 1036 BP.

AAA61697;

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The invention relates to novel serine proteases designated BSSP4 (AABI1700-B11709). The invention also relates to vectors and transformants comprising BSSP4 mucleic acids, relates to vectors and transformants comprising BSSP4 mucleic acids, relates to vectors and transformants comprising BSSP4 mucleic acids, transgenic animals in which the expression level of BSSP4 can be varied, and an mBSSP4 knockout mouse. The invention additionally encompasses anti-BSSP4 antibodies and methods of production of such antibodies, methods of ESSP4 antibodies and methods of production of such antibodies, methods of ESSP4 antibodies are creating the mass of actine proteases. The invention medical conditions. Nucleotides encoding BSSP4 were initially isolated in a human brain cDMA library using degenerate PCR initially isolated in a human brain cDMA library using degenerate PCR initially isolated in a human brain cDMA library using degenerate PCR initially isolated in a human brain conserved regions of serine proteases. The BSSP4 serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological campers. Blood diseases associated with altered BSSP4 expression levels. Such diseases include Alzheimer's disease, oedema (dropsy), cancer or inflammation of brain, prostate, testis or bone. Sequences AAAG1793 ans AAAG1704 represents cDNA encoding murine conserved and consing mutine conserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease BSSP4 and antibodies recognizing BSSP4 for assay and diagnosis of diseases in which BSSP4 expression is altered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; oedema; dropsy; cancer; inflammation; prostate; testis; bone; ss.
                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human serine protease BSSP4 (hBSSP4) SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 0.7%; Score 25.4; DB 1; Length 1036; Similarity 53.5%; Pred. No. 15; 53; Conservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1036 BP; 205 A; 310 C; 301 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okui A, Kominami K, Yamaguchi N, Mitsui S;
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                                                                                                  AAA61697 standard; cDNA; 1036 BP
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                                                                                                                                                                                                                                                                                       23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400084/34.
P-PSDB; AAB11702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200031277-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jemura H,
RESULT 24
AAA61697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The invention relates to novel serine proteases designated BSSP4

(AMB11700-B11709), and to nucleic acids encoding them (AAA61695-A61704,
AAA61799). The invention also relates to vectors and transformants
comprising BSSP4 mucleic acids, transgenic and massSex, the comprise of production aciditionally encompasses anti-BSSP4 antibodies and methods
of production of such antibodies, methods of ESSP4 detection using the
arkers for certain medical sease, methods of ESSP4 detection using the
antibodies, and the use of BSSP4 proteins or fragments as diagnostic
markers for certain medical conditions. Nucleotides encoding BSSP4 were
initially isolated in a human brain cDNA library using degenerate PCR
initially isolated in a human brain cDNA library using degenerate PCR
primers (AAA61745-ABA178) based on conserved regions of serine proteases
The BSSP4 serine proteases and nucleotides encoding them are useful in
detecting homologues, mutants and polymorphic variants in biological
cancer of midlemars for diseases associated with altered BSSP4 expression
levels. Such diseases include Alzheimer's disease, oedema (dropsy),
cancer or inflammation of brain, prostate, testis or bone. Sequences
AAA61655-A61703 ans AAA61799 represent oblys encoding murine
preced (massed), and sequence AAA61704 represents cDNA encoding murine
                                                                                                                                                BSSP4; serine protease; human; hBSSP4; mouse; mBSSP4; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; oedema; dropsy; cancer; inflammation; prostate; testis; bone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease BSSP4 and antibodies recognizing BSSP4 for assay and diagnosis of diseases in which BSSP4 expression is altered.
                                                                                                          cDNA encoding human serine protease BSSP4 (hBSSP4) SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 25.2; DB 1; Length 1036; 71.7%; Pred. No. 16; tive 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence.1036 BP; 205 A; 310 C; 301 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 71-73; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          99WO-JP006472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FUSO ) FUSO PHARM IND LTD
                                                               23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 71.7
nes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400084/34.
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                                                                                                                                                                                                                                                                                    WO200031277-A1.
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                                                                                                                                                                                                                                                                                                                                                                       19-NOV-1999;
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                               02-JUN-2000.
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Gaps

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Matches

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ABV97809 standard; cDNA; 448 BP

RESULT 26 ABV97809 ABV97809;

RESULT 25

d d ò Human; NOV14a; cytostatic; Cardiant; Antinflammatory; Immunosuppressive; Antiallergic; Hamenstatic; Anti-HIV; Antidiabetic; Anorectic; Anorectic; Antiashmatic; Nephrotropic; Heparotropic; Neuroprotective, Nootropic; Antibacterial; Vitucide; Antibarseitic; Relaxant; Anticonvulsant;

Partial Human NOV14a DNA sequence, 162662711.

Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IQA nephropathy; cirrhosis; arthritis; 162662711; Alahaimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; prostasin-like protein; chromosome 16; ds.

09-JAN-2002; 2002WO-US000554.

WO200255704-A2. Homo sapiens.

18-JUL-2002.

09-JAN-2001; 2001US-0260417P. 10-JAN-2001; 2001US-0260831P. 28-FEB-2001; 2001US-0272338P. 09-MAR-2001; 2001US-0274876P. 18-APR-2001; 2001US-0284704P

(CURA-) CURAGEN CORP.

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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP6859) encoded by (I) and oligomucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polymecleotides, on the protesting relations and antigen presenting calls expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymecides can be used as propagation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour colls, in vaccines and for gene contrary contrary contrary contrary former of the tumour colls, in vaccines and for gene and in the deal for this patent did not form part of the contrary contrary contrary contrary. Note the requence date for this patent did not form part of the contrary contrary contrary contrary contrary contrary contrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Persing DH, Hepler WT, Jiang Y;
                                                                                                                                                                                              Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 3217; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 25; DB 1; Length 448; Best Local Similarity 68.0%; Pred. No. 15; Matches 34; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 448 BP; 95 A; 112 C; 111 G; 114 T; 0 U; 16 Other;
                                                                                                 Human pancreatic cancer expressed cDNA SEQ ID NO 3217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001, 2001US-0278651P.
28-APR-2001, 2001US-0287112P.
16-MAY-2001, 2001US-0291631P.
12-JUL-2001, 2001US-0313999P.
                                                                                                                                                                                                                                                 cytostatic; tumour; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2002; 2002WO-US002781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2001; 2001US-0265682P.
09-FEB-2001; 2001US-0267568P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001US-0265305P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-2001; 2001US-0333626P
14-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benson DR, Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-627435/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200260317-A2.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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2620 GGCAGGAGAGAAGGGGACGACAGAGATGAGATGGCTGGATGGCATCACTGACTCGATG 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an insert assembly sequence for NOV14a protein. WoV14a is a prostasin-like protein, and the NOV14a coding sequence localises to chromosome 16. The NOV proteins and coding sequence invention are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, 1gA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), asroke muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 GGCCACATGACCCCAGCCAGTGACAGTGCAGTGGAGGCCGTTGGGGAAGGAGGCGTTGGC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2680 G-----ACGIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAGGGAGG 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 GAGTECAATGTCGCCCTCGAGCCCTCCTGAAGGTAGCTGGGGTGCGGGTG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 0.7%; Score 25; DB 1; Length 882; Local Similarity 50.0%; Pred. No. 18; es 86; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 882 BP; 165 A; 304 C; 254 G; 159 T; 0 U; 0 Other;
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Matches
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3233 GCTTTAATAAAGTTTTTTTTTTTTTTTTTTAAAGAATGTCATTCTTT 3282

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GCTTTTTTTTTTTTTTTTTTTTTTTTTTTAANAGCAGGGTCACTTTAA

ABN85394 standard; DNA; 882 BP.

ABN85394/c

(first entry)

21-OCT-2002 ABN85394;

54

NOVX polypeptides and encoding polynucleotides, useful for preventing or treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or

Claim 9; Page 100; 358pp; English.

pharmacogenomics.

Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM, Arajur S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Bllerman K; Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G;

Stone DJ;

Gunther E,

WPI; 2002-590674/63.

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The partial factor VII cDNA sequence is produced by joining portions of CDNA clones lambda VII2115 and lambda VII1923. It is used in a DNA construct which contains a nucleotide sequence encoding a protein which, on activation, has the same biological activity for blood coagulation as Factor IIa. The nucleotide codes at least partially for Factor VII and comprises a sequence encoding a calcium binding domain joined to a scend sequence downstream of this encoding a catalytic domain for the serine protease activity of Factor VIIa. The calcium binding domain comprises a gene encoding Factor VII. IX, X Protein C, prothrombin or Protein S. The construct is used to transfect host cells to produce the protein which, on activation, yields Factor VIIa. (Updated on 31-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkner KL, Insley MY, Woodbury RG, Gray CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA construct used to transfect hosts - to produce protein which activates to give factor VIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 0.7%; Score 24.8; DB 1; Length 2177; Local Similarity 72.7%; Pred. No. 26; les 32; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2177 BP; 569 A; 624 C; 605 G; 379 T; 0 U; 0 Other;
                                                                                                                                                                                            Factor VII; Factor VIIa; DNA construct
                                                                                                                                                                                                                                                     Location/Qualifiers
13. .1128
'/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1A; 55pp; English.
                               AAN60063 standard; cDNA; 2177 BP.
                                                                                                                                                                                                                                                                                                                                                                                        86EP-00302855.
                                                                                                                                                                                                                                                                                                                                                                                                                                       85US-00810002,
                                                                                                                                                                                                                                                                                                                                                                                                                       85US-00724311
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                            Partial Factor VII cDNA,
                                                                                              (revised)
                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hagen FS, Murry MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1986-326899/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAP60055.
                                                                                                                                                                                                                                                                                                                                                                                         L6-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-1985;
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1985;
                                                                                                            31-OCT-2002
23-MAY-1991
                                                                                             25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                        10-DEC-1986
                                                                                                                                                                                                                                                                                                                        EP200421-A.
                                                             AAN60063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RESULT 28
                 AAN60063
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08-AUG-2001 (first entry)

Human secreted protein-encoding gene 4 cDNA clone HWHIH10, SEQ ID NO: 14.

Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson; 6 disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; gene therapy; ss.

Homo sapiens

/*tag= a "Human secreted protein precursor" /product= "Mature human secreted protein" Location/Qualifiers /*tag= b 108. .911 . .107 /*tag= WO200136440-A1 sig_peptide mat_peptide

25-MAY-2001

19-NOV-1999; 99US-0166414P. 21-JUL-2000; 2000US-0219665P. 15-NOV-2000; 2000WO-US031282.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Komatsoulis GA, Birse CE, Moore PA;

P-PSDB; AAE03821

2001-343795/36.

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

Claim 1; Page 440-441; 553pp; English.

ADD002283-AAD00335 represent cDNAs corresponding to 23 human secreted protein genes, and ABC0380 represent the proteins they encode. AAE0380-AAE0380 represent the proteins they encode. AAE0380-AAE0380 represent human secreted proteins they encode. The secreted proteins and their genes are useful for preventing, treating or amaliorating medical conditions, e.g., by protein or gene therapy. The secreted protein in a sample or by determining the presence of mutations in the protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 23 genes, the new genes. Specific uses are described for each of the 23 genes, the new genes. Specific uses are described for each of the 23 genes, the developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, locatal and developmental abnormalities, heematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, contrive disorders, schizophrenia, asthma, skin disorders, contrive disorders, schizophrenia, asthma, skin disorders, pregnancy-related disorders, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proteins can also be used to aid wound healing and epithelial cell proteins can also be used to aid wound healing and epithelial cell proteins to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a protein of the invention can be used as a food additive or a preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated

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3245 ITTITITITITITITITITAAAGAAIGICAIICITIGIGAAG 3288

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AAD08286 standard; cDNA; 1151 BP.

RESULT 29

AAD08286

AAD08286;

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14 SEP-2000; 2000US-0232399P.
14 SEP-2000; 2000US-0232400P.
14 SEP-2000; 2000US-0232400P.
14 SEP-2000; 2000US-0233064P.
14 SEP-2000; 2000US-0233064P.
14 SEP-2000; 2000US-0233064P.
15 SEP-2000; 2000US-0234274P.
25 SEP-2000; 2000US-0234274P.
27 SEP-2000; 2000US-023424P.
27 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
29 SEP-2000; 2000US-0235484P.
20 CCT-2000; 2000US-0235484P.
20 CCT-2000; 2000US-0235484P.
20 CCT-2000; 2000US-0235486P.
20 CCT-2000; 2000US-023546F.
20 CCT-2000; 2000US-0235997P.
20 CCT-2000; 2000US-0235997P.
20 CCT-2000; 2000US-0234647F.
20 CCT-2000; 2000US-0244647F.
20 NOV-2000; 2000US-024647F.
20 NOV-2000; 2000US-0246525P.
20 NOV-2000; 2000US-0246525P.
20 NOV-2000; 2000US-0246525P.
20 NOV-2000; 2000US-0246525P.
20 NOV-2000; 2000US-0246525P.
20 NOV-2000; 2000US-0246528P.
22-AUG-2000; 2000US-0226868P.
23-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227182P.
30-AUG-2000; 2000US-0229824P.
01-SEP-2000; 2000US-0229834P.
01-SEP-2000; 2000US-0229844P.
01-SEP-2000; 2000US-0229944P.
05-SEP-2000; 2000US-0229944P.
05-SEP-2000; 2000US-0229944P.
06-SEP-2000; 2000US-0229948P.
06-SEP-2000; 2000US-023943P.
06-SEP-2000; 2000US-023943P.
06-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023144P.
08-SEP-2000; 2000US-023141P.
08-SEP-2000; 2000US-023141P.
08-SEP-2000; 2000US-023141P.
08-SEP-2000; 2000US-023141P.
08-SEP-2000; 2000US-023198P.
14-SEP-2000; 2000US-023398P.
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with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blodd-related disorder; infectious disorder; spene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                              1103 CTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1149
                                                                                                                                                       . Match 0.7%; Score 24.6; DB 1; Length 1151; Local Similarity 70.2%; Pred. No. 24; es 33; Conservative 0; Mismatches 14; Indels 0.
                                                                                                                                                                                                                                               1517 CTGTGAAAAGAAGAGAAGTGAAAAGCAAAGGAAAAAAGGAAAGATAA 1563
                                                                                                               Sequence 1151 BP; 252 A; 370 C; 336 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding novel human enzyme polypeptide #301.
                                                                                                                                                                                                                                                                                                                                                                                                     AAS41085 standard; cDNA; 1352 BP.
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18-MAR-2000; 2000US-0189874P.
18-MAY-2000; 2000US-019913P.
19-MAY-2000; 2000US-019913P.
19-MAY-2000; 2000US-020515P.
28-JUN-2000; 2000US-0205186P.
30-JUN-2000; 2000US-021688P.
11-JUL-2000; 2000US-021688P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-0217496P.
26-JUL-2000; 2000US-0217496P.
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2000US-0224519P.
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14-AUG-2000; 2000US-025526FP.
14-AUG-2000; 2000US-0255268P.
14-AUG-2000; 2000US-0255268P.
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14-AUG-2000;
14-AUG-2000;
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                                                                    invention
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Matches
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. carcer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. archivitis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. paemphila), reproductive disorders (e.g. altherosclerosis), blood-related disorders (e.g. paemphila), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenca). The polynucleotides of the invention can also be used in gene therapy. AAAS40785-AAA31684 represent circular access encoding for the novel human enzyme polypeptides of the invention. Note: a sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                  17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025199P.
08-DEC-2000; 2000US-025198P.
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1241 TITTGTGTATATAAATGTTAATGATTTTTTATAAGTATTTGTAACCCTGCCCACATATCT 1300

0; Gaps

DB 1; Length 1352;

Match 0.7%; Score 24.6; DB 1; Length 1: Local Similarity 53.7%; Pred. No. 26; GB 51; Conservative 0; Mismatches 44; Indels

Query Match

Matches

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Human; immunosuppressive, antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; vincide; fungicide, opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebral schaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                   Human cDNA encoding a novel secreted protein, SEQ ID 134.
                    1301 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1335
3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                          AAS26942 standard; cDNA; 1352 BP
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24-FEB-2000; 2000US-018662BP.
22-MAR-2000; 2000US-01864564P.
16-MAR-2000; 2000US-0188350P.
11-MAR-2000; 2000US-0198315P.
11-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
28-JUN-2000; 2000US-0219486FP.
28-JUN-2000; 2000US-0219487P.
11-JUL-2000; 2000US-0219488P.
11-JUL-2000; 2000US-0219488P.
11-JUL-2000; 2000US-021948P.
11-JUL-2000; 2000US-021948P.
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11-JUL-2000; 2000US-021948P.
11-JUL-2000; 2000US-021949P.
11-JUL-2000; 2000US-022556P.
11-JUC-2000; 2000US-022556P.
11-JUC-2000; 2000US-022556P.
11-JUC-2000; 2000US-022559P.
11-JUC-2000; 2000US-022559P.
11-JUC-2000; 2000US-0225759P.
11-JUC-2000; 2000US-0225759P.
11-JUC-2000; 2000US-0225759P.
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11-JUC-2000; 2000US-022598P.
11-JUC-2000; 2000US-022598P.
11-JUC-2000; 2000US-022938P.
11-JUC-SEP-2000; 2000US-022938P.
11-JUC-SEP-2000; 2000US-022938P.
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2000US-0231242P.
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000US-0241826P.
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Rosen CA, Barash SC, Ruben SM;
                  17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
                                                                                                         06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
                                                                                                                      08-DEC-2000; 2000US-0251868P, 08-DEC-2000; 2000US-0251869P.
                                                           000US-0249299P
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                                                                                                                                                 11-DEC-2000; 2000US-0254097P.
                                                                 17-NOV-2000; 2000US-0249300P
                                                                                      2000US-0251030P
                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                WPI; 2001-476222/51.
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Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 1; SEQ ID NO 134; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proceins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, gasts, horses, casts, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a nathological condition or susceptibility to be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoascabant assays (ELISA). Disorders which are diagnosed or treated include autoimmune companies of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. carbovascular disorders e.g. corneal infection, carbovascular disorders e.g. corneal infection, carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. corneal infection, carbovascular disorders e.g. carbovascular disorders e.g. corneal infection, carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascular disorders e.g. carbovascul

0; Gaps / Match 0.7%; Score 24.6; DB 1; Length 1352; Local Similarity 53.7%; Pred. No. 26; os 51; Conservative 0; Mismatches 44; Indels 0. Query Match Best Loca Matches

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3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077

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ABK72087 standard; cDNA; 1352 BP RESULT

ABK72087;

13-AUG-2002

(first entry)

Human; ss; ovarian antigen; gene; ovary disorder; breast disorder; nepolastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; autoimmune disorder; hair loss; utinary system disorder; cardiovascular disorder; hair loss; respiratory disorder; cardiovascular disorder; arrhythmia; respiratory disorder; musculoskeleral system disorder; endocrine disorder; gastrointestinal disorder; liver disorder; denocratic disorder; gall bladder disorder; lare intestine disorder; denocratic disorder; intestine disorder; denocratic disorder; cancerate disorder; cancerate disorder; cancerate disorder; cancerate disorder; denocratic disorder; denocratic disorder; cancerate disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic disorder; denocratic denocratic disorder; denocratic denocratic disorder; denocratic denocratic disorder; denocratic den Human cDNA encoding ovarian antigen #46. preservative.

Homo sapiens.

WO200155329-A2.

02-AUG-2001

17-JAN-2001; 2001WO-US001360.

04-PEB-2000; 2000US-0180628P. 07-JUN-2000; 2000US-0209467P. 14-SEP-2000; 2000US-0232398P. 17-NOV-2000; 2000US-0249300P. 01-DEC-2000; 2000US-0250160P. 08-DEC-2000; 2000US-0251868P. 31-JAN-2000; 2000US-0179065P.

(HUMA-) HUMAN GENOME SCI INC.

08-DEC-2000; 2000US-0251990P.

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-476195/51. P-PSDB; ABG60284.

Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive disorders

Claim 1; SEQ ID NO 56; 524pp; English.

The invention relates to isolated ovarian related polypeptide (ovarian antigan) comprising a sequence at least 90% identical to a sequence elected from a polypeptide fragment, domain, epitope or full length protein of a sequence (81) appearing as ABG6029-ABG60296 having contain or a variant, allelic variant or species homologue of 81. Also included are the CDNA clones encoding the proteins of 81. Si, an anti-S1 antibody and the CDNA are useful for diagnosing, preventing, treating or ameliorating a medical condition in mammalian subject respicially diseases and/or disorders of the ovary and/or breast such as neoplastic disorders (such as ovarian Krukenberg tumour and cancer), infectious diseases (e.g., mastitis, opphoritis), inflammatory diseases (e.g., mastitis, opphoritis), inflammatory diseases (e.g., mastitis, system disorders (fasted disorders (sichle cell anaemia), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthitis), blood-related disorders (sichle cell anaemia), respiratory disorders, urinary system disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and

2000US-0189874P. 2000US-0190076P. 2000US-0198123P. 2000US-0205515P. 2000US-0209467P.

16-MAR-2000; 17-MAR-2000; 18-APR-2000;

19-MAY-2000;

28-JUN-2000; 30-JUN-2000;

2000US-0215135P. 2000US-0216647P. 2000US-0216880P. 2000US-0217487P.

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           information disorders (daison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, diseases at the callular level, and wound healing and epithelial cell profileration. They are also useful to prevent skin aging, for preventing hair loss, to maintain organs before transplantation or for supporting cell culture of primary tissues, to modulate mammalian characteristics such as body height, to modulate mammalian characteristics such as body height, to modulate and as food additive or preservative. The present sequence is a cDNA encoding
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neurological disorders (Alzheimer's disease and Parkinson's disease),
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tive 0; Mismatches 44; Indels
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24-FEB-2000;
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1241 İTTTGİĞTATATAAAĞTTATĞATTTTATAĞĞTATTTĞTAACCCTGCCACATATCTT 1300
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17-JAN-2001; 2001WO-US001340.
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17-JAN-2001; 2001WO-US001344.
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                                                              (RUBI/) RUBIN S M.
(BARA/) BARASH S C.
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of exidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, transferances, prevention and/or prognosis of a wide range of diagnosis, transferances of the invention are useful in the diagnosis, transferances of the invention are useful in the clasment prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), continuities, neurological disorders (e.g. Alzhaimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. athma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. unfluences). The polymucleotides of the infectious disorders (e.g. Influences). The polymucleotides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polympoptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly trom WIPO at fitp.wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249209P.
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## (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476222/51. P-PSDB; AAU17038.

Novel polypeptides and polynucleotides useful as diagnostic reagents the diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

# Claim 1; SEQ ID NO 135; 601pp; English.

The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or amalicitate a medical condition in e.g. humans, mice, rabbits, grats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELSA). Disorders which are diagnosed or treated include autoimmune diseases e.g. the breast or liver, cardiovascular disorders e.g. carbital isorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. carbital isorders e.g. nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corhaal infection carbot used to aid wound healths and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to repenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, ocfactors and other nutritional components. The present The Sequence Trees and the nutritional components. The present The

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RESULT 37
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                                         2983 ICTATITIACTITAATIGCACTIATITITATIGATITITICIAATAAAATCCAGTCCTIGT 3042
                                                                  1231 İTTTGİÇIATATAAATGTTAATGATTİTTATAĞĞTATİTGİAACCCTGCCCACATATCTİ 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of cDNA clone DNA43318 (ATCC 209481) coding for human PRO343 (UNQ302) (see AAY06482). The clone was isolated from a foctal lung library. Amplification of DNA4318 (chromosome 16) was association with tumour formation or growth. Antagonists (e.g. antibodies) directed against PRO343 may have utility in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be sasociated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment.
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                     Gaps
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                                                                                                                                                                                                                                                                         cDNA clone encoding human PRO343, amplified in tumour cells.
                  44; Indels
                                                                                               TITAAAAAGACITIAAAAITATIAATITCICI 3077
                                                                                                                      1291 AİTTATTCCTCCAAİTİCAATAAAİTATTİATİCT 1325
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    Pred. No. 26;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
53. .1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 11; 162pp; English.
                                                                                                                                                                                         AAX87259 standard; cDNA; 1378 BP
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98US-0083500P.
98US-0086414P.
98US-0107783P.
98US-0109304P.
  53.7%;
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149. .1003
/*tag= c
                                                                                                                                                                                                                                               (first entry)
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53. .148
Best Local Similarity 53.7
Matches 51, Conservative
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                                                                                              3043 TTT
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10-JUN-1998;
10-NOV-1998;
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treatment

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                                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; Alz, neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; ss.
                                                                Gaps
                                              ó
                       Length 1378;
Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                              44; Indels
                                                                                                            3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                                                 1332 ATTTATTCCTCCAATTTCAATAATTATTTATTCT 1366
                       DB 1;
                      Score 24.6; I
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                         Protein PRO343 cDNA clone DNA43318-1217.
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97US - 0059115P.
97US - 0059119P.
97US - 0059121P.
97US - 0059121P.
97US - 0059184P.
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970S-0059266P.
970S-0062125P.
970S-0062285P.
970S-00632887P.
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97US-0062816P.
97US-0063045P.
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97US-0063127P.
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970S-0063542P.
970S-0063544P.
970S-0063549P.
970S-0063560P.
                     0.7%;
ilarity 53.7%;
Conservative
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                    Query Match
Best Local Similarity,
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
21-OCT-1997;
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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17-SEP-1997;
17-SEP-1997;
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                                                                                                                                                                                                              AAX52262;
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10664775-2.rng

PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO863; Lumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation; ss.

Location/Qualifiers 53. .1007

Homo sapiens

Key

/*tag= a

WO200037640-A2

cDNA encoding novel polypeptide PRO343.

03-OCT-2000 (first entry)

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AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO210 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. entercoclitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. poriasis, epithelial cancers such as lung squamous cell carcinoma of the prolases related to growth or survival of nerve cells including Parkinson's disease, Alzhaimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal carring. PRO264 can be used as a tari-thrombotic agent, PRO287 polypeptides and portions may be used as an anti-thrombotic agent, PRO287 polypeptides and portions may be used for treatment of Usher Syndrome or Atrophia areata; PRO29 can be used as an anti-thrombotic agent, PRO287 polypeptides and portions may can be used for treatment of Usher Syndrome or Atrophia areata; PRO317 can be used for treatment of Usher Syndrome or Atrophia areata; PRO317 can be used for treatment of Usher Syndrome or Atrophia erepair; PRO317 can be used for treatment of Usher Kidney, uterus, endometrium, processels, or related tissue, e.g. in the heart of genital tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and polypeptides used in, e.g. treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard A, Pennica D, Chen J, Yuan J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 97; 320pp; English.
97US-0063734P.
97US-0063735P.
97US-006421SP.
97US-006421SP.
97US-0064243P.
97US-0064243P.
97US-0064809P.
97US-0064809P.
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97US-0066120P.
97US-0066364P.
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97US-0066466P.
97US-0066511P.
97US-0066770P.
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Best Local Similarity 53.74
Matches 51, Conservative
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31-OCT-1
31-OCT-1
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2983 TCTATTTTRCTTTAATTGCACTTATTTTTATTGATTTTTTTAATAAAATCCAGTCCTTGT 3042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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Local Similarity 53.7%;
les 51; Conservative (
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AAA46914 standard; cDNA; 1378 BP

RESULT 38 AAA46914

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AAA46914;

SKB

4.4 • # 4

New anti-polypeptide antibody useful in the treatment and diagnosis of neoplastic cell growth and proliferation.

Claim 50; Fig 11; 220pp; English.

Roy MA;

Gurney AL, Hillan K, Lawrence DA,

Goddard A,

Botstein D,

Wood WI;

WPI; 2000-452188/39.

P-PSDB; AAY93689

(GETH ) GENENTECH INC.

99WO-US012252.

-1999

99WO-US021090 99WO-US028409 99WO-US028565

99WO-US028313

30-NOV-1999 02-DEC-1999

3600E0S0-0M66 98US-0113296P

16-DEC-1999;

22-DEC-1998 08-MAR-1999 01-SEP-1999 LS-SEP-1999 30-NOV-1999 11-DEC-1999

29-JUN-2000

99WO-US028301.

antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antianglogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation; sr.

WO200104311-A1.

18-JAN-2001

Homo sapiens

dermatological; antipsoriatic; cytostatic; antiinflammatory;

(first entry)

24-APR-2001

Human PRO343 cDNA.

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antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neuroprotective; vasotropic; chemotaxic; angiogenic; antiarthritic; antirheumatic; antiarteriosclerocic; cardiant; antidabetic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy, dermal scarring; wound healing; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; asthma: rheumatoid arthritis; multiple sclerosis; inflammatory disorder; diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
                                                                                                                                                                                                                                                                                                                                                                                           Pennica D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                         Gurney AL, Hillan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 262; 355pp; English.
                                                                                                                                                                                                                                                                                                            99WO-US021090
                                                                                                                                                                                                                                                                                                                                      98WO-US019330
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                         Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-271434/23.
                                                  Human PRO343 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ADC78575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA of the
                                                                                                                                                                                                                                                           WO200015796-A2
                           01-JAN-2004
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                              15-SEP-1999;
                                                                                                                                                                                                                                                                                    23-MAR-2000
 ADC78574;
                                                                                                                                                                                                                                                                                                                                                                                       Chen J,
Yuan J;
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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polymucleotides of the invention may be useful as research tools and as therapeutics for treating entercoditis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarting and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, thrombosis, bone and/or sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging, ALDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human ö 2983 ICTAITITACTITAATIGCACTIAITITITATIGATITITICIAATAAAATCCAGICCTIGT 3042 1272 irrigigiananaaiginaangarririahaggiarrigiaaccongcodacaratorr 0; Gaps DB 1; Length 1378; Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other; 44; Indels 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 0; Mismatches 0.7%; Score 24.6; 1 53.7%; Pred. No. 26; Local Similarity 53.7 les 51; Conservative Query Match Matches

1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366

g ò

δ a AAF72420 standard; cDNA; 1378 BP.

40 RESULT 40 AAF72420 ID AAF7 XX

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Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriais), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. lung stransmony disease), wound repair, cardiovascular disorders (e.g. Parkinson) disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherios:, multiple solerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerriteen NE, Goddard A; Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in chromosome and gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 97; 393pp; English.
                                                                                                                                                                                                                                                                                                                                                                    99WO-US023089.
                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US028564.
                                                                                                                                                                                                                                                22-FEB-2000; 2000WO-US004414
                                                                                                                                                                                                                                                                                        99US-0145698P
99US-0146222P
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1, Wood WI;
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Filvaroff E, Fc
Godowski PJ, G1
Mather JP, Pan
Williams PM, WK
                                                                                                                                                                                                                                                                                     26-JUL-1999;
28-JUL-1999;
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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02-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
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29-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease)
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0.7%; Score 24.6; DB 1; Length 1378; 53.7%; Pred. No. 26; Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other; Query Match Best Local Similarity

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TCTATITIACTITAATIGCACTIATITATIGATITITICIAATAAAATCCAGTCCTIGT 3042
                                      1272 TTTTGTGTATATAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
                                                                                                                                                                                                                Human, PRO, gene, ss, secreted polypeptide, transmembrane polypeptide; pathological disorder; cardiac insufficiency disorder; protein secretion; pancreas, diabetes; gastrointestinal mucosa, mucosal lesion; psoriasis; skin disease, keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma, epidermoid carcinoma, vulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.
0; Gaps
44; Indels
                                                         3043 ITITITAAAAAGACITIAAAAITAITAATITCICI 3077
                                                                             1332 ATTTATTCCTCCAATTTCAATAATTATTTATTCT 1366
0; Mismatches
                                                                                                                                 ACA59110 standard; cDNA; 1378 BP
                                                                                                                                                                                                                                                                                                                                                                               9705-0059113P
9705-0059113P
9705-0059113P
9705-0059121P
9705-0059184P
9705-0059263P
9705-0059265P
9705-0062265P
9705-0062265P
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9705-006354P
9705-0063564P
9705-0063564P
9705-0063564P
                                                                                                                                                                                            Human PRO polynucleotide #48.
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                                                                                                                                                                         16-JUN-2003 (first entry)
51; Conservative
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                                                                                                                                                                                                                                                                                                 Homo sapiens.
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17-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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17-SEP-1997
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Matches
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22-FSB-2000; 2000WG-US004414.
24-FSB-2000; 2000WG-US00504.
02-MRX-2000; 2000WG-US005841.
20-MAX-2000; 2000WG-US00537.
30-MAX-2000; 2000WG-US008439.
22-MXY-2000; 2000WG-US014042.
02-UUN-2000; 2000WG-US014042.
28-JUL-2000; 2000WG-US015264.
24-AUG-2000; 2000WG-US02020710.
24-AUG-2000; 2000WG-US023328.
     970S-0064248P
970S-0064809P
970S-0065846P
970S-006563P
970S-0066120P
970S-0066453P
970S-0066454P
970S-0066454P
970S-0066770P
970S-0066770P
970S-0066772P
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99WO-US028214
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01-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
20-DEC-1999;
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29-NOV-1
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### (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Boni NF, Roy WA, Stewart TA, Tumas D; Williams PM, Wood WI;

#### WPI; 2003-328338/31. P-PSDB; ABU71637.

Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.

# Claim 2, Fig 97; 473pp; English.

The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polymucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and in therapeutic treatment of disorders involving protein secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseasés associated with abnormal keratinocyte differentiation (e.g., psoriases, epithelial cancers such as lung squamous call carcinoma, epidermoid carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein electrophoresis purposes and can be utilised in protein-

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Claim 2; Fig 97; 474pp; English.
               970S-0064215P.
970S-0064307P.
970S-0064208P.
970S-005186F.
970S-005186F.
970S-0055846F.
970S-0065633P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
970S-0066433P.
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20-MAR-2000; 2000MO-US005641.
30-MAR-2000; 2000MO-US008439.
22-MAY-2000; 2000MO-US014642.
22-UJN-2000; 2000MO-US015264.
28-UJL-2000; 2000MO-US02561.
24-AUG-2000; 2000MO-US023328.
18-SEP-2000; 2000MS-00665350.
                                                                                                                                                                                                       99WO-US020594
99WO-US020944
99WO-US021090.
99WO-US021547.
99WO-US023089.
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99WO-US028313.
99WO-US028301.
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98WO-US019437
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P-PSDB; ABU71492.
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20-DEC-1999;
20-DEC-1999;
05-JAN-2000;
                                                   07-NOV-1997;
12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
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15-SEP-1999;
05-OCT-1999;
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Williams PM,
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30-NOV-1999
       2983 TCTATTTTACTTTAATTGCACTTATTTTATTGATTTTTCTAATAAAATCCAGTCCTTGT 3042
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                                                                                                      1272 İTTIGIĞIRLALAARARGATITİTİRİRGGIATİTIĞIRACCCTGCÇCACATATCT 1331
assays, biochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polynucleotide of the invention
                                                                                                                                                                                                                                                                   Human; secreted and transmembrane protein; PRO polypeptide, cancer;
Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
                                                                     ..
0
                                              Ouery Match
0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0
                            Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                                                                                        3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                                                              ATTTATICCICCAATTICAATAAATTATTTATTCT 1366
                                                                                                                                                                                                                                                 cDNA encoding human PRO polypeptide #48.
                                                                                                                                                                                           ACA58507 standard; cDNA; 1378 BP.
                                                                                                                                                                                                                                                                                                                                                                                           97US-0059115P
97US-0059117P
97US-0059121P
97US-0059121P
97US-0059268P
97US-0062285P
97US-0062285P
97US-0062486P
97US-006346P
97US-006346P
97US-006314P
97US-006314P
97US-006312P
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97US-006312P
97US-006334P
97US-006354P
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97US-006354P
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97US-0063734P.
97US-0063735P.
                                                                                                                                                                                                                                (first entry)
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ACA58507
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

The present invention relates to the isolation of novel human secreted and transmembrane proteins (PRO polypeptides), and the polynucleotide sequences are useful in molecular biology, as hybridisation probes, in chromsome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide sequences may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals oknock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or

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                                                                                                                                                                                                                                                                                                                         1272 TTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
their antibodies are useful in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as cancer. Alzheimer's disease or ischaemia, and in various diagnostic assays. The present sequence encodes a human PRO polypeptide of the invention
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                                                                                                                                                                            DB 1; Length 1378;
                                                                                                                            Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                       Match 0.7%; Score 24.6; DB 1; Length 1 Local Similarity 53.7%; Pred. No. 26; es 51; Conservative 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA for secreted/transmembrane protein PRO343.
                                                                                                                                                                                                                                                                                                                                                                         3043 ITTTTTAAAAGACTTTAAAATTATTTTTCTCT 3077
                                                                                                                                                                                                                                                                                                                                                                                                      1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366
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97US-0063127P.
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97US-0063321P.
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97US-0063435P.
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97US-0063732P.
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2000WO-US007377
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2000WO-US015264
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18-SEP-2000; 2000US-00665350
97US-0063735P
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02-DEC-1999;
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16-DEC-1999;
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17-NOV-1997;
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02-MAR-2000;
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29-NOV-1999;
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### (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

### WPI; 2003-329602/31. P-PSDB; ABU71938.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, in generating probes and in tissue typing.

# Claim 2; Fig 97; 484pp; English.

The invention relates to an isolated nucleic acid with at least 80% nucleic acid sequence identity to a nucleotide sequence encoding one of a secreted/transmembrane polypeptides, or PRO polypeptides or encoding a PRO protein extracellular domain. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the PRO polypeptide for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (

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cc a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC cumber (detailed in the specification); or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimaeric molecule computating a PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a process or PRO1868 in a sample euspected of containing the polypeptide, correctly a process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or process or proces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic; biosensor; bioreactor; Parkinson's disease;
Alzheimer's disease; inflammation; nephritis; wound healing;
herve.repair; collateral blood vessel formation; cancer;
colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
infertility; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted and transmembrane protein; PRO; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.7%; Score 24.6; DB 1; Length 1378; Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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970S-0059112P.
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97US-0062816P.
97US-0063120P.
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27-0CT-1
27-0CT-1
28-0CT-1
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Ferrara N;

Desnoyers L, Eaton DL,

Ashkenazi A, Botstein D,

Homo sapiens.

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The invention describes a new isolated nucleic acid molecule comprising
the full length coding sequence of the DNA deposited with the American
Type Culture Collection (e.g. ArCC Deposit No. 209228), or a sequence
with at least 80% identity to a DNA encoding a RNO polypeptide comprising
any of 61 sequences having 164.1119 amino acids fully defined in the
competification. The RNO polypeptides or polymodicatides are useful as
plarmaceuticals, diagnostics, biosensors or bioreactors. These are
particularly useful for detecting or treating e.g. Parkinson's disease,
compair, collateral blood vessel formation, cancers (e.g. colorectal
cancer), haemorrhage for reduce risk for haemorrhage), rheumatoid
carthritis, diabetes, cirrhosis of the liver, librosis of the lungs,
restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
reterility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
pigs, goats, or rabbits) The RNO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The RNO
geness are useful as hybridisation probes, or for screening libraries of
human cDNA, genomic DNA or mRNA. The RNO genes may also be used in gene
therapy, particularly for replacing a defective gene. This sequence
therapy, particularly for replacing a defective gene. This sequence
                                                                                                                                                                                                     New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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                                                                                                                           WPI; 2003-370793/35.
P-PSDB; ABO01821.
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Query Match

0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0; Gaps Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other; Query Match

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ABX71662 standard; cDNA; 1378 BP. RESULT 45

10-MAR-2003 (first entry) ABX71662;

Human cDNA encoding secreted/transmembrane protein PRO343.

Human; PRO; secreted protein; transmembrane protein; enterocolitis; gastrointestinal ulceration; skin disease; ss; gene; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; squamous cell carcinoma; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; inflammatory disease; rheumatoid arthritis; asthma; multiple sclerosis; organ failure; attherosclerosis; cardiac injury; infertility; birth defect; premature aging; ALDS; acquired immunodeficiency syndrome; cancer; diabetic complication; wound repair. 

9705-0063486F 9705-00630416F 9705-00630416F 9705-0063120F 9705-0063121F 9705-0063128F 9705-0063128F 9705-0063541F 9705-0063541F 9705-0063541F 9705-0063541F 9705-0063704P 9705-0063732P 9705-0063732P 9705-0063738P 9705-0063708P 9705-006420P 9705-006420P 9705-006420P 9705-006420P 9705-006420P 9705-0065693P 9705-0065693P 9705-0059115P 9708-0059119P 9708-0059121P 9708-0059122P 9708-0059184P 9708-0059268P 9708-0059266P 9708-0062285P 9708-0062285P 97US-0063550P. 97US-0063564P. 97US-0063435P. 97US-0066511P. 97US-0066770P. 97US-0066772P. 97US-0066466P. 98WO-US019330. 18-JUL-2001; 2001US-00909320 98WO-US019177 98WO-US019437 98WO-US025108 99WO-US020594 99WO-US020944 99WO-US028565 US2002132240-A1. 24-NOV-1997; 14-SEP-1998; 19-SEP-2002 29-OCT-1 -NON-1 03-NOV-- NON- 6 1-NOV--VON-70 

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16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US00399.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US005041.
24-FEB-2000; 2000WO-US005041.
20-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US005977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequences given in the specification (accession numbers 62 acid sequences given in the specification); (b) an amino acid sequence encoded by the nucleotide sequence (apposited under American Type Culture Collection (accession numbers of listed in the specification); (c) an extracellular domain of the PRO by Olypeptide with its associated signal peptide; (d) an extracellular domain of the PRO polypeptide with its associated signal peptide; or (e) an extracellular domain of the PRO polypeptide with its associated signal peptide. Also include are the nucleic acids encoding the PRO polypeptides and nucleic acids are useful in diagnosing or treating of concerns, host calls and anti-PRO antibodies. The PRO polypeptides and nucleic acids are useful in diagnosing or treating abnormal keratingoryce differentiation, skin diseases associated with abnormal keratingoryce differentiation, e.g. posiasis or epithelial cancers such as aquamous cell carcinoma, Alzheimer's disease, Parkinson's disease, anyotrophic lateral solerosis, inflammatory disease, e.g. creamers such as aquamous cell carcinoma, Alzheimer's disease, e.g. creamers such as action and repair and associated therapies or polypeptides are also useful for wound repair and associated therapies conformed with re-growth of tissue. The nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in the describement and screening of therapeutically useful reagents, for chromosome identification, and the in turn are useful reagents, for chromosome identification, and created in pene therapy, and as molecules and nucleic acid and encodes may be used in assays for PRO polypeptides and uncleic acid acid molecules are also useful or mechalism are also useful the archiberacial percentage or acid molecules are also useful or recom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrara N;
1 ME, Goddard A;
Kljavin IJ;
Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, I
Filyaroff B, Fong S, Gao W, Gerber H, Gerritsen N
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, P
Marber JP, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI,
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                                                                                                                                                                                                                                              22-MAY-2000; 2000WO-US014042.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
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ICTATITIACITIAAITGCACITAITITIAITGATITITICIAATAAAAICCAGICCITGI 3042
                   1272 TTTTGTGTATATAAAGTTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
                                                                                                                                                                                                                            Human, gene; ss; abnormal bleeding; gynaecological disease; asthma, hysterectomy; angiogenesis; coronary ischaemic condition; skin disease; gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; ALS; chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; uncontrolled cell growth, cancer, blood coagulation cascade; thrombosis; haemorrhage; endometrial bleeding; angiogenesis; wound healing; tumour; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing:
                                                                                                                                                                                                         Human secreted/transmembrane polypeptide PRO343 cDNA.
                                               3043 ITITITAAAAGACITITAAAAITATIAATITCICI 3077
                                                                     1332 ATTTATTCCTCCAATTCAATAAATTATTTATTCT 1366
                                                                                                                                  ACH06994 standard; cDNA; 1378 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0059113P.
97US-0059115P.
97US-0059117P.
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97US-0063045P.
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97US-0063544P.
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97US-0062285P.
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97US-0063127P.
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97US-0062814P
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97US-0064215P
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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31-OCT-1997;
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
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17-0CT-1997;
17-0CT-1997;
21-0CT-1997;
24-0CT-1997;
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2983
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                                                                                                                       ACH06994
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97US-0063870P

Gaps . 0

Query Match
0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0;

10664775-2.rng

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97US - 0064103P
97US - 0064808P
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97US - 0065186P
97US - 0065120P
97US - 0066120P
97US - 0066120P
97US - 006612P
97US - 0066454P
97US - 0066472P
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97US - 0069425P
98US - 0100262P
98US - 0100262P
98US - 0100262P
98US - 0100262P
98US - 0100262P
98US - 0100262P
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99US-0143048P.
99US-0145698P.
99US-014622P.
99WO-US020944.
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11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
02-MAR-2000;
20-MAR-2000;
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14-SEP-1998;
14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
17-SEP-1998;
13-OCT-1998;
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20-DEC-1999;
20-DEC-1999;
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                                   18-NOV-1
                                                21-NOV-
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## (GETH ) GENENTECH INC.

Ferrara N; NE, Goddard A; Kljavin IJ; Tumas D; Botstein D, Desnoyers L, Eaton DL, Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA, Pan J, Paoni NF, Wood WI; Ashkenazi A, P Filvaroff E, Godowski PJ, Mather JP, P Williams PM,

#### WPI; 2003-492258/46. P-PSDB; ABO47409.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases.

Claim 3; Fig 97; 478pp; English.

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The invention relates to an isolated PRO polypeptide. PR0317 is useful in diagnosing or treating abnormal bleeding involved in gynecological diseases e.g. to avoid or lessen the need for hysterectomy. PR0317 may also be useful as an agent that affects and pr0317 is useful controlled to be useful as an agent that affects angiogenesis and PR0317 lis useful controlled to treating disorders.

CC PR0211 and PR0217 polypeptides are useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases. CC associated with abnormal keratinocyte differentiation (e.g. psoriasis). PR0187 polypeptide is useful for treating parkinson's disease. Telated to uncontrolled cell growth, e.g. cancer. PR0319 polypeptide plays a regulatory role in the blood coagulation cascade. PR0246 polypeptides which serves as tumour specific antigens may be explorated as therapeutic targets for anti-tumour drugs. PR0269 polypeptide is useful as an antithromboric agent with reduced risk for haemorrhage as compared with heparin. PR0317 polypeptide is useful in portion have therapeutic applications in wound healing and tissue repair. PR034 polypeptides are useful for treating asthma, rheumatoid arthritis, portion have therapeutic applications in wound healing and tissue repair. PR034 polypeptides are useful for treating asthma, rheumatoid arthritis, portions and multiple sclerosis. The polypeptide and its nucleic acid immunohistochemical staining and/or assay of sample fluids. Anti-PR0 are useful in diagnostic assays for PR0 e.g. detecting its error purification of PR0 from recombinant cell culture or natural sources. The polyment setting a human secreted/transmenter process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 53.7%;
nes 51; Conservative
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#### RESULT 47

ABX96231 standard; cDNA; 1378 BP. 13-MAY-2003 (first entry) ABX96231;

Human secreted/transmembrane protein cDNA, #50.

Human, gene, ss; PRO; secreted, transmembrane, pharmaceutical; diagnostic; biosensor; bioreactor; therapeutic; hyperplasia; endometriosis; cancer; tumour; ischaemia; coronary arterial disease; polycystic kidney disease; renal failure; inflammatory response; asthma; rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy; cytostatic; gynecological; cardiant; nephrotropic; hepatotropic; antiinflammatory. 

#### Homo sapiens,

US2002160374-A1.

31-OCT-2002

12-JUL-2001; 2001US-00905291.

97US-0059113P. 97US-0059115P. 97US-0059117P. 17-SEP-1997; 17-SEP-1997; 17-SEP-1997;

10664775-2.rng

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97US-0059119P.
97US-0059121P.
97US-0059182P.
97US-0059263P.
97US-0059266P.
97US-0062266P.
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97US-0063045P.
97US-0063120P.
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9705-00642159-
9705-006421039-
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97US-0065186P.
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2983 ICTATITIACTITAATIGCACTIATTITIATTGATTITICTAATAAAATCCAGTCCTIGT 3042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. hyperplasia, concers (e.g. those involving solid tumours), ischaemia, coronary arterial disease, polycystic kidney disease, chronic or acute renal failuxe, or inflammatory responses (e.g. asthma, rheumatoid arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may also be used in agene therapy, particularly for replacing a defective gene. The sequences presented in ABXS6017.ABXS6378 are the genes encoding, the primers amplifying and the probes detecting the PRO
                                                                                                                                                                                                                                                                                                       New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245) and genes encoding them, useful for detecting or treating e.g. hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease or inflammations.
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                                                                                                                         Ferrara N;
n ME, Goddard A;
Kljavin 1J;
, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 24.6; DB 1; Length 1378; Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                                                                                       Ashkenazi A, Botstein D, Desnoyers L, Baton DL, E
Flyazoff E, Fong S, Gao W, Gerber H, Gerritsen N
Godowski PJ, Grimaldi JC, Gurney AL, Hillan XJ, I
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 97; 477pp; English.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
38-SEP-2000; 2000US-00665350.
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Williams PM, Wood WI;
                                                                               (GETH ) GENENTECH INC.
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Human, gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease; psoriasis; cancer; lung cancer; colon cancer; nerve cell disease; Alzheimer's disease; Parkinson's disease; Usher syndrome; anglogenesis; atrophia areata; inflammatory disease; asthma; rheumatorid arthritis;

ischaemia; ss; gene

US2003023054-A1

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9705-0059113P
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99WO-US020944.
99WO-US021090.
                 16-JUL-2001; 2001US-00906742
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17-007-1997;
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The invention relates to sixty one nucleic acids encoding PRO
polypeptides (Secreted and transmembrane). The polynucleotide is useful
in molecular biology, including uses as hybridisation probes, in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
chromosome and gene mapping, in generating antisense RNA and DNA, and in
gene therapy. The polynucleotide may also be used in preparing PRO
polypeptides by recombinant techniques, and in generating either
transgenic animals or knock-out animals which, in turn, are useful in the
transgenic animals or knock-out animals which, in turn, are useful in the
chevelopment and screening of therapeutically useful reagents. The PRO
polypeptide or the antibody is used in preparing a medicament for
treating a condition responsive to the polypeptide or antibody, such as
mucosal lesions e.g. ulcers and enterocolitis, skin disease e.g.
poriasis, cancer e.g. lung cancer and colon cancer, nerve cell disease
e.g. Alzheimer's disease and Parkinson's disease, Usher syndrome,
e.g. Alzheimer dispublicatis, inflammatory disease e.g. suthma and
rheumatorid arthritis, isochaemia, and in various diagnostic assays. The
present sequence represents an cDNA which encodes a PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixty one isolated nucleic acids encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in chromosome and gene mapping, in generating antisense RNA and DNA, and in treating cancer and Alzheimer's disease.
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0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Marber JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Rood WI;
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                                      29-NOV-1999; 99WO-US02219.
30-NOV-1999; 99WO-US022113.
30-NOV-1999; 99WO-US022113.
30-NOV-1999; 99WO-US02813.
30-DEC-1999; 99WO-US02866.
30-DEC-1999; 99WO-US0300095.
30-DEC-1999; 99WO-US030095.
30-DEC-1999; 99WO-US030091.
30-DEC-1999; 99WO-US030091.
30-DEC-1999; 99WO-US030091.
30-DEC-1999; 99WO-US030091.
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30-DEC-1999; 99WO-US03091.
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30-DEC-1999; 99WO-US03091.
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30-DEC-1999; 99WO-US03091.
30-DEC-1999; 99WO-US03091.
30-DEC-1999; 99WO-US03091.
30-DEC-1999; 99WO-US03091.
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30-DEC-1999; 99WO-US03091.
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P-PSDB; ABU67392.
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The invention relates to an isolated, secreted and transmembrane polypeptide, termed PRO polypeptide. The polypeptide is useful for identifying agonists or antagonists of the polypeptide, for preparing variants of the polypeptide, as molecular weight markers for preparing cariants of the polypeptide, as molecular weight markers for protein electrophoresis purpose and the nucleic acid is useful for recombinantly agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The nucleic acid is useful as therapeutic antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes the PRO and for the genetic analysis of individuals with genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030091.

20-DEC-1999; 99WO-US030911.

11-FEB-2000; 2000WO-US03056.

24-FEB-2000; 2000WO-US005641.

24-FEB-2000; 2000WO-US005841.

22-MAR-2000; 2000WO-US005841.

30-MAR-2000; 2000WO-US005841.

31-MAR-2000; 2000WO-US01564.

22-MAY-2000; 2000WO-US01564.

23-MAY-2000; 2000WO-US01564.

24-MU-2000; 2000WO-US015564.

28-JUL-2000; 2000WO-US015564.

28-JUL-2000; 2000WO-US015564.
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                  98US-0088026P.
98US-0099803P.
98WO-018018824.
98US-0100262P.
98WO-US0193177.
                                                                                           98US-0100858P.
98WO-US019437.
98US-0104080P.
                                                                                                                               98US-0109304P.
98WO-US025108.
98US-0113296P.
99US-0143048P.
99US-0145698P.
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99WO-US021090.
99WO-US021547.
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15-SEP-1999
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29-NOV-1999
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      Human; ss; gene; gene therapy; tumour; tissue typing; obesity; diabetes; hypoinsulinaemia; hyperinsulinaemia; vascular permeability; cardiac insufficiency disorder; immune response; regeneration; cartilage; auditory hair cell; hearing loss; bone disorder; sports injury; arthritis.
                                                                                    Human secreted / transmembrane polypeptide PRO343 cDNA
           ACD20219 standard; cDNA; 1378 BP
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97US-0059113P.
97US-0059112P.
97US-0059112P.
97US-0059112P.
97US-0059112P.
97US-005912B.
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                                                            (first entry)
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17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
18-SEP-1997;
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24-OCT-1997
                                     ACD20219;
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disorders, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes for polymerase chain reaction (PCR).

Northern analysis, Southern analysis and Western analysis. PRO antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO antibody is useful for the preparation of medicament for treating conditions which is responsive to the PRO polypeptide or anti-PRO conditions which is responsive to the PRO polypeptide or anti-PRO conditions which is responsive to the PRO polypeptide or anti-PRO conditions which is responsive to the prolypeptide and the modelet exid is useful for tissue typing. The polypeptide and the modelet exid is useful for tissue typing. The polypeptide and the modelet exid is useful for tissue typing. The polypeptide and the modelet exid is useful for tissue typing tumour growth, enhances vacclast permeability and immune response, for inducing regeneration of auditory hair cells and for response, for inducing regeneration of auditory hair cells and for response, such as sports injuries and arthritis. The present sequence represents cDNA encoding a human secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2983 ICTATTTTACTTTAATTGCACTTATTTTTTATTGATTTTTCTAATAAAATCCAGTCCTTGT 3042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, secreted and transmembrane protein, gane therapy, psoriasis, enterocolitis, gastrointestinal ulceration, skin disease, keratinocyte differentiation, epithelial cancer, Alzheimer's disease, squamous cell carcinoma, Parkinson's disease, inflammatory disease, amyotrophic lateral sclerosis, rheumatoid arthritis, asthma; multiple sclerosis, organ failure, atherosclerosis, cardiac injury, diseatility, birth defect; premature aging, AIDS, cancer, diabetic complication, wound repair; tissue re-growth; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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97US-0059113P
97US-0059113P
97US-0059121P
97US-0059124P
97US-0059184P
97US-0059265P
97US-0062266P
97US-0062266P
97US-0062285P
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17-SEP-1997;
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18-SEP-1997;
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neurodegenerative disease; endometrial bleeding; wound healing;
tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing
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                                                            Homo sapiens.
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17-OCT-1997;
17-OCT-1997;
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21-NOV-1997
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        Georgeed and transmembrane). The PRO polypoptides and mucleic acids are useful in diagnosing or treating entercoclitis, gastrointestinal useful in diagnosing or treating entercoclitis, gastrointestinal ulceration, skin disease associated with abnormal keratinocyte differentiation, sign disease, associated with abnormal keratinocyte differentiation, and profile associated with abnormal keratinocyte disease, parkinson's disease, amyotrophic actionamy, Alzheimer's disease, Parkinson's disease, amyotrophic atteral sclerosis, inflammatory diseases, eg. rheumatoid arthritis, asthma or multiple sclerosis, organ failure, atherosclerosis, cancer, injury, infertility, birth defects, premature aging, AIDS, cancer, injury, infertility, birth defects, premature aging, AIDS, cancer, also useful for wound repair and associated therapies concerned with regrowth of tissue. The PRO polypeptides and mucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in recombinant cell culture or natural sources. This sequence encodes a cover the natural sources. This sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2983 TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTCTAATAAAATCCAGTCCTTGT 3042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1272 İTTGGGGATALAAAGGTATATGATAGGTATİTGTAACCCTGCCCACATATCTİ 1331
                                                                                                                                                                                                                                                                                                                                                                                                        invention describes sixty one nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; gene; gene therapy; apoptosis; bleeding; tumour; ALS; gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer; coronary; schaemic condition; gastrointestinal mucosa disorder; asthma; mucosal lesion repair; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;
                                                                                                                                                                                                                                                                                    New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                      Ferrara N;
ME, Goddard A;
Kljavin IJ;
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                                                                                                                                     Botstein D, Desnoyers L, Eaton DL, Pong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ, an J, Paoni NF, Roy MA, Stewart TA,
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Pred. No. 26;
0; Mismatches
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22-MAY-2000; 2000WO-US014042.
02-UUN-2000; 2000WO-US015564.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
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M. Wood WI;
                                                                                                   (GETH ) GENENTECH INC.
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P-PSDB; ABU69669.
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Best Local Similarity
                                                                                                                                 Ashkenazi A,
Filvaroff E,
Godowski PJ,
                                                                                                                                                                                                      Williams PM,
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Matches

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2000WO-US014042
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                             99WO-US021090
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                   99WO-US020594
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99WO-US028564
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Williams PM,
                                                                                  05-7AN-2000;
11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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Filvaroff E,
                                                     -DEC-1999;
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-DEC-1999;
-DEC-1999;
-DEC-1999;
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                                            1999;
                   08-SEP-1999;
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Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases. , Botstein D, Desnoyers L, Eaton DL, Ferrara N;
, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
, Wood WI;

Claim 2; Fig 97; 467pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptides are useful for modulating biological activity of a cell, in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy, for treating angiogenesis, tumour, coronary isohaemic condition, disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte amountation (e.g. psoriasis), Parkinson's disease, Alzheimer's differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's disease, amyotrophic lateral scherosis (ALS), neuropathies, disease related to uncontrolled cell growth (e.g. cancer), blood coagulation cascade disorders, neurodegenerative disease, thrombosis, haemorinage, endommetrial bleeding, wound healing, tissue repair, asthma, rheumatoid arthritis, multiple sclerosis. Nucleic acid encoding PRO polypeptides are useful in molecular biology including uses as hybridisation probes and in the generating transganic animals or knockout animals. The PRO antibodies are useful for immunolistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sour expense. and transmembrane PRO polypeptide

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

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2983 TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTTCTAATAAAATCCAGTCCTTGT 3042
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                                                                     1272 IIIIGIGIATATAAAIGITAAIGAITITITATAGGIATITIGIAACCCIGCCCACAIAICIT 1331
                                                                                                                                                                                                                                                                        Human, gene, ss; PRO; secreted; transmembrane, gastrointestinal mucosa; mucosal lesion, skin disease, keratinocyte differentiation; psoriasis; parkinson's disease; Alzheimer's diseases, amyotrophic lateral sclerosis; ALS; neuropathy; cell growth, cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; and medical paragiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
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DB 1; Length 1378;
                       44; Indels
                                                                                             3043 TITITIAAAAAGACTITAAAAITAITAATITCICT 3077
                                                                                                                 1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366
                                                                                                                                                                                                                                                    Human secreted/transmembrane protein cDNA, #52.
0.7%; Score 24.6; D
53.7%; Pred. No. 26;
ive 0; Mismatches
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9705-0063814P
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97US-0063734P
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         Best_Local Similarity 53.7
Matches 51, Conservative
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98US-0113296P.
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30-MAR-2000; 2000WO-US008439
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Filvaroff E,
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, Botstein D, Desnoyers L, Eaton DL, i Fong S, Gao W, Gerber H, Gerritsen N , Grimaldi JC, Gurney AL, Hillan KJ, F Pn J, Paoni NF, Roy MA, Stewart TA, , Wood WI,

Ferrara N; ME, Goddard A; Kljavin IJ; Tumas D;

Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal P-PSDB; ADB29468.

ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.

Claim 2; Fig 97; 469pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and then uncleic acid encoding them. The PRO polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptides are useful bloadive molecule to a cell sepressing a PRO polypeptides are useful conformation and for modulating the bloadive molecular conformation and maintenance of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. peoriasis) Parkinson's disease, halveing PRO polypeptides. PRO polypeptides are also useful for treating diseases associated with abnormal keratinocyte differentiation (e.g. peoriasis) Parkinson's disease, amyotrophic lateral solerosis (ALS), neuropathies and differentiation (e.g. peoriasis) Parkinson's disease, amyotrophic lateral solerosis (ALS), neuropathies and diseases any polypeptides also serves as tumour specific antigers which may be exploided as therepeutic targets for anti-tumour drugs, and are also infection. The PRO polypeptides can be also used in assays to determine the capture of the proposition and propositions and part of the proposition and propositions are solered in assays to determine the capture of the propositions affect the expression of mithering other PRO sexpeptides and their portions affect the expression of mithering other proposes, as the properties are useful in molecular biology including uses as hybridisation probes for conducting the protein and gene mapping in the generating rob properties, so probe person in the development and sort the generating of propositions affect the expression of midividuals which are useful in the development and sort the generating for properties of propositions are useful in the development and sort process as which 

Seguence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

0; Gaps DB 1; Length 1378; 0.7%; Score 24.6; DB 1; Length 13 53.7%; Pred. No. 26; tive 0; Mismatches 44; Indels 51; Conservative Best Local Similarity Query Match Matches à

1272 irringigiararaaargriaargarriaraaggrarringraaccergceeacararer 1331 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 à

1332 Arrrarrccrccaarrrcaaraaarrarrrarrcr 1366

ADA18323 standard; cDNA; 1378 BP. RESULT 53
ADA18323
ID ADA1
XX
AC ADA1
XX
DT 20-N

ADA18323;

20-NOV-2003 (first entry)

Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzeimers disease; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding anadiogenesis; kidhey tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant. Human secreted/transmembrane protein cDNA, #52.

Homo sapiens.

980S-0109304P. 98WO-US025108. 98US-0113296P. 99US-0143048P. 99US-0145698P.

20-NOV-1998; 01-DEC-1998; 22-DEC-1998; 07-JUL-1999;

99WO-US020944

99WO-US020594

98US-0100858P. 98WO-US019437. 98US-0104080P.

US2003039971-A1.

27-FEB-2003

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30-MAR-2000; 2000WG-US008439. 22-MAY-2000; 2000WG-US014042. 02-JJN-2000; 2000WG-US015264. 28-JJL-2000; 2000WG-US020710. 24-AUG-2000; 2000WG-US022328. 18-SEP-2000; 2000US-00665350. 99WO-US028S64. 99WO-US028B65. 99WO-US030091. 99WO-US030911. 2000WO-US0002119. 2000WO-US000315. 99WO-US028214. 99WO-US028313. 99WO-US028301. 99WO-US021090. 99WO-US021547. 99WO-US023089. 2000WO-US005004. 2000WO-US007377 05-JAN-2000; 11-FEB-2000; 24-FEB-2000; 24-FEB-2000; 02-MAR-2000; 30-MAR-2000; 30-MAR-2000; 22-MAY-2000; 22-MAY-2000; 28-JUL-2000; 28-JUL-2000; 15. SEP-1999; 15. SEP-1999; 16. SEP-1999; 16. SEP-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 16. DEC-1999; 

(GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-503392/47. P-PSDB; ADA18324. New secreted and transmembrane polypeptides useful for treating skin, neurodegenezative diseases, asthma, rheumatoid arthritis, psoriasis and multiple sclerosis,

Claim 2; SEQ ID NO 262; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucleic acid encoding them. The Polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bloactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing a PRO polypeptides are also useful for reating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal classes, amyotrophic lateral sclerosis (ALS), neuropathies and differentiation (e.g. psociasts), Parkinson's disease, Alzhedmer's diseases, amyotrophic lateral sclerosis (ALS), neuropathies and addifferentiation (e.g. psociasts), Parkinson's disease, Alzhedmer's diseases, amyotrophic lateral sclerosis (ALS), neuropathies and cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also

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97US-0066770P. 97US-0066840P.

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comployed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine attit thes a role in neurodegenerative diseases or their reversal, as an attithrombotic agent with reduced risk for haemorrhage as compared with heparin, in treating other PRO-associated disorders, in modulating the reduced risk for haemorrhage as compared with heparin, in treating angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of consolate which have a role in apoptosis. The polymucleotides are useful in molecular biology including uses as hybridisation probes for CDNA library to isolate the full-length PRO CDNA or to isolate other CDNA; in molecular angionist, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgemic animals or knockout animals which are useful in the development and screening of the reapeutically useful requested as as well as for recombinantly expensively the propertied expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as the respectic agents, for screening compounds to identify those that mimic of angonists, the polymucleotides and proteins are useful for tissue typing PRO etc. Generally for replacing of PRO etc. Gagonists). The polymucleotides and proteins are useful in diagnostic assays for PRO etc. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from cissue the protein and for affinity purification of PRO from cells, tissues or serum and for affinity purification of PRO from the effect of the protein and and protein and defective gene and any also be used in gene therapy, particularly for replacing a defective gene. The invarious protein and serve and proteins are useful in section of polyment of the protein and protein and protein and protein and any serve and any serve and any serve and any serve
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New genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO1868), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in
                                                                                                                                                                              Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerrissen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
20-DEC-1999; 99WO-US030911.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US030565.
11-FEB-2000; 2000WO-US003566.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US006414.
24-FEB-2000; 2000WO-US005841.
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30-MAR-2000; 2000WO-US005841.
22-MAY-2000; 2000WO-US016449.
22-JUN-2000; 2000WO-US015264.
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Claim 2; Fig 97; 476pp; English.

The invention relates to an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide expearing as sequence with at least 80% identity to: (a) a nucleotide sequences having 50.4053bp (10.1867) and transmembrane protein) polypeptides papearing as AB032756-AB032816; or (b) any of 61 nucleotide sequences having 50.4053bp (11) defined in the specification; or the full length coding sequence of any these 61 nucleotide sequences. Also included are the isolated PRO oplypeptide (lacking its associated signal peptide), a vector comprising the nucleotide signal peptide), a vector comprising the nucleotic acid molecule, a host cell comprising the vector (used to produce the PRO polypeptide), a chimmeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868 polypeptide and modulating at least one biological activity of a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides or polypeptide and modulating at least one biological activity of a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides or polymercleotides are useful as pharmaceuticals, diagnostics, biosensors or ploreactors. These are particularly useful for diagnosing or treating corporation matterns, particularly, birth defects, premature aging, malignancy increations, Partinson's diseases, Alzheimer's disease, or AIDS in mammals. These are also useful for modulating cholesterol uptake in the body, and in wound healing or tissue repair. The PRO polypeptides are also useful as weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening alpharmace is a cDNA encoding a PRO plypeptide are also useful as proprised or therapy, generic DNA, genening a PRO polypeptide are also useful as proprised or therapy, served and in gene therapy.

Seguence 1378 BP; 235 Å; 461 C; 412 G; 270 T; 0 U; 0 Other;

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0.7%; Score 24.6; Di
Local Similarity 53.7%; Pred. No. 26;
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Human, PRO; gene, ss; secreted polypeptide, transmembrane polypeptide, abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion; coronary ischaemic condition; gastrointestinal mucosa; skin disease; ALS; keratinocyte differentiation; psoriasis; Parkinson's disease; asthma; Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer; amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth. 1332 ATTTATTCTCCTCCAATTCATAATTATTTATTCT 1366 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 ACD83165 standard; cDNA; 1378 97US-0059263P. 97US-0059266P. 97US-0062125P. 97US-0062285P. 97US-0063486P. 97US-0062814P. 97US-0062816P. 97105 0063045P 9705 0063120P 9705 0063122P 9705 0063123P 9705 0063329P 9705 0063542P 9705 0063542P 9705 0063542P 9705 0063542P 9705 0063542P 9705 0063542P 9705 0063543P 9705 0063732P 9705 0063732P 9705 0063733P 9705 0063733P 9705 0063733P 9705 0063733P 9705 0063733P 9705 0063732P 97US-0059113P. 97US-0059115P. 97US-0059117P. Human PRO polynucleotide #48. 11-JUL-2001; 2001US-00903786 97US-0059184P 22-SEP-2003 (first entry) US2003044793-A1. 06-MAR-2003, 997 997 ACD83165; RESULT 55 ACD83165 ઠે 엄  preservation and maintenance of gastrointestinal mucosa and the repair of

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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fal'Varoff E, Fong S, Gao W, Gerber H, Gerriteen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides can be used in diagnosing or treating abnormal bleeding involved in gynaecological diseases e.g. to avoid or lessen the need for hysterectomy. They can also be used in treating coronary ischaemic conditions, disorders associated with the Novel secreted and transmembrane PRO polypeptides and polynucleotides encoding them, useful for treating abnormal bleeding involved in gynecological diseases, skin diseases and neurodegenerative diseases. Claim 2; Fig 97; 475pp; English.

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                                                                                                                                                                                                 acute and chronic mucosal lesions, skin diseases associated with aborrant keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alabaimer's disease, asthma, rheumatoid arthritis, multiple sclerosis, amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to uncontrolled cell growth, such as cancer. This sequence represents a human PRO polynucleotide of the invention
                                                                                                                                                                                                                             1272 TTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene; ss; PRO; secreted, transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal beart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; cimulated T-lymphocyte; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; bone disorder; cartilage disorder; arthitis; cardiant; vulneary; cytostatic; ophthalmological; osteopathic; antiatthritic; anorectic.
                                                                                                                                                                       0; Gaps
                                                                                                                                          DB 1; Length 1378;
                                                                                                              Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                                                                                                                                       44; Indels
                                                                                                                                                                                                                                                         3043 ITTITIAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                                                                                                                                                                                                      1332 ATTTATTCCTCCAATTCCAATAATTATTTATTCT 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane protein cDNA, #52.
                                                                                                                                                              0; Mismatches
                                                                                                                                          0.7%; Score 24.6;
33.7%; Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                           ADA16298 standard; cDNA; 1378 BP.
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9703-0059121P
9703-0059124P
9703-0059263P
9703-0059266P
9703-0062125P
9703-0062125P
9703-0062181P
9703-0062814P
9703-0062814P
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9703-0062814P
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97US-0063128P.
97US-0063327P
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                                                                                                                                                                       51; Conservative
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17-0CT-1997
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27-OCT-1997
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                                                                                                                                          Query Match
Best Local (
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02-MAR-2000; 2000WO-US00S841.
20-MAR-2000; 2000WO-US00377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-UJN-2000; 2000WO-US015564.
28-JUL-2000; 2000WO-US012564.
                              9705-0063549P
9705-0063559P
9705-0063435P
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9705-00637335P
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99WO-US028214.
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98WO-US019330.
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98US-0113296P.
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99US-0145698P.
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      28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
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21-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
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15-SEP-1999;
15-SEP-1999;
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17-NOV-1997;
18-NOV-1997;
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25-NOV-1997;
12-DEC-1997;
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16-SEP-1998;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather UP, Broni NP, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-521801/49. P-PSDB; ADA16299. 

New genes encoding for secreted and transmembrane PRO polypeptides, useful for treating e.g. cardiac insufficiency disorders, wounds, cancers, obesity, diabetes, hyperinsulinemia, hypoinsulinemia, or arthritis.

Claim 2; SEQ ID NO 262; 476pp; English.

The invention discloses isolated PRO secreted/transmenbrane polypeptides and the nutcleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide. for linking a bloactive molecule to a call expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bloactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell. PRO polypeptide or the PRO polypeptide are useful for modulating the biological activity protection and conference. The PRO polypeptide or the protection of cells, modulating the proliferation of central as pharmaceuticals, diagnostics, blosensors or polymolocides are useful for simulating mypertrophy of menaral heart, inhibiting vascular encothelial growth factor (VEGP) stimulated proliferation of central activity of the proliferation of central activity associate enhancing the survival or proliferation of crimulated T-lymphocytes, enhancing the survival or proliferation of crimulated T-lymphocytes, enhancing the survival or proliferation of crimulated plucase or PRA upeak, inducing proliferation and/or refulle modulating glucose or PRA upeak, inducing proliferation and/or cells, modulating proliferation or crimilated choracovers. In particular, these are useful for the cells, modulating proliferation or crimilated in survival or particular in the action of chonacovers. In particular, these are useful for cells, modulating proliferation of chonacovers. In particular, these are useful for centing or treating cardiac insufficiency disorders, wounds, cancerous refunding by more propersion of genes which have a role in cell death, me polymolecular polypeptides, for generation and or knockout animals with generation of genetic analysis of individuals with generations are useful in cells cardial as molecular are useful in the development and undown, for p

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

0; Gaps DB 1; Length 1378; Query Match
0.7%; Score 24.6; DB 1; Length 1
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 2983 ICTAITITACTITAATIGCACTTAITITITITITITITITITITITAATAAATCCAGTCCTTGT 3042 1272 İTİTGİĞİATATAAAİGTIAAİGATİTİTATAĞGİATTİĞİAACCCTGCCCACATAİCT 1331 g

3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 ઠ

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WPI; 2003-755054/71.
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                                       24-NOV-1997
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Human; gene, ss; PRO; secreted; transmembrane; gastrointestinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson; disease; Albeimer's disease; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic, tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                                 Human secreted/transmembrane protein cDNA, #52.
                                      ADA42443 standard; cDNA; 1378 BP
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970S-0059113P.
970S-00591119P.
970S-0059121P.
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970S-006312P.
970S-006312P.
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                                                                             20-NOV-2003 (first entry)
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                                                                                                                                                                                                                Homo sapiens
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24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
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29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
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                  RESULT 57
ADA42443
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24-EAR-2000; 2000WO-US005841
20-MAR-2000; 2000WO-US005841
30-MAR-2000; 2000WO-US008439
22-MAY-2000; 2000WO-US014042
02-UUN-2000; 2000WO-US015264
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US02328
18-SEP-2000; 2000WS-US023328
970S-0066511P.
970S-0066770P.
970S-0066840P.
970S-0069425P.
980S-0088026P.
980S-009803P.
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98WO-US019437.
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99WO-US021090.
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99WO-US028564.
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99WO-US030095.
99WO-US030911.
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05-UAN-2000; 2000WO-US000219.
11-FEB-2000; 2000WO-US03565.
22-FEB-2000; 2000WO-US0054044.
24-FEB-2000; 2000WO-US00500414.
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#### (GETH ) GENENTECH INC.

Desnoyers L, Baton DL, Ferrara N;
I, Gerber H, Gerritesen NE, Goddard A;
Graney AL, Hillan KJ, Kljavin IJ;
Graney AL, Stewart TA, Tumas D;
P, Roy MA, Stewart TA, Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Filvaroff E, Fong S, Gao W, Gerber H, Godowski L, Grimaldi JC, Gurney AL, H Mather JP, Pan J, Paoni NP, Roy MA, S Williams PM, Wood WI; Novel PRO polypeptides useful for treating Parkinson's disease, Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome, psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological diseases.

# Claim 2; SEQ ID NO 262; 479pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a

cc del expressing RRO polypeptides. RPO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases associated with abnormal Keratinocyte (diseases, amycrophic lateral sclerosis (ALS), neuropathies and adiseases, amycrophic lateral sclerosis (ALS), neuropathies and adiseases, amycrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be explored a therapeutic targets for anti-tumour faruge, and are also employed therapeutically in vivo for lessening the effects of viral cinfection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with chepatin, in treating or cher PRO-appropries, and may also have an effect on kidney clister. PRO polypeptides and their portions affect the expression of cissue. PRO polypeptides, for an effect on kidney genes which have a role in appotosis. The polymuclocides are useful in molecular biology including uses as hybridiaation probes for cDNA, in consome and gene mapping, in the generation of antisense RNA and DNA, chomosome and gene mapping, in the generation respection and for the genetic animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic animals which are useful in the development and screening of the PRO polypeptide (agonists) or protein electrophoresis as the reagentic assays for screening compounds to identify those that mimic contistes and proteins are useful in the BRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent meanuples are useful in gene therapy, par invention. 

13-JUL-2001; 2001US-00904485

US2003064367-A1. Homo sapiens.

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

2983 TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTCTAATAAATCCAGTCCTTGT 3042 1272 irrigigiataraahgeraangarrirraanggrarrigaangeeergeeeegeera 1331 0; Gaps 0.7%; Score 24.6; DB 1; Length 1378; 53.7%; Pred. No. 26; 0; Mismatches 44; Indels 3043 TTTTTTAAAAAGACTTTAAAATTATTATTTCTCT 3077 1332 AİTİAFITCCICCAAİTİCAATAAİTİATİTATİCİ 1366 ACD23343 standard; cDNA; 1378 BP. 51; Conservative Local Similarity ACD23343; Query Match Best Loca Matches ACD23343 à 

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Human; PRO; gene; ss; Parkinson's disease; Alzheimer's disease; ALS; amyotrophic lateral sclerosis; neuropathy; cancer; viral infection; AIDS; blaber's syndrome; haemorrhage; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; psoriasis; skin disease; endometrial bleeding; angiogenesis; ischaemic condition; atherosolatoid architis; multiple sclerosis; inflammatory disease; diabetic complication.
                                                                                             Human PRO polynucleotide #48.
26-AUG-2003 (first entry)
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9705-0663486P 9705-0663486P 9705-0663486P 9705-06630485P 9705-0663012P 9705-066312P 9705-066312P 9705-066332P 9705-066332P 9705-066332P 9705-066352P 9705-066352P 9705-066352P 9705-066354P 9705-066354P 9705-066354P 9705-066354P 9705-066354P 9705-066364P 9705-066364P 9705-06636P 9705-06636P 9705-06636P 9705-06636P 9705-06636P 9705-066486P 9705-066486P 9705-066486P 9705-066486P 9705-066486P 9705-06646P 9705-06646P 9705-06646P 9705-06646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 9705-066646P 97US-0059122P. 97US-0059184P. 97US-0059263P. 97US-0059115P. 97US-0059117P. 97US-0059119P. 98WO-US018824. 98US-0100262P. 98WO-US019177. 12-NOV-1997; 17-NOV-1997; 18-NOV-1997; 4-OCT-1997; 4-OCT-1997; 12-DEC-1997; 17-SEP-1998; 24-NOV-1997; 24-NOV-1997; 25-NOV-1997; 28-OCT-1997 28-OCT-1997 .4-SEP-1998, 16-SEP-1998 .7-SEP-1997 29-0CT-1 29-0CT-1 31-0CT-1 5-0CT-1 7-0CT-1 -VON-70 

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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are used for treating diseases related to growth or survival of nerve cells such as Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and neuropathies, diseases related to uncontrolled cell growth such as cancer, viral infections, Usher's syndrome, haemorrhage, entercoolitis, 2011inger billison syndrome, gastrointestinal ulceration, congenital microvillus atrophy, skin diseases such as psoriasis and epithelial encencer, endometrial bleeding, anglogenesis, isonamic conditions, asthma, rheumatoid arrhritis, multiple sclerosis, inflammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature also useful in chromosome and gene mapping. This sequence represents a human PRO polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerriteen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.7%; Score 24.6; DB 1; Length 1378; Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels 0;
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18-SEP-2000; 2000US-00665350.
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99WO-US028301
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24-FEB-2000;
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Human; gene; 95; PRO; secreted; transmembrane; gastrointestinal mucosa, mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; haemorrhage; endometrial bleeding angiogenesis; kidney tissue, apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                                                                  Human secreted/transmembrane protein cDNA, #52.
                    ADA16722 standard; cDNA; 1378 BP.
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22-MAY-2000; 2000WO-U5014042.
02-JUN-2000; 2000WO-U5012564.
28-JUL-2000; 2000WO-U5012564.
24-AUG-2000; 2000WO-U502710.
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Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritens ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI; Pan J, Ashkenazi A, Filvaroff E, Godowski PJ, Williams PM, Mather JP,

#### WPI; 2003-503391/47. P-PSDB; ADA16723.

New secreted and transmembrane PRO polypeptides e.g. PRO187, which is a member of the epidermal growth factor-8 (EGF-8) family of proteins, useful for treating cancer.

## Claim 2; SEQ ID NO 262; 471pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide, for linking at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides.

for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. peoriasis) Parkinson's disease, Alzheimer's diseases, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral content of the same ar role in neurodegenerative diseases or their reversal, as an it in treating other PRO-associated disorders, in medulating endometrial bleeding andiogeness, and may also have an effect on kidney content and properties and thair portions affect the expression of endometrial bleeding andiogeness, and may also have an effect on kidney to endometrial bleeding andiogeness, and may also have an effect on kidney to endometrial bleeding andiogeness, and thair portions and game mapping. The polymucleotides are useful in moreous and game mapping, in the generation of antisense RNa and DNA, to isolate the full-length PRO cDNA or to isolate other companing of the protein and for chromosome and game mapping, in the generation of antisense RNa and DNA, to consolate the full and proteins are useful in the generation and for cerominals with genetic disorders as well as protein are useful or expression in specific correspentic agents, for screening compounds to identify those that mimic correlations and or an endome and electrophoresis growed the PRO polypeptide (angonists) or prevent the effect of the PRO polypeptide (angonists) or prevent the effect of the PRO polypeptide same useful for immundiscondering and or 

# Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

/ Match 0.7%; Score 24.6; DB 1; Length 1378; Local Similarity 53.7%; Pred. No. 26; to Conservative 0; Mismatches 44; Indels 0; Query Match Matches

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### 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 1332 ATTHATTCCTCCAATTCAATAAATTATTTATTCT 1366

ADA13151 standard; cDNA; 1378 BP.

ADA13151;

06-NOV-2003 (first entry)

Human secreted/transmembrane protein cDNA, #52.

Human, gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriaais; parkinson; disease; Albeimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease; antithrombotic agent; heemorrhage; endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant. ADA13151
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20-MAR-2000; 2000WO-US005841.
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02-UUN-2000; 2000WO-US015264.
28-UUL-2000; 2000WO-IS015264.
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99WO-US021547.
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18-SEP-2000;
              05-OCT-1999;
29-NOV-1999;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AJ, Hillan KJ, Kljavin IJ; Mather JP, Ban J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-521802/49. P-PSDB; ADA13152. New secreted and transmembrane PRO polypeptides, useful for treating cancer, skin disorders, neurodegenerative diseases, and for lessening the effects of viral infection.

### Claim 2; SEQ ID NO 262; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise bloadies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a call expressing a PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for Inhing a collocative molecule to a call expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a call expressing a PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of a call expressing a Minh the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled call growth, e.g. cancer. Completed as last parametric targets for anti-tumour drugs, and are also exploited as therapeutic targets for anti-tumour drugs, and are also exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine the manufactural production and any algority in the genes which have a role in neurodegenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of condomerrial bloeding angiogenesis, and may also have an effect of molecular biology including uses as hybridisation probes for copy, to issue the full-length PRO copy or tesolate the full-length PRO copy or tesolate the full-length PRO copy or tesolate the full-length PRO copy or tesolate the full-length PRO polypeptides, for generation of antisense RNA and DNA croisolate call and and ge

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of individuals with genetic disorders as well as for recombinantly argressing the protein and for chromosome identification. The proceins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that minic polypeptide (agonists) or prevent the effect of the RRO mildolypeptide (antagonists) or prevent the effect of the RRO polypeptide (antagonists). The polymucleotides and proteins are useful for tissue typing. RRO antibodies are useful for immunohistochemical staining and/or assay for RRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a RRO polynucleotide of the
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29-NOV-1999;
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24-NOV-1997;
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enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis and Usher syndrome. Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerrissen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Fan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI; New PRO polypeptides useful for treating Parkinson's disease, Claim 2; SEQ ID NO 262; 468pp; English. 24-AUG-2000; 2000WO-US023328. 18-SEP-2000; 2000US-00665350. (GETH ) GENENTECH INC. WPI; 2003-755103/71. P-PSDB; ADA42020.

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

Homo sapiens. 23-JAN-2003. 7-SEP-1997 28-OCT-1997 29-OCT-1997 29-OCT-1997 29-OCT-1997 ADA17366; 28-0CT-1 29-0CT-1 28-OCT-1 RESULT 62 ADA17366 à The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucleis card encoding them. The polypeptides can be used to raise and the mucleis card encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide. For linking a to loadtive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful confidence to a cell expressing a PRO polypeptide. The PRO polypeptide are useful confidence to a cell expressing a PRO polypeptide. The PRO polypeptide are useful confidence to a cell expressing a PRO polypeptide. The PRO polypeptide are useful confidence to a cell expressing PRO polypeptide. PRO polypeptide are as a law one can accompanies that a cell expressing properties are useful for treating diseases associated with the preservation and maintenance of gastrointestual mucosa and the repair of accel properties and are associated with the preservation and maintenance of gastrointestual mucosa and the repair of accel gastrointestual mucosa at umour specific antigens which may be differentiation (e.g. psoriasis), Parkinson's disease, Albreimer's diseases amyortrophic lateral sclerosis (ALS), neuropathics and careful and additionally, disease related to uncontrolled cell growth e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutically in vivo for lessening the effect on kidney in the capetide can be also used in assays to decemine of the parkin, in treating other PRO sesociated disorders, in which have a role in neurodegenerative diseases on their reversal, as an antithrombotic agent with have a role in apoptosis. The generation of antisens RNA and DNA, chromosome and gene mapping in the generation of antisens RNA and DNA, chromosome and gene mapping in the generation of antisens RNA and DNA chromosome and gene mapping in the generation of antisens RNA and DNA chromosome and gene mapping in the generation of antisens RNA and DNA chromosome and gene mapping in the generation of an DB 1; Length 1378; Query Match 0.7%; Score 24.6; DB 1; Length 13° Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels

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1272 TITIGIGIATATABAHGITAATGATITITATAGGTATITIGIAACCCTGCCCACATAICT 1331
                                                                                                                                                                                                          Human, gene, ss; PRO, secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease, keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's disease; awyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection; neurodegenerative disease, antithrombotic agent; haemorrhage; endometrial bleeding anglogenesis; kidney tissue; apoptosis; therapeutic; tissue typing; immunohistochemical staining; gene therapy; noctropic; neuroprotective; cytostatic; virucide; anticoagulant.
                                    3043 TITITIAAAAGACITIAAAAITATTATTTCICI 3077
                                                   1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366
                                                                                                                                                                                       Human secreted/transmembrane protein cDNA, #52.
                                                                                                                  ADA17366 standard; cDNA; 1378 BP.
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9708 - 00622859
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97US-0064248P

03-NOV-1997

97US-0064809P

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24-FEB-2000, 2000WO-US00S004.
20-WAR-2000; 2000WO-US00S641.
20-WAR-2000; 2000WO-US009377.
30-WAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
22-UNY-2000; 2000WO-US012264.
28-UUL-2000; 2000WO-US012264.
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2000WO-US000219,
2000WO-US003565,
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21-NOV-1997;
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29-NOV-1999
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#### (GETH ) GENENTECH INC.

Ferrara N; ME, Goddard A; Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N, Frivarcif E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard Godowski PJ, Grimaldi JC, Gurney ME, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D; Pan J, Paor M. Wood WI; Williams PM,

WPI; 2003-531434/50.

P-PSDB; ADA17367.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or PRO1868, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; SEQ ID NO 262; 475pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to rais

antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protesh and for modulating at a teast one biological activity of a cell. PRO polypeptides are useful car detecting other PRO polypeptides in a sample and for linking a coll expressing a PRO polypeptide. The PRO polypeptides are also useful concerned modernie to a cell expressing a PRO polypeptides are also useful cor treating disorders asociated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases asociated with the preservation and maintenance differentiation (e.g. psoriasis). Parkinson's disease, lamyotrophic lateral scherosis (ALS), neuropathies and differentiation (e.g. psoriasis). Parkinson's disease, lamyotrophic lateral scherosis (ALS), neuropathies and activation additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tunour specific antigens which may be exploited as therapeutic latered to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tunour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also cantibrombots as therapeutic argets for anti-tumour drugs, and are also cantibrombots as therapeutic associated disorders as compared with hepatin, in treating other PRO-associated disorders, in modulating of endomerrial bleedings and their portions affect on kidney tissue, PRO polypeptides, and may also have an effect on kidney discuss mother have a role in apoptosis. The polymolectides are useful in molecular biology including uses as hybridisation of antisense RNA and but conscend and spen mapping, in the generation of antisense RNA and the conscense and gene mapping, in the generation of antisense RNA and conscipled the protein and for chromosome and gene mapping, in the generation of antisense RNA and the resemble protein and for chromosome and gene mapping, in the generation of artisense resemble 

Seguence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

2983 ICTATTTTACTTTAATTGCACTTATTTTATTGATTTTTTCTAATAAATCCAGTCCTTGT 3042 0; Gaps 0.7%; Score 24.6; DB 1; Length 1378; 53.7%; Pred. No. 26; tive 0; Mismatches 44; Indels 0 51; Conservative Sest Local Similarity Query Match Matches ò 1272 irringigiararaargirargarrinrinaragiarringiaaccorgcocacatarori 1331

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3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 1332 ATTIATTCCTCCAATTTCAATAATTATTATTT 1366 ò 요

RESULT 63 ADA42869

ADA42869 standard; cDNA; 1378 BP. · KKKKKK KKKK YKK

ADA42869;

20-NOV-2003 (first entry)

Human secreted/transmembrane protein cDNA, #52.

Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa; mucosal lesion; skin disease; keratinocyte differentiation; psoriasis; Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis; ALS; neuropathy; cell growth; cancer; tumour; viral infection;

neurodegenerative disease, antithrombotic agent; haemorrhage, and andometrial bleeding angiogenesis; kidney tissue, apoptoais; therapeutic, tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.

Homo sapiens.

US2003054351-A1.

20-MAR-2003

13-JUL-2001; 2001US-00904462

970S-0059113P 970S-0059113P 970S-0059113P 970S-0059114P 970S-0059124P 970S-0059124P 970S-0059124P 970S-005286P 970S-006287P 970S-006287P 970S-006287P 970S-006287P 970S-0063874P 970S-0063127P 970S-0063127P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-0063128P 970S-006312P 970S-006312P 970S-006312P 970S-006312P 970S-006312P 970S-0063178P 970S-0063178P 970S-0063178P 970S-0063178P 970S-0064178P 970S-0066472P 970S-0066472P 970S-0066472P 970S-0066472P 970S-0066472P

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980.S-01132956 990.S-0143048P 990.S-0145698P 990.S-0145698P 990.S-0145622P 990.O-01502094 990.O-015021090 990.O-015021090 990.O-015021040 990.O-015021040 99WO-US028564 99WO-US028565 99WO-US030095 99WO-US030091 99WO-US030091 2000WO-US030219 2000WO-US005841. 2000WO-US007377. 2000WO-US008439. 2000WO-US014042. 2000WO-US015264. 2000WO-US020710. 2000WO-US023328. 2000WS-00665350. 2000WO-US004414. 2000WO-US005004. 99WO-US028301 11-FEB-2000; 22-FEB-2000; 24-FEB-2000; 02-MAR-2000; 20-MAR-2000; 30-MAR-2000; 15-SEP-1999 15-SEP-1999 05-OCT-1999 29-NOV-1999

(GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NP, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-755052/71.

P-PSDB; ADA42870.

Novel isolated secreted and transmembrane PRO polypeptide, useful for tissue typing, treating Parkinson's disease, Alzheimer's disease, birth defects, cancer.

Claim 2; SEQ ID NO 262; 464pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antithedies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a call expressing a PRO polypeptide, for modulating a contective molecule to a call expressing a PRO polypeptides are useful to redecting other PRO polypeptides in a sample and for linking a colypeptide antibodies are useful for modulating the biological activity of a call expressing a PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of a call expressing which has promain a sample and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal festing disorders associated with haboramal keratinocyte of gastrointestinal mucosa and the repair of acute and chronic mucosal diseases, amyotrophic lateral sclerosis (ALS), neuropathies and cancer. Consolvated as therapeutic targets for anti-tumour drugs, and are also exploited as therapeutic targets for anti-tumour drugs, and are also exploited as therapeutic targets for anti-tumour drugs, and are also capped propertion. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antibenting and other PRO-associated disorders, in modulating endommerrial bleeding anglogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of

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genes which have a role in apoptosis. The polymucleotides are useful in molecular biology including uses as hybridisation probes for cDNA library choisolate the full-length PRO cDNA or to isolate other CDNAs, in chromosome and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therappeutically useful reagents, in the development genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as the PRO polypeptide (aponists) or protein electrophoresis purposes, the PRO polypeptide (aponists) or protein electrophoresis purposes that mimic the PRO polypeptide (aponists) or protein electrophoresis schaul proteins are useful for tissue typing. PRO antibodies are useful for tissue typing. PRO antibodies are useful for immunohistochemical diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affanity purification of PRO from tecombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The entire of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the pr
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leukocyte homing; rheumatoid arthritis; psoriasis; multiple sclerosis;
mucosal lesion; enterocolitis Zollinger Ellison syndrome; asthma;
antiasthmatic; antirheumatic; antiarthritic; neuroprotective.
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Local Similarity 53.7%; Pred. No. 26;
Los 51; Conservative 0; Mismatches 44; Indels 0;
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tissue typing; immunohistochemical staining; gene therapy; nootropic; neuroprotective; cytostatic; virucide; anticoagulant.
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97US-0059113P.
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       The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The polypeptides are useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the polypeptides, where the bloactive molecule to a cell expressing the polypeptides. The bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptides or antibodies specific to the polypeptides are useful for modulating at least one biological activity of a cell expressing the polypeptides. The collypeptides are useful for treating disorders associated with leukocyte coloning such as asthma, rheumatoid arthritis, psoriasis and multiple colonings such as asthma, rheumatoid arthritis, psoriasis and multiple colonicitis and Zollinger Ellison syndrome and for identifying agonists or antagonists of the polypeptides. The polymucleotides are useful as hybridization probes, in chromosome and gene mapping, in generating of antisense RNA and DNA, in the preparation of PRO polypeptides and for generating probes for polymerase chain reaction (PCR), Northern analysis, and molonial and plant analysis.
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                                                                                                                                                                                                                                                                                           Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                    Botstein D, Desnoyers L, Eaton DL, Ferrara N; Pong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D;
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Pred. No. 26;
0; Mismatches
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              02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
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1 Similarity 53.7%;
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M, Wood WI;
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P-PSDB; ABO17602.
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22-MAY-2000;
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Filvaroff E,
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Mather JP, F
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20-DEC-1999; 99W0-US030911.
20-DEC-1999; 99W0-US030999.
05-JAN-2000; 2000W0-US000219.
11-FEB-2000; 2000W0-US004565.
22-FEB-2000; 2000W0-US0050604.
02-MAR-2000; 2000W0-US0050641.
20-MAR-2000; 2000W0-US0050641.
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22-MAY-2000; 2000W3-US014042.
02-UUN-2000; 2000W3-US012564.
28-UUL-2000; 2000W3-US012564.
24-AUG-2000; 2000W3-US023328.
18-SEP-2000; 2000US-00665350.
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99US-0145698P.
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                      08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-765399/72. P-PSDB; ADB77789 New isolated secreted and transmembrane polypeptide, useful for treating diseases, e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.

Claim 2; Fig 97; 467pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antitudedies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protean and for linking a the least one biological activity of a cell. PRO polypeptides are useful conditions at least one biological activity of a cell. PRO polypeptides are useful bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing a PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte of gastrointestinal mucosa and the repair of acute and chronic mucosal differentiation (e.g. psoriasis), Parkinson's disease, Alzheiner's diseases, amyotrophic lateral sclerosis (ALS), neuropathics and acuter. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also exploited as role in neurodesencrative diseases or their reversal, as an infection. The PRO polypeptides can be also used in assays to determine if the has a role in neurodesencrative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with heparin, in treating other PRO-associated disorders, in modulating cendometrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides an apoposis. The polymotleetides are useful in molecular biology including uses as hybridisation probes for CDNA library

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c to isolate the full-length PRO cDNA or to isolate other cDNAs, in chromosome and gene mapping, in the generation of antieense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the generic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for infamunohistocohemical for itssue typing. PRO antibodies are useful for immunohistocohemical cataining and/or assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The ending entering its a gene encoding a PRO polymucleotide of the
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53.7%; Pred. No. 26;
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97US-0063486P
97US-006346P
97US-0063120P
97US-0063121P
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97US-0063124P
97US-0063324P
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97US-006638P
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97US-006638P
97US-006638P
97US-006638P
97US-010838P
98WO-USO119370
98WO-USO119370
98WO-USO119370
98WS-0113396P
98WS-0113396P
99WS-0113296P
99WS-0114322P
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Novel isolated native PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating enterocolitis, Zollinger-Ellison
                                                                                                                                                                                                                                            Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D;
                                                                                                                                                                                                                                          Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, F
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen M
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, K
Mather D, Pan J, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI;
2000WO-US007377.
2000WO-US008439.
2000WO-US014042.
2000WO-US015264.
                                                                                              28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-765412/72.
P-PSDB; ADB74925.
20-MAR-2000; 2
30-MAR-2000; 2
22-MAY-2000; 2
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                 Mather JP, Pe
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Claim 2; Fig 97; 475pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleid and encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide for inhking a carie demoding them. The PRO polypeptide in the specifically bind to the PRO polypeptide for inking a telest one belongical activity of a cell. PRO polypeptide are useful for modulating the biological activity of a cell. PRO polypeptide are as also useful for detecting other PRO polypeptides. PRO polypeptide are as also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of actue and chronic mucosal fifferentiation (e.g. psoriasis) Parkinson's disease, Altheimer's diseases ascociated with abnormal keratinocyte (c.g. psoriasis) Parkinson's disease, Altheimer's diseases are received with the preservation and maintenance of gastrointestinal mucosa and the repair of actual properties of gastrointestinal macosa activity of seases. As a character of the properties of the properties of gastrointestinal macosa activity of seases. As a character of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the prop

nvention.

22-FEB-2000; 2000WO-US004414 24-FEB-2000; 2000WO-US005004 02-MAR-2000; 2000WC-US005841

2000WO-US003565

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                                                                                    1272 TTTTGTGTATATAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; tissue typing; immunohistochemical staining; gene therapy; endothelial acat; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; simulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FRA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulnaemia; home disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                   0; Gaps
               DB 1; Length 1378;
             Query Match 0.7%; Score 24.6; DB 1; Length 13° Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels
                                                                                                                                                            3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                                                                                                 1332 ATTTATTCCTCCAATTTCAATAAATTATTATTCT 1366
                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein cDNA, #52.
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98US-0100858P.
98WO-US019437.
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98US-0088026P.
98US-0099803P.
98WO-US018824.
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99US-0143048P.
99US-0145698P.
99US-0146222P.
99WO-US020594.
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99WO-US030911.
99WO-US030999.
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11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US004414.
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02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
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22-MAY-2000; 2000WO-US014042.
02-UUN-2000; 2000WO-US015264.
28-UUL-2000; 2000WO-US020710.
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98WO-US019177
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18-SEP-2000; 2000US-00665350
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12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
21-NOV-1997;
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16-SEP-1998;
17-SEP-1998;
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05-OCT-1999;
29-NOV-1999;
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03-NOV-1997;
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24-NOV-1
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Ashkenazi A, Botstein D, Desnoyers L, Baton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski bJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Ban J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Rood WI;

WPI; 2003-540670/51. P-PSDB; ADC28571.

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nutolated and encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a call expressing a PRO polypeptide. For linking a to bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide and for modulating the bioactive molecule to a cell expressing a PRO polypeptides or useful for modulating the biological activity of polypeptides or polypeptide are useful for modulating the biological activity of polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypeptides or polypept
Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.
                                                                                          Claim 2; SEQ ID NO 262; 470pp; English.
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17-NOV-1997;
18-NOV-1997;
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e 0; Mismatches 44; Indels 0
                                                                                                                                                        Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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ADC39770
TD ADC39'
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14-JUN-1998

(first entry)

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Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VBGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; cap photoraceeptor cell; c-fos; glucose; FRA; chordarocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
 Human secreted/transmembrane protein cDNA, #52.
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9703-0059119P.
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98WO-US01330
98WS-U100858P
98WS-01040807
98WS-0104304P
98WS-0109304P
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99WO-US030095.
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2000WO-US008439.
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2000WO-US000219,
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17-SEP-19
13-OCT-19
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Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI; Pan Ashkenazi A, I Filvaroff E, I Godowski PJ, ( Mather JP, Pa Williams PM,

### WPI; 2003-540675/51. P-PSDB; ADC39771.

an Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as antithrombotic agent and for inducing endothelial cell apoptosis.

### Claim 2; SEQ ID NO 262; 477pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for linking a taleast one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bloactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polymorlecides are useful for simulating hypertrophy of neonatal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated proliferation of endothelial cells, modulating the proliferation of stimulated retinulated T-lymphocytes, enhancing the survival or proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating the proliferation of stimulating proliferation and/or receips.

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cc differentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. 169s of sight due to retinitis pigmentosum), obesity, diabetes, hyperinsulinaemia, hypothsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a colle in cell death. The polytuclectides are useful in molecular biology including uses as hybridisation probes of for cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, in chromosome and gene mapping, in the generating transgenic and minals which are useful in the development and comminals or knockout annimals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for coroninantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis uproposes, as therapeutic agents, for screening compounds to identify the PRO polypeptide (antagonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for distinct of the PRO polypeptide (antagonists). The polymucleotides and proteins are useful in diagnostic assays of sample fluids. Anti-PRO expression in specific cells, tissues or serum and for affinity or replacing a defective gene may also be used in gene therapy, particularly for replacing a gene encoding a PRO polypeptide of the invention.
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ADC40284 standard; cDNA; 1378 BP ADC40284; 

RESULT 69

(first entry) 18-DEC-2003 Human secreted/transmembrane protein cDNA, #52.

Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; andothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete, hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnezary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.

Homo sapiens.

JS2003059829-A1.

27-MAR-2003.

13-JUL-2001; 2001US-00905381

17-SEP-1997; 97US-0059113P.

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970S-0059117P
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970S-0059122P
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30-MAR-2000; 2000MO-US008439. 22-MAY-2000; 2000MO-US014042. 02-UJN-2000; 2000MO-US015264. 28-UJL-2000; 2000MO-US023328. 18-SEP-2000; 2000MS-0065350. 99WO-US028565. 99WO-US030095. 99WO-US030911. 99WO-US030999. 2000WO-US003565 2000WO-US004414. 2000WO-US005841 2000WO-US007377 22-FEB-2000; 24-FEB-2000; 02-MAR-2000; 20-MAR-2000; 30-MAR-2000; 22-MAY-2000; 05-JAN-2000; 11-FEB-2000; 20-DEC-1999; 20-DEC-1999; 

#### (GETH ) GENENTECH INC.

Ŕ Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MS, Goddard Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Godowski PJ, Grimaldi Mather JP, Pan J, Par Williams PM, Wood WI;

WPI; 2003-540676/51. P-PSDB; ADC40285.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating skin, neurodegenerative diseases, as an antithrombotic agent and for inducing endothelial cell apoptosis.

### Claim 2; SEQ ID NO 262; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides on the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a contibodies that specifically bind to the PRO polypeptide in a sample and for modulating at least one bloiogical activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bloadcale to a cell expressing a PRO polypeptides in a sample and for linking a bloadcate medicule to a cell expressing PRO polypeptides. The PRO polypeptides are useful sparmaceuticals, diagnostics, pices are useful as pharmaceuticals, diagnostics, biosensors or polymedicating versions. These are useful for stimulating hypertrophy of meantal nearth in a cell expressing PRO polypeptides. The PRO polypeptides or boreactors. These are useful for stimulating hypertrophy of meantal colls, induction of endothelial growth factors (VEFF) estimulated colls, modulating the proliferation of for for the proliferation of endothelial growth factors (VEFF) estimulated colls, modulating glucose or FFA uptake, inducing proliferation of endothelial growth factors are useful for cells, modulating glucose or FFA uptake, inducing proliferation of endothelial growth are cells, inducing proliferation and/or retrinitis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders, wounds, cancerus crimitis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders, sprokes and profession of genes which have a role in cell death. The polymucleotides con by polymential biology including uses as hybridisation probes (CC or oDNA library to isolate the full-length PRO oDNA or to isolate other and plans, in chromosome and gene mapping, in the generation of thraspeutically useful in manuals which are useful in the development and creaming of thraspeutically useful as molecular marker for protein electrophoresis contends are useful for tissed the proteins are

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expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The RRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neconatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartiade disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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0.7%; Score 24.6; DB 1; Length 1
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels
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Ferrara N; ME, Goddard A;

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides on be used to raise antibodies that specificially bind to the PRO polypeptide, for linking a cariabodise that specificially bind to the PRO polypeptide for inking a transmembrane polypeptide. For Inking a transmembrane polypeptide antibodies are useful for modulating the biological activity of a cell PRO polypeptides. The PRO polypeptide antibodies are useful for modulating the biological activity of conference. The PRO polypeptides or polymorecents are useful for modulating the biological activity of conferences. The PRO polypeptides or polymorecents. The PRO polypeptides or polymorecents. The PRO polypeptides or polymorecents. The properties of a cell expressing PRO polypeptides. The PRO polypeptides or polymorecents. The PRO polypeptides or polymorecents. The PRO polypeptides or polymorecents. The properties of a cell expressing PRO polypeptides. The PRO polypertrophy of meonatal heart. Inhibiting vascular endothelial growth factor (VEGP)-stimulated proliferation of endothelial cells, modulating pulcose or FPA uptake, inducing proliferation of chondrocytes. In particular, these are useful for cells, modulating glucose or FPA uptake, inducing proliferation of disorders or inputies (e.g. loss of sight due to differential disorders or inputies (e.g. loss of sight due to cerinitis prigmantomy or bossity, diabetes hyperinsulary prolymorecents the properties or inputies (e.g. sports minarial or genes which have a role in cell for sometime of antisense RNA hypoisusulates or processor or polymorecents or control of second or second properties or entities of the properties or entities or second properties or entities of the properties or entities with generation of sense as hybridisation properties or subalized with generation of sense and properties are useful in diagnostic assays for Processor or interpolation of properties are useful in diagnostic assays for process, as therapeutically usef
                                                                                                                                                Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
  Kljavin IJ;
Tumas D;
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Hillan KJ,
Stewart TA,
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3.7%; Pred. No. 26;
ve 0; Mismatches
Grimaldi JC, Gurney AL,
In J, Paoni NF, Roy MA,
                                                                                                                                                                                                                                Claim 2; SEQ ID NO 262; 476pp; English.
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Godowski PJ, Grimaldi
Mather JP, Pan J, Pe
William PM, Wood WI;
                                                                                  WPI; 2003-615762/58.
P-PSDB; ADC19109.
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Best Local Similarity
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Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; encoratal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoraceeptor cell; c-fcs; glucose; FRA; chondrocyte; retinal cinsufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hope disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                                               Human secreted/transmembrane protein cDNA, #52.
           ADC34408 standard; cDNA; 1378 BP.
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970S-0059263P-
970S-0062125P-
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970S-0063814P-
970S-0063114P-
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970S-0063120P-
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970S-0063542P.
970S-0063544P.
970S-0063549P.
970S-0063560P.
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97US-0059122P.
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970S-0063704P.
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970S-0063738P.
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97US-0064103P.
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                                                        18-DEC-2003 (first entry)
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                                  ADC34408;
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ADC34408
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                      2983 TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTTCTAATAAAATCCAGTCCTTGT 3042
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97US-0066453P

24-NOV-1997

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RESULT 71

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02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-UJN-2000; 2000WO-US012564.
28-JUL-2000; 2000WO-US012564.
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2000WO-US004414.
2000WO-US005004.
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99US-0146222P.
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18-SEP-2000; 2000US-00665350.
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99WO-US028565
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13-SEP-1999;
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14-SEP-1998;
16-SEP-1998;
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13-OCT-1998;
20-NOV-1998;
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Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; an J, Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI; Ashkenazi A, Botst Filvaroff E, Fong Godowski PJ, Grima Mather JP, Pan J, Williams PM,

#### WPI; 2003-615763/58. P-PSDB; ADC34409.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancers, asthma, rheumatoid arthritis, neurological diseases, and skin diseases.

## Claim 2; SEQ ID NO 262; 478pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or

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polymuclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonatal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated proliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of retinal neurons or rod photoreceptor cells, inducing proliferation and/or recinal neurons or rod photoreceptor cells, inducing proliferation and/or reding glucose or FRA uptake, inducing proliferation and/or reding glucose or FRA uptake, inducing proliferation and/or reding glucose or red uptake, inducing proliferation and/or reding flow of chondrocytes. In particular, these are useful for cells, inducing of chondrocytes in particular, these are useful for retinitis pigmentosum) obesity, diabetes, hyperinsulinaemia, manals. PRO polypeptides and their portions affect the articular printing in mammals. PRO polypeptides and their portions affect the are useful in molecular biology including uses as hybridisation probes for constant in molecular biology including uses as hybridisation probes for one printing and play, for preparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, so probes and for the commands or knockout animals which are useful in the development and for chromosome that mimic the PRO polypeptide (agonists) or prevent the effect of the proteins are useful as molecular marker for protein electrophoresis or useful for tissue typing. PRO polypeptide (agonists) or prevent the effect of immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in agentification of PRO from recombinant cell culture or natural sources. The PRO polypeptide of the invention.

PRO properses, are useful as general properses or serum and for affinity and general p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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I Similarity 53.7%; Pred. No. 26; 
51; Conservative 0; Mismatches 44; Indels 0;
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Best Local Similarity
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RESULT 72 ADC29463

ADC29463 standard; cDNA; 1378 BP

ADC29463;

18-DEC-2003 (first entry)

Human secreted/transmembrane protein cDNA, #52.

Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart, vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; home disorder; cartilage disorder; sport injury; arthitis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic. 

Homo sapiens.

7.14

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97US - 0059121P
97US - 0059182P
97US - 0059263P
97US - 0059266P
97US - 0062285P
97US - 0062285P
97US - 0063285P
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98WO-US019330
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US2003049676-A1.
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99WO-US028214.
99WO-US028313.
99WO-US028301.
99WO-US028564.
99WO-US028565.
                                                                  2000WO-US008439
2000WO-US014042
   99WO-US021090
                                 99WO-US030095
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2000WO-US020710
                                                                                 24-AUG-2000; 2000WO-US023328
18-SEP-2000; 2000US-00665350
                                                                                            (GETH ) GENENTECH INC.
                                                   22-FEB-2000;
24-FEB-2000;
                                                              20-MAR-2000;
                                               11-FEB-2000;
                                                           02-MAR-2000;
                                                                      22-MAY-2000;
                                            05-JAN-2000;
                                 16-DEC-1999;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather UP, Paoni NF, Ann Roy M, Stewart TA, Tumas D; Williams PM, Wood WI; WPI; 2003-585107/55. P-PSDB; ADC29464.

Novel isolated PRO polypeptides e.g. PRO234 (useful for treating rheumatoid arthritis, psoriasis and multiple sclerosis) and PRO187 (useful for treating Alzheimer's disease, cancer).

Claim 2; SEQ ID NO 262; 451pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise and the nucleic acid encoding them. The polypeptides can be used to raise articodies that specifically bind to the PRO polypeptides, for linking a bloactive molecule to a cell expressing a PRO polypeptides are useful for modulating a bloactive molecule to a cell expressing a PRO polypeptides are useful complement of a cell expressing a properties are useful as properties. The PRO polypeptides are useful as plantaceuticals, diagnostics, blosensors or polymented antibodies are useful for modulating the biological activity of a cell expressing a properties. The PRO polypeptides or polymented are useful as pharaceuticals, diagnostics, blosensors or polymented are useful for stimulating hypertrophy of meonatal heart, inhibiting vascular endothelial growth factor (VEGF)-stimulated proliferation of endothelial cells, modulating the proliferation of endothelial cells, inducing proliferation of endothelial cells, inducing proliferation and/or retinal neurons or rod photoreceptor cells, inducing proliferation and/or recing or treating cardiac insufficiency disorders, wounds, cancerous cumours, retinal disorders or injuries (e.g. loss of sight due to detecting or treating cardiac insufficiency disorders, soports injuries or arthritis planents, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides, and their portions affect the expression of genes which have a role in cell death. The polymucleotides are useful in molecular biology including uses as hybridisation probes or conval biology including uses as hybridisation of antimals or knockout animals which are useful in the generation of antisce construction of herspectual procession of penes which have a role energing of therspectuals which are useful in the generation of or the general or recombinantly expressing the protein and for chromosome and gene which are useful energing of thers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rrirgiciararaangaraangarrirrahaggrarrigraaccergceeararer 1331
The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polymoteotides and proteins are useful for tissue typing. PRO antibodies are useful for mimurohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The progress may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polymucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene; ss; PRO; secreted; transmembrane; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1332 ATTTATTCCTCCAATTTCAATAATTATTTATTCT 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane protein cDNA, #52.
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9705-0059113P
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9705-0059121P
9705-0059124P
9705-0059164P
9705-0059266P
9705-0052268P
9705-005228FP
9705-005288P
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18-SEP-1997;
15-OCT-1997;
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17-SEP-1997
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02-DEC-1999; 99WO-US028865. 16-DEC-1999; 99WO-US030095. 20-DEC-1999; 99WO-US030991. 20-DEC-1999; 99WO-US030991. 05-JAN-2000; 2000WO-US030899. 11-FEB-2000; 2000WO-US03865. 22-FEB-2000; 2000WO-US03865. 24-FEB-2000; 2000WO-US03665. 02-MAR-2000; 2000WO-US036841. 9705-00631212 9705-00631217 9705-0063127 9705-0063329 9705-0063342 9705-0063344 9705-0063344 9705-0063344 9705-0063364 9705-0063364 9705-0063364 9705-0063364 9705-0063735 9705-0063735 9705-0063735 9705-0063735 9705-006374 9705-006374 9705-006374 9705-006476 9705-006476 9705-006476 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006645 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 9705-006646 98US-0104080P. 98US-0109304P. 98WO-US025108. 98US-0113296P. 99US-0143048P. 99US-0145698P. 99US-0146222P. 99WO-US020594. 98US-0100858P 98WO-US019437 99WO-US020944 99WO-US028564 98WO-US019330 99WO-US021090 99WO-US028214 99WO-US028313 99WO-US021 20-MAR-2000; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 27-0CT-1997; 28-0CT-1997; 28-0CT-1997; 28-0CT-1997; 16-SEP-1998; 17-SEP-1998; 17-SEP-1998; 28-OCT-1997; 28-OCT-1997; 29-OCT-1997; 29-OCT-1997; 29-OCT-1997; 29-OCT-1997; 31-OCT-1997; 31-OCT-1997; 03-NOV-1997; 21-NOV-1997; 17-NOV-1997; 18-NOV-1997; 14-SEP-1998; 14-SEP-1998; 13-OCT-1998; 20-NOV-1998; 01-DEC-1998; 22-DEC-1998; 13-SEP-1999 15-SEP-1999, 05-OCT-1999 29-NOV-1999 5-NOV-1997 04-JUN-1998 29-OCT-1997 24-NOV-1997 L2-DEC-1997 10-SEP-1998 08-SEP-1999 24-NOV-1997 07-NOV-19 21-NOV-12 eta

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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen I Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI,
                                                                                       Claim 2; SEQ ID NO 262; 470pp; English.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
              (GETH ) GENENTECH INC.
                                                     WPI; 2003-615797/58.
P-PSDB; ADC28995.
                                                                   Novel secrence
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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides cone bused to raise and the nucleic acid encoding them. The polypeptide to raise antibodies that specifically bind to the PRO polypeptide. For linking a bloactive molecule to a cell expressing a PRO polypeptide. The PRO Discrete in the SPO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO perpeptides in PRO PRO PROPERTIES. The PRO PRO PROPERTIES of a cell expressing PRO polypeptide antibodies are useful for modulating the biological activity of polypeptide antibodies are useful for modulating the proliferation of proceedors. These are useful for the survival or proliferation of colymolocytes, enhancing the survival or proliferation of retinal neurons or rod photoreceptor cells, inducing c-fcs in endothelial cells, modulating proliferation of condroverses. In particular, these are useful for cells, modulating proliferation of chondrocytes. In particular, these are useful for cells, modulating proliferation of chondrocytes. In particular, these are useful for cells, modulating proliferation of chondrocytes. In particular, these are useful for cells, modulating proliferation of chondrocytes. Inducing proliferation of chondrocytes. Inducing proliferation of chondrocytes. Inducing proliferation probes cumours, retinal disorders or injuries (e.g. loss of sight due to cells, modulating plucose or FRA uptake, inducing proliferation probes constitution of genes which have a role incells, modulating proliferation of genes which have a role incell proliferation of genes which have a role incell proliferation of genes which have a role incell proliferation of genes which have a role incell proliferation of genes which have a role incell proliferation of the rapeutically useful reagents, as probes and for the combinantly expressing the protein and engagents, as therapeutically useful reagents, 
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Ferrara N;
n ME, Goddard A;
Kljavin IJ;
, Tumas D;
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Best Local Similarity 53.7%;
Matches 51; Conservative
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tissue typing; immunohistochemical staining; gene therapy;
enconatal heart; vascular endothelial growth factor; VEGF; proliferation;
endothelial cell; stimulated T-lymphocyte; retinal neuron;
rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;
cardiac insufficiency disorder; wound; cancer; tumour; retinal
retinitis pigmentosum; obesity; diabete; hyperinsulinaemia;
hypoinsulinaemia; bone disorder; cartilage disorder; sport injury;
arthritis; cardiant; vulnerary; cytostatic; ophthalmological;
osteopathic; antiarthritic; anorectic.
                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; PRO; secreted; transmembrane; therapeutic;
3043 TITITIAAAAAGACITIAAAATTAITAATTICICT 3077
                                             1332 Arriarrecrecaarricaaraarrarriarrici 1366
                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein cDNA, #52.
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9703-005926BP
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970S-0063735P.
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970S-0064215P.
970S-0063870P.
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27-OCT-1
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97US-0064809P. 97US-0065186P. 97US-0065632P. 97US-0066120P. 97US-0066364P. 97US-006646P. 97US-006646P. 97US-006646P. 98WO-US019330. 98WS-0100858P. 98WO-US019437. 98US-0104080P. 98US-0109304P. 99US-0113296P. 99US-0143048P. 99US-0145698P. 97US-0066840P. 97US-0069425P. 98US-0088026P. 98US-0099803P. 98WO-US018824. 2000WO-US003565 2000WO-US004414 2000WO-US005004 2000WO-US005841 98US-0100262P 98WO-US019177 99US-0146222P 99WO-US021090 99WO-US021547 99WO-US028313 99WO-US028301 2000WO-US007377 98WO-US025 22-FEB-2000; 24-FEB-2000; 02-MAR-2000; 20-MAR-2000; 08-DEC-1999; 16-DEC-1999; 20-DEC-1999; -DEC-1999; 30-MAR-2000; 22:MAY-2000; -SEP-1998; -SEP-1998; -SEP-1998; 02-JUN-2000; NOV-1999 -SEP-1998 -NOV-18-NOV-1 21-NOV-1 22-DEC-1 

(GETH ) GENENTECH INC

Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Istluaroff E, Fong S, Gao W, Gerber H, Gerritsen Schowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Wood WJ Williams PM,

2003-708343/67. P-PSDB; ADC40880 Novel PRO polypeptides useful for treating Parkinson's disease, Alzheimer's disease, enterocolitis, Zollinger-Ellison syndrome, psoriasis, epidermoid carcinoma of the vulva and gliomas, gynecological diseases.

Claim 2; SEQ ID NO 262; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides

can the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO potypeptide are useful conflored and the specifically bind to the PRO polypeptides are useful conflored and polypeptides are useful as phanneculicals, diagnostics, biosensors of a cell expressing PRO polypeptides. The PRO polypeptides or conflored antibodies are useful for mediating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or conflored are useful as phanneculicals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of mediating the biological activity of proliferation of endothelial cells, modulating hypertrophy of mediating conflored to proliferation of endothelial cells, modulating che proliferation of endothelial cells, modulating proliferation of endothelial cells, modulating proliferation of conflored cells, modulating proliferation of conflored cells, modulating diucose or FPA upper cells, inducing cries in endothelial cells, modulating proliferation of conflored cells, modulating processor or injuries (e.g., post significantion of conductorial cells, modulating proliferation of conductorial conflored cells, hyperingulation of conductorial cells, modulating of conductorial cells, modulating carried in an endothelial cells, modulating carried conflored cells, hyperingulation of genes which have a role in cell death. The polypoints diagnostics in mannals. PRO polypeptides and their portions affect the are useful in molecular biology including uses as hybridisation probes for convenient and some mapping, in the development and conflored cells, mannals or knockout animals which have a role in cell death. The polypoperide complantly expersing the procein and for themselved conflored cells and polypeptides and procein and procein and procein and procein and procein and procein and procein and procein and procein and procein and procein and procein 2983 TCTATITIACTITAATIGCACTIATITITATIGALTITITCTAATAAAATCCAGTCCTIGT 3042 .; 0 Score 24.6; DB 1; Length 1378; Pred. No. 26; 0; Mismatches 44; Indels 0. Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other; 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366 0.7%; Query Match Best Local Similarity 53.77 Matches 51; Conservative à Db ઠે

ADC19536 standard; cDNA; 1378 ADC19536; RESULT 75 ADC19536 EXEX EXEX EXEX EX

18-DEC-2003 (first entry)

Human secreted/transmembrane protein cDNA, #52.

Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart, vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;

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cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoisusulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic. 970S-0663120P.
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970S-0663128P.
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98US-0109304P. 98WG-US025108. 98US-0113296P. 99US-0143048P. 99US-0146222P. 99WG-US02059. 99WO-US021090, 99WO-US020944 99WO-US023089 99WO-US028214 99WO-US028313 99WO-US028564 99WO-US028565 99WO-US030095 99WO-US030911 99WO-US030999 2000WO-US000219 2000WO-US003565 2000WO-US004414 2000WO-US005841 2000WO-US007377 2000WO-US008439 2000WO-US014042 99WO-US028301 18-SEP-2000; 2000US-00665350 11-FEB-2000; 02-MAR-2000; 20-DEC-1999; 

#### (GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski DJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; William PM, Wood WI,

WPI; 2003-695902/66. P-PSDB; ADC19537. Novel isolated PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis.

### Claim 2; SEQ ID NO 262; 478pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise can tabedies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful cor documents as ample and for modulating a bioactive molecule to a cell expressing a PRO polypeptide are useful cor modulating the biological activity of a cell expressing PRO polypeptide and for linking a collocative molecule to a cell expressing a PRO polypeptide or inking a collocative molecule are useful as pharmaceuticals, diagnostics, biosensors or collocators. These are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polymucleotides are useful for stimulating hypertrophy of neonatal collocations. These are useful for colliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of cells, modulating proliferation of cells, modulating proliferation of cells, modulating proliferation of cells, modulating processor PRA uppake, inducing proliferation and cells, modulating proliferation and chondrocytes, in particular, these are useful for cells, modulating or treating cardiac insufficiency disorders, wounds, cancerous cumours, retinal disorders or injuries (e.g. sports injuries or retinitis pigmentcaum), obesity, diabetes, hyperingulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthitis) in mammals. PRO polypeptides and their portraions affect the expression of genes which have a roll dienthy proliferation of cholypeptides.

98WO-US019330. 98US-0100858P. 98WO-US019437.

98WO-US018824

97US-0066120P 97US-0066364P 97US-0066453P 97US-0066466P

97US-0066511P 97US-0066770P 97US-0066772P 97US-0066840P

24-NOV-1

97US-0064809P 97US-0065846P 97US-0065693P

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17-SEP-1998;
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20-NOV-1998;
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       are useful in molecular biology including uses as hybridisation probes for cDNA library to isolate the full-length PRO cDNA or to isolate other CDNA, in chromosome and gene mapping, in the generation of antisense RNA can DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The process, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO to presented is a gene encoding a PRO plynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VBGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FRA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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Matches 51, Conservative
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Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                        (GETH ) GENENTECH INC.
                                          WPI; 2003-695953/66.
P-PSDB; ADC33985.
                             Ashkenazi A,
Filvaroff E,
Godowski PJ,
Mather JP, Pa
                                      Williams PM,
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RESULT 77 ADC13054 셤 ઠે The invention discloses isolated PRO secreted/transmembrane polypeptides and the mutolist acid encoding them. The polypeptides can be used to taise and the mutolist acid encoding them. The polypeptides for linking a can call with the properties and the modulating the bioactive molecule to a cell expressing a PRO polypeptide. The PRO bloactive molecule to a cell expressing a PRO polypeptides. The PRO polypeptides are useful for modulating the biological activity of polypeptide antibodies are useful for modulating the biological activity of polypeptide antibodies are useful for modulating the biological activity of polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polymolocities are useful for stimulating hypertrophy of mechanic beart, inhibiting vascular endothelial growth factor (VDEP) stimulated broceactors. These are useful for stimulating hypertrophy of mechanic cells, modulating glucose or FRD works, inducing proliferation of retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial endit for cells, modulating glucose or FRD works, inducing proliferation of chondrocytes. In particular, these are useful for cells, modulating glucose or FRD works, inducing proliferation of chondrocytes or insufficiency disporters, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to cells, modulating glucose or FRD works, inducing proliferation probes tumours, retinal disorders or injuries (e.g. loss of sight due to correct the proprint of antibody including uses as hybridisation probes tumours, retinal disorders or injuries (e.g. loss of sight due to correct the proprint of genes which have a role in cell for the proprint and proprints and provides and for the combinant or secondarial with generating transgenic corrections of therapeutically useful reagents, as probes and for the cecombinantly expressing the protain and for chromosome and genetic cells, module defecting and proprints are useful , Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Wood MI, Paoni NF, Roy MA, Stewart TA, Tumas D; wood MI; Novel isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis. Claim 2; SEQ ID NO 262; 476pp; English. 22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
20-MAR-2000; 2000WO-US006843.
30-MAR-2000; 2000WO-US00643.
22-MAY-2000; 2000WO-US014642.
23-JUN-2000; 2000WO-US015264.
24-JUL-2000; 2000WO-US0215264.
24-AUG-2000; 2000WO-US02328.

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0.7%; Score 24.6; D
53.7%; Pred. No. 26;
iive 0; Mismatches
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9-NOV-1
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-743809/70. P-PSDB; ADC13055.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specificially bind to the PRO polypeptide. for linking a cariotative for acid encoding them. The PRO polypeptide for mindoles that specificially bind to the PRO polypeptide. The PRO polypeptide in the PRO polypeptide are useful for acid encoding the PRO polypeptide in PRO polypeptide antibodies are useful for modulating the biological activity of a cell ** PRO polypeptide on the PRO polypeptide antibodies are useful for modulating the biological activity polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides. The PRO polypetides of cells, modulating proliferation of conductoryes. In particular, inducing control proliferation of chocarcoytes. In particular, these are useful for cells, modulating plucose or FRV uptack, inducing proliferation of fhondrocytes. In particular, these are useful for cells, modulating plucose or FRV uptack, inducing proliferation of chocarcoytes. In particular, these are useful for cells, modulating clustering cardiac insufficiancy disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. sports injuries or articular or secondarion of annisense RNA proprisulinaemia, or bone or carrilage disorders, wounds, cancerous centing in proliferation of genes which have a role in cell and proliferation of genes which have useful in the development and construction of therapeutically useful reappets as a probes and for the genetic analysis of individuals with generating control and proved in parellal or modulary or process, as therapeutically useful reapports, or prevent an Novel isolated secreted and transmembrane PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotropic lateral sclerosis, cancer, neuropathies, diabetes and Claim 2; SEQ ID NO 262; 473pp; English. psoriasis. 

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;.

Gaps . 0 Query Match 0.7%; Score 24.6; DB 1; Length 1378; Best Local Similarity 53.7%; Pred. No. 26; Matches 51; Conservative 0; Mismatches 44; Indels 0;

ADC12506 standard; cDNA; 1378 BP ADC12506; RESULT 78 ADC12506

18-DEC-2003 (first entry)

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18-SEP-1997;
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22-FEB-2000;
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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;

WPI; 2003-743881/70. P-PSDB; ADC12507. New secreted transmembrane PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in identifying chromosomes, as chromosome markers, in generating probes and in tissue typing.

# Claim 2; SEQ ID NO 262; 487pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antithodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for inking a tileast one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell expressing PRO polypeptides or polypeptides are useful for stimulating hypertrophy of neonacal polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonacal heart, inhibiting vascular endothelial growth factor (VEGF) stimulated the tilefration of stimulated 1-lymphocytes, enhancing the survival or proliferation of stimulated retinal neurons or rod photoreceptor cells, inducing c-fos in endothelial

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        cells, modulating glucose or FFA uptake, inducing proliferation and/or redifferentiation of chondrocytes. In particular, these are useful for detecting or treating cardiac insufficiency disorders, wounds, cancerous crumours, retinal disorders or injuries (e.g. loss of sight due to cretinitis pigmentosum), obesity, diabetes, hyperinaulinaemia, choose or injuries (e.g. loss of sight due to arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polymuclectides are useful in molecular biology including uses as hybridisation probes or commands in chromosome and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, for generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic commands or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the correction and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis or prevent the effect of those that minit the PRO polypeptide (antagonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for mandomistochemical staining and/or assay of sample fluids. Anti-PRO expression in specific cells, tissues or serum and for affinity continued for membrohies are useful in diagnostic assay for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity or PRO genes may also be used in gene therapy, particularly for replacing a protyce polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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0.7%; Score 24.6; DB 1; Length 1378;
Best Local Similarity 53.7%; Pred. No. 26;
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ADD05061
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                                         2000WO-US005841.
2000WO-US007377.
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                 99WO-US030911
                     99WO-US030999
                                                  30-MAR-2000; 2000WO-US008439.
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20-MAR-2000;
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## (GETH ) GENENTECH INC.

, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Finmaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Wood WI; Ashkenazi A, Filvaroff E, Godowski PJ, Mather JP, P

RESULT 80 ADD0406

#### WPI; 2003-801231/75 P-PSDB; ADD05062.

Novel isolated native PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating enterocolitis, Zollinger-Ellison syndrome.

# Claim 2; SEQ ID NO 262; 474pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO plypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide are useful for modulating the biological activity of a cell expressing a PRO polypeptides. The PRO polypeptide or linking a polypeptide are useful for modulating hypertrophy of neonatal complements. These are useful for stimulating hypertrophy of neonatal heart, inhibiting vascular endothelial growth factor (WEGF) stimulated CC proliferation of endothelial cells, modulating hypertrophy of neonatal complements. There are useful for stimulated T-lymphocytes, enhancing the survival or proliferation of complements. The survival or proliferation of detecting glucose or FRA uptack, inducing proliferation of colls, modulating glucose or FRA uptack, inducing proliferation of detecting of treating cardiac insufficiency disorders, wounds, cancerous cumulated T-lymphocytes, enhancing the survival or proliferation of detecting or treating cardiac insufficiency disorders, ensemble of the colls, inducing proliferation and or cartilage disorders, wounds, cancerous cumulation of theorems of artifactions of sight due to crimitis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders of engage as hybridisation probes or arthuring of thermanian, or bone or cartilage disorders of consecution of genes which have a role in cell death. The polymoched arthuring of thermanian properties and their portions affect the arthuring of thermanian properties and processed in decenting of thermanian properties and provesses, as therapeutic agents, for screening compounds to identify the proteins are useful an engelula m

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antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                           1272 TTTTGTGTATATAAATGTTAATGATTTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
                                                                                                                                                                                                                                                                        Gaps
immunohistochemical staining and/or assay of sample fluids. Anti-PRO
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                                                                                                                                                                                                                                                                                                                                                                                                      3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077
                                                                                                                                                                                                                                                                                                                                                                                                                                              1332 ATTTATTCCTCCAATTTCATAAATTATTTTTTTT 1366
                                                                                                                                                                                                                         0.7%; Score 24.6; D
53.7%; Pred. No. 26;
Live 0; Mismatches
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Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VBGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FRA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; arthritis, cardiant; vulnerary; cytostatic, ophthalmological; osteopathic; antiarthritic; anorectic. Human secreted/transmembrane protein cDNA, #52. BP ADD04067 standard; cDNA; 1378 01-JAN-2004 (first entry)

#### Homo sapiens.

US2003104381-A1.

#### 05-JUN-2003.

11-JUL-2001; 2001US-00903823

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GETH ) GENENTECH INC

Ferrara N; ME, Goddard A; Kljavin IJ; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goodowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas Williams PM, Wood WI; WPI; 2003-801226/75. P-PSDB; ADD04068. 

Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher Syndrome.

Claim 2; SEQ ID NO 262; 487pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucleic acid encoding them. The polypeptides can be used to raise and the mucleic acid encoding them. The polypeptides for linking a bioactive molecule to a cell expressing a PRO polypeptide for modulating a bioactive molecule to a cell expressing a PRO polypeptide are useful for detecting other PRO polypeptides are useful for modulating the biological activity of a cell PRO polypeptides of the properties are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides of a cell expressing PRO polypeptides in a sample and for linking a confidence are useful for modulating the proliferation of polymentides are useful for modulating the proliferation of conducting the confidence of a cell expressing PRO polypeptides. The PRO polypeptides of polymentides or polymuclectides are useful for scientific properties or red photococceptor cells, modulating proliferation of conducting glucose or FRA uptack, inducing proliferation of chonduccytes. Enaminated or red photococceptor cells, modulating proliferation of chonduccytes. In particular, these are useful for cells, modulating proliferation of chonduccytes. In particular, these are useful for cells, modulating proliferation of chonduccytes. In particular, these are useful for cells, modulating plucose or FRA uptack. Inducing proliferation of chonduccytes or injuries (e.g. loss of sight due to creinitis pigmentosum), obesity, diabetes hyperitacis in molecular bloody including uses as hybridisation probes or retinitis pigmentosum, or bone or cartilinge disorders wunds, cancerous retinitis pigmentosum, or bone or cartilinge and their portions affect the combas, in chromosome and gene mapping, in the generation of annisens RNA minic the inforduction of solate the full-ingeth RNA in thromosome and gene mapping, in the generation of the red in the process of the process of the process of the process of the process of the process of the process of the p

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated native PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating enterocolitis, Zollinger-Ellison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski DJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood WI;
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tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; redothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fcs; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hypoinsulinaemia; house disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritis; anorectic.
                                                                                                                             transmembrane; therapeutic;
                                                                                                       Human secreted/transmembrane protein cDNA, #52
                                         ADD03643 standard; cDNA; 1378 BP
                                                                                                                             secreted;
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9705-0059113P
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                                                                                  (first entry)
                                                                                                                            Human; gene; ss; PRO;
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for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a RPO polypeptide. The PRO polypeptide antibodical activity of bioactive molecule to a cell expressing the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or considerable are useful as pharaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of meanal consideration of endothelial growth factor (VBGP)-stimulated proliferation of endothelial growth factor (VBGP)-stimulated proliferation of endothelial growth factor (VBGP)-stimulated proliferation of endothelial growth factor (VBGP)-stimulated collis, modulating glucose or FRA uptake, inducing proliferation of fordatoryes. In particular, these are useful for elinal neurons or rod photoreceptor cells, inducing proliferation of chordrocytes. In particular, proliferation and/or rectinal neurons or rod photoreceptor cells, inducing proliferation of chordrocytes. In particular, proliferation and/or cells, modulating glucose or FRA uptake, inducing proliferation of chordrocytes. In particular, proliferation and/or cells, modulating glucose or cartilage disorders, wounds, cancerous cummunities of some or cartilage disorders (e.g. joss of sight due to rethinist planemia, or bone or cartilage disorders (e.g. sports injuries or rethinitis) in molecular biology including uses as hybridistation probess for cDNA library to isolate the full-length PRO cDNA or to isolate other CDNAs, in chromosome and gene mapping, in the generation of antisense RNA animals without are useful in the development and screening of therapeutically useful reagents, as probes and for the generation of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for the proteins are useful as molecular marker for protein strengent or specific and produces, as therapeutic agents, for screening compounds to identify the proteins are useful in diagnostic assays for P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1272 TTTGGGTATATAAAGGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
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osteopathic, antiarthritic, anorectic. 97US-0059113P. 97US-0059115P. 97US-0059117P. 97US-0059113P. 97US-0059121P. 97US-0059184P. 97US-0059263P. 97US-0059266P.

ADE34895;

RESULT 82 ADE34895 ID ADE3

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise can intiodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating a confident that specifically upperides in a sample and for linking a conformation other PRO polypeptides in a sample and for inking a conformation other PRO polypeptides are useful conformation for linking a conformation of a cell expressing a PRO polypeptides or conformation of a cell expressing a PRO polypeptides or conformation of a cell expressing a properties or conformation of a cell expressing a properties or conformation of solvential as pharmaceuticals, diagnostics, biosensors or polymucleotides are useful for simulating hypertrophy of neonatal conformation of endothelial growth factor (VEGP)-stimulated proliferation of conformation of stimulated T-lymphocytes, enhancing the survival or proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of conformation of conformation of conformation of conformation of chondrocytes. In particular, these are useful for cells, modulating glucose or FPA uptake, inducing proliferation and/or reciting or treating cardiac insufficiency disorders, wounds, cancerous cumpurs, retinal disorders or injuries (e.g. loss of sight due to rethintis pigmentosum), obesity, diabetes, hyperinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or arthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polymucleorides conformation of molecular biology including uses as hybridisation probes for conformation and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara N;
n ME, Goddard A;
Kljavin IJ;
Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated PRO polypeptides e.g. PRO245 and PRO1868, useful for treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, ElYaxoff E, Fong S, Gao W, Gerber H, Gerritsen Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,
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animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (agonists). The polymucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant coll culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a collumnicative gene and procession as a sequence of presented is a gene encoding a PRO 2983 ICTAITITACTITAATIGCACTIATITITATIGATTITICTAATAAATCCAGTCCTIGT 3042 1272 irringigiararaaangrraangaririnahaggraringraaccergcccacararerr 1331 Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; beneatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal retinitis pigmentosum; obesity; diabete; hyperinaulinemia; hypoinsullinaemia; hone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritis; anorectic. Gaps ; 0 DB 1; Length 1378; Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other; 44; Indels 3043 TITITIAAAAAGACTITAAAAATTATTAATTTCTCT 3077 1332 atitratrecrecaatiteaaraaatitaritarier 1366 Human secreted/transmembrane protein cDNA, #52. 0.7%; Score 24.6; D. 53.7%; Pred. No. 26; Ative 0; Mismatches polynucleotide of the invention. ADE79340 standard; cDNA; 1378 97US-0059113P. 97US-0059117P. 97US-0059117P. 97US-0059121P. 97US-0059122P. 97US-0059124P. 97US-0059264P. 97US-006212SP. 97US-006212SP. 12-JUL-2001; 2001US-00904992 29-JAN-2004 (first entry) Conservative Similarity US2003135025-A1. Mac. Local Sim. 51; C Homo sapiens. 15-OCT-1997; 17-OCT-1997; 17-OCT-1997; 17-JUL-2003. 7-SEP-1997 7-SEP-1997 .7-SEP-1997 .7-SEP-1997 .7-SEP-1997 8-SEP-1997 17-SEP-1997 .8-SEP-1997 ADE79340; Query Match RESULT 83 ADE79340 datches a à ò 셤

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28-0CT-1
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22-MAY-2000; 2000WO-US014042.
02-UTN-2000; 2000WO-US015564.
28-UUL-2000; 2000WO-US020710.
24-MUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00665350.
               (GETH ) GENENTECH INC.
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Ä Ferrara N;
ME, Goddard R Kljavin IJ;
Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, F Filvaroff B, Fong S, Gao W, Gerber H, Gerritsen M Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, K Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Williams PM, Wood WI,

### WPI; 2004-031331/03. P-PSDB; ADE79341.

New nucleic acid encoding a PRO polypeptide, for producing a recombinant PRO polypeptide and for treating e.g. cancer, infertility, kidney disorders, and cardiac disfunctions.

# Claim 2; SEQ ID NO 262; 473pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide. For linking a bloactive molecule to a cell expressing a PRO polypeptide. For linking a bloactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptides or linking a propagation of the processing PRO polypeptides. The PRO polypeptides or linking a propagation of a cell expressing PRO polypeptides. The PRO polypeptides or the process of a cell expressing PRO polypeptides. The PRO polypeptides or polymucleotides are useful for modulating the proliferation of polymeropy or neonateral beart inhibiting vascular endochalial growth factor (VBGP) estimulated proliferation of condothelial cells, modulating the proliferation of chondrocytes. Inhuriting proliferation of chondrocytes. Inhuriting proliferation of chondrocytes. Inhuriting proliferation of chondrocytes. Inhuriting proliferation of chondrocytes. Inhurities proliferation of chondrocytes. Inhurities proliferation of chondrocytes. Inhurities or retinities pigmentosum), obesity, dishetes, hyperities, are useful for expression of genes which have a role in cell propried the control of antisense or extrating propried and their portions affect the arbitries provided the propression of genes which have a role in cell of sorters or inhurities (e.g. sports injuries or control of sorters or broad or carrilage disorders wounds, cancerved to control of sorters or propried in the development and sorten broad the properties of the properties are useful in the development and content and bub, to preparating PRO polypeptides, for generation of antisense RNA combinantly versesing the protein and for control in the development and second properties are useful in diagnostic assays for PRO e.g. detecting its econ

# Sequence 1378 BP; 235.A; 461 C; 412 G; 270 T; 0 U; 0 Other;

Gaps ö 0.7%; Score 24.6; DB 1; Length 1378; 53.7%; Pred. No. 26; ive 0; Mismatches 44; Indels 0; Conservative Query Match Best Local Similarity Matches 51; Conserv

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New PRO nucleic acid, useful for manufacturing a medicament for diagnosing or treating tumor or for tissue typing.
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Filvaroff E, Fong S, Gao W, Gerber H, Gerriteen S
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA,
Williams PM, Wood WI;
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           970S-0064809P-970S-0064208P-970S-0064809P-970S-0065846P-970S-0065846P-970S-0065631P-970S-0066453P-970S-0066453P-970S-0066453P-970S-0066453P-970S-0066472P-970S-0066472P-970S-0066472P-970S-006942B-980S-00098026-980S-010019433-980S-010019433-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-980S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-010019437-990S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01001943-9-90S-01
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P-PSDB; ADE79765.
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1272 İTTTGİGİATATAAAİGTTAATGATİTTİATAĞGİATİTĞIAACCCTGCCĞĞCATATÇTT 1331
                                                                                                                                                                                                                                                                                                          Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; tosonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FRA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartialege disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
                                                                           3043 TITITIAAAAAGACIITAAAATIAITAATITCECT 3077
                                                                                             Human secreted/transmembrane protein cDNA, #52.
                                                                                                                                                                                     ADE79764 standard; cDNA; 1378 BP.
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9705-0062814P
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9705-0063120P
9705-0063121P
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97US-0062125P.
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Ferrara N; 1 ME, Goddard A; Kljavin IJ; Tumas D;

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the mucled caid encoding them. The polypeptides can be used too raise antibodies that specifically bind to the PRO polypeptide, for linking a bind the mucled caid encoding them. The polypeptides for modulating at a teast one biological activity of a cell. PRO polypeptides are useful for modulating the biological activity of a cell. PRO polypeptides are useful for similarial propertopes, biosensor of polypeptides are useful for similarial propertopes, biosensor or biological are useful for similarial propertopes, biosensor or biological are useful for similarial propertopes, biosensor or bioractors. These are useful for similarial propertopes, biosensor or bioractors. These are useful for similarial prover factor (VEGP)-stimulated propertopes, cancer or beart, inhibiting vascular endothelial growth factor (VEGP)-stimulated T-lymphocytes, enhancing the survival or proliferation of crimulated T-lymphocytes, enhancing the survival or proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of criminal neurons or robe propertor cells, inducing proliferation of criminal glorders or injuries (e.g. loss of sight due to differentiation of chondrovtes. In particular, these are useful for retaining cardiac insifficancy disorders, wounds, cancerous cumours, retinal sorders or injuries (e.g. loss of sight due to rethinitis pignemicsum), obesity, diabetes, hyperinsillinaemia, or bone or azarilage disorders (e.g. sports injuries or artilage disorders (e.g. sports injuries or expension of genes which have a role in cell death. The polymucleotides are useful in molecular biology including uses as hybridistation probes con the DNA, for preparing PRO polypeptides, for generating transgence or the processing the process and their portions and polymphase or induced analysis of individuals with genetic disorders as well as minerally expressing the procein marker for proteins are useful as molecular marker for proteins are useful as
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1272 iringigianaiaaangniangahiririanaggiaririghaccengceeacararer 1331 Gaps , 6 0.7%; Score 24.6; DB 1; Length 1378; 53.7%; Pred. No. 26; 0; Mismatches 44; Indels 3043 TTTTTAAAAAGACTTTAAAATTATTAATTTCTCT 3077 1332 ATTTATTCCTCCAATTTCAATAAATTATTTATTCT 1366 51; Conservative Query Match Best Local Similarity g ò

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Human, gene; ss; PRO; secreted; transmembrane; therapeutic;
tissue typing; immunohistochemical staining; gene therapy;
neonatal heart; vascular endothelial growth factor; VEGF; proliferation;
                                                                                      Human secreted/transmembrane protein cDNA, #52.
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ADE73440 standard; cDNA; 1378

RESULT 85 ADE73440 (first entry)

29-JAN-2004 ADE73440;

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endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
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9708-0065846P-
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9708-0066124P-
9708-0066466P-
9708-006646P-
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                                                                        Homo sapiens
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98WO-US025108
98US-0113296P.
99US-0143048P.
99US-0145698P.
99US-0146222P.
    98WO-US019437.
98US-0104080P.
98US-0109304P.
                                                                  99WO-US028214.
99WO-US028313.
99WO-US028301.
                                               99WO-US020944
                                                             99WO-US023089
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99WO-US030095
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05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
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24-FEB-2000;
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02-JUN-2000;
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              20-NOV-1998
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Ferrara N; ME, Goddard A; Kljavin IJ; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddi Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin I. Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Pan J, Paoni NF, Wood WI; Mather JP, Pa Williams PM,

## WPI; 2004-020333/02. P-PSDB; ADE73441.

New nucleic acids encoding polypeptides designated PRO have sequence identity to various secreted proteins and transmembrane proteins and are useful in molecular techniques and as therapeutic agents.

# Claim 2; SEQ ID NO 262; 474pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for modulating a pleactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptides are useful for modulating the biological activity of a cell expressing a PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing a PRO polypeptides or polypeptides are useful for stimulating the biological activity of a cell expressing PRO polypeptides or polymuclectides are useful for stimulating hypertrophy of neonatal colliferation of bioreactors. These are useful for stimulating hypertrophy of neonatal colliferation of endothelial cells, modulating the proliferation of stimulated T-lymphocytes, enhancing the survival or proliferation of conditions or relia, inducing c-fos in endothelial cells, modulating proliferation and/or recipieration of chondrocytes. In particular, these are useful for cells, inducing c-fos in endothelial cells, modulating orbitical cardiac insufficiency disorders, wounds, cancerous tumours, retinal disorders or injuries (e.g. loss of sight due to bypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or hypoinsulinaemia, or bone or cartilage disorders (e.g. sports injuries or

carthritis) in mammals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polynucleotides are subtrained probes for connain in molecular biology including uses as hybridisation probes cor connain in molecular biology including uses as hybridisation probes con the connain in the connain and contained the propertial propertials. For generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic continuals or knockcut animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the screening of therapeutically useful reagents, as probes and for the screening of the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify the PRO polypeptide (agonists). The polymucleotades and proteins are useful for tissue typing. PRO antibodies are useful for tissue typing. PRO antibodies are useful for tissue typing and/or assay of sample fluids. Anti-PRO immunohistochemical staining and/or assay for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity countification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polypeptide of the invention. 

Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;

3042 1272 TTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331 Gaps ; DB 1; Length 1378; 44; Indels 3043 TITITIAAAAAGACTITAAAATTATTAATTTCTCT 3077 1332 ATTTATTCCTCCAATTCAATAATTATTTATTCT 1366 ch 0.7%; Score 24.6; DB Similarity 53.7%; Pred. No. 26; 51; Conservative 0; Mismatches Query Match Local Best Loca Matches g à ઠ

RESULT 86

ADE73975 standard; cDNA; 1378 BP.

ADE73975;

(first entry) 29-JAN-2004

Human secreted/transmembrane protein cDNA, #52.

Human; gene; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; enconateal heart; vascular endothelial growth factor; VBGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoraceeptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; bone disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.

Homo sapiens.

US2003148370-A1

07-AUG-2003

13-JUL-2001; 2001US-00904838

17-SEP-1997; 17-SEP-1997; 17-SEP-1997;

97US-0059113P. 97US-0059115P. 97US-0059119P. 97US-0059121P. 97US-0059121P.

17-SEP-1997; 17-SEP-1997; 17-SEP-1997; 

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9705-0059184P.
9705-0059265P.
9705-0052285P.
9705-0062287P.
9705-0062287P.
9705-0063144P.
9705-00631120P.
9705-00631120P.
9705-0063122P.
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97US-0066770P.
97US-0066772P.
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97US-0069425P.
98US-0088026P.
98US-0099803P.
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98US-0109304P.
98WO-US025108.
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99US-0143048P.
99US-0145698P.
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98US-0100858P.
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07-JUL-1999;
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05-OCT-1999;
29-NOV-1999;
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11-FEB-2000; 2000WO-US003555. 22-FEB-2000; 2000WO-US003565. 24-FEB-2000; 2000WO-US0056414. 20-MAR-2000; 2000WO-US005841. 20-MAR-2000; 2000WO-US00843. 20-MAR-2000; 2000WO-US00843. 21-MAY-2000; 2000WO-US01264. 28-JUN-2000; 2000WO-US01264. 28-AUG-2000; 2000WO-US01264. 28-AUG-2000; 2000WO-US012564. 28-AUG-2000; 2000WO-US012564. 

(GETH ) GENENTECH INC.

Ferrara N; n ME, Goddard A; Kljavin IJ; Tumas D; Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, F Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen M Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, K Mather JP, Pan J, Beoni NF, Roy MA, Stewart TA, Williams PM, Wood WI; Mather JP, Pe Williams PM,

WPI; 2004-020440/02. P-PSDB; ADE73976.

Isolated secreted and transmembrane PRO nucleic acids and the proteins they encode, e.g. PRO245, PRO269 and PRO1868, useful for preventing, diagnosing and treating e.g. disorders relating to blood coagulation.

Claim 2; SEQ ID NO 262; 1pp; English.

defective gene. The sequence polypeptide of the invention. 9

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1 TCGGTACCTGTTAAATCTTGTGAATCTAATCCTTGTCTTAATGGAGGATCTTGTAAAGAT
                                                                                                                              AAA31550;
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                                                                                 3042
                                                                                                     1272 TTTTGTGTATATAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid substitutions were designed in the growth factor domain of tissue plasminogen activator (tPA) with the goal of disrupting possible specific receptor interactions. Oligonuclectides (AAT27589-25) encoding the growth factor region replacement domains A-D (AAR96224-27) were generated from 14 different oligonuclectides. Fragment B results in replacement of tPA amino acids 52-91 with the entire growth factor region of human Factor IX. Mutant tPAs were expressed in BHX cells and characterised for plasma half life and fibrin binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid plasminogen activator comprises human tPA activator and N-terminal crosslinking domain from alpha2-plasmin inhibitor - useful to treat thrombosis and image blood clots.
                                                                                2983 TCTATTTTACTTTAATTGCACTTATTTTTATTGATTTTTTCTAATAAAATGCAGTCCTTGT
                                                        Gaps
                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; tPA; alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting; protein engineering; growth factor domain; Factor IX; ds.
                                                        ;
0
                                 DB 1; Length 1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24.2; DB 1; Length 132; Pred. No. 17; 0; Mismatches 43; Indels
          Sequence 1378 BP; 235 A; 461 C; 412 G; 270 T; 0 U; 0 Other;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 132 BP; 39 A; 15 C; 28 G; 50 T; 0 U; 0 Other;
                                                        44;
                                                                                                                                                   1332 ATTTATTCCTCCAATTTCAATAATTATTTATTCT 1366
                                                                                                                             3043 TTTTTTAAAAGACTTTAAAATTATTATTTCTCT 3077
                                O.7%; Score 24.6; DB Similarity 53.7%; Pred. No. 26; 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                Novel growth factor domain fragment B DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Fig 15; 35pp; English.
                                                                                                                                                                                                             AAT27590 standard; DNA; 132 BP.
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Best Local Similarity 53.8%;
Matches 50; Conservative (
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                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-187699/19.
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28-JAN-1992;
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06-AUG-1996
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                                                        51;
                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foster DC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868 ACCAGTAATGCTGAAGAGGTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCAGACATGGCGGAGGGCTGCACCTGAAGGGGACGATGAAGGCCCACACGGACATGGT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New plant microsatellite markers and associated flanking species for the detection of polymorphic genetic markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
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2975 TTACTTATTCTATTTTACTTTAATTGCACTTAT 3007
                                                                   GATATTAATTCATATGAATGTTGGTGTCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FOREST LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant microsatellite marker #511.
                                                                                                                                                                                                                                              AAA31550 standard; DNA; 260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-NZ000092.
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis.
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RESULT 89 ABX42370/c

260 TGCTTCCAAAATTCAGTAGTTTTCTCAGTGTTTTCAAAAACTTGTCGTGCTTCTTCAAAA 201

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Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                      3ovine EST associated with lactation/muscle/fat deposition #7535.
ABX42370 standard; cDNA; 361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1999; 99US-0115707P.
                                                                                           20-FEB-2003 (first entry)
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WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                    JS2002137139-A1.
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                                             ABX42370;
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Mathialagan N, Tao N, Warren WC;

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Claim 2; SEQ ID NO 7535; 245pp; English

The invention relates to a purified nucleic acid molecule associated with catcation or muscle and fat deposition (designated LMFD), derived from catcation or muscle acid can specifically hybridise to a second nucleic acid can specifically hybridise to a second nucleic acid comprising an upper file of them. Also included are acid a transformed cell having a nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid comprising an LMFD nucleic acid dinked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule. On the molecule; and (b) detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for level or pattern of the molecule in a bovine cell or tissue. The molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the listue sequence was not shown in the specification but was obtained in celectronic format from the upporton=20020137139

Sequence 361 BP; 117 A; 62 C; 83 G; 99 T; 0 U; 0 Other;

.. Query Match 0.7%; Score 23.6; DB 1; Length 361; Best Local Similarity 54.7%; Pred. No. 33; Matches 47; Conservative 0; Mismatches 39; Indels (

2919 TACTIATITIAAITITIGGGAITITIAACIAITICTICAAIGACTIGIAITICIAAIAITIAC 2978

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Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                                         Colon tumour related determined cDNA sequence for clone R0096:E09
2979 TTATTCTATTTACTTTAATTGCACT 3004
             200 Gracarrrrrrrrrrrrrrrand
                                                 AAI29377 standard; cDNA; 596 BP
                                                                                                                                                                                   30-DEC-1999; 99US-00476296.
10-7M-2000; 2000US-0048031.
15-FEB-2000; 2000US-00504629.
06-MAR-2000; 2000US-0057251.
19-MY-2000; 2000US-0057251.
29-UIN-2000; 2000US-00609448.
28-AUG-2000; 2000US-00609448.
                                                                                                                                                                      29-DEC-2000; 2000WO-US035596.
                                                                            12-OCT-2001 (first entry)
                                                                                                                                          WO200149716-A2.
                                                                                                                              Homo sapiens.
                                                                                                                                                        12-JUL-2001.
                                                              AA129377;
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Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer. Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA; King GE, Wang T, Jiang Y; WPI; 2001-441847/47.

(CORI-) CORIXA CORP.

Claim 2; Page 390-391; 472pp; English.

The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity.

(I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of context of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCA) and hybridisation assays to detect and quantitate the presence of similar or nucleic acids in samples, and therefore which patients may be in need of cantibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) and stays to identify modulators of TCAP carbession and activity. Anti-(I) and activity. The anti-(I) antibodies may also be used as antigonists may also be used to down regulate TCAP expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of TCAP in samples (e.g. by enzyme linked immunosofbalt assay to the nucleotide and amino acid sequences given in the exemplification of the present invention

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Gaps

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81;

Mismatches

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Conservative

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85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes compounds (I) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or. expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; (6) a method for development of cancer in a patient. (1) have immunostimulant and cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t H, Benson DR, Meagher MJ, Stolk JA;
CL, King GE, Wang A, Clapper JD, Skeiky YAW;
Carter D;
                                                                                                                                                                                                                                                                                                                                  colon cancer; colon tumour; immunotherapy; diagnosis; cancer; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
                                                                                                                                      101 TGCAGGAGGCAGATGGGCCGGATGTAGCGGGAGAAGGTGATGGGTCTGCTGAGTTGGAG
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                     DB 1; Length 596
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Pred. No. 42;
Sequence 596 BP; 106 A; 172 C; 212 G; 105 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                           Human colon tumour cDNA for clone R0096:E09 SEQ ID NO:931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 596 BP; 106 A; 172 C; 212 G; 105 T; 0 U; 1 Other;
                                            Indels
                                            81;
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49.4%; Pred. No. 42;
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                                                                                                                                                                                                                                        ABZ33563 standard; cDNA; 596
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03-AUG-2001; 2001US-00922217.
19-DEC-2001; 2001US-00025380.
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41 GECCACATGACCCCAGCCAGTGACAGTGCAGTGGAGGCCGTTGGGGAAGGAGGCGTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial Human NOV14a DNA sequence, 162662716.
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; 2001US-0260831P.
; 2001US-0272338P.
; 2001US-0274876P.
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28-FEB-2001;
09-MAR-2001;
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10664775-2.rng

fusion gene with a human serine protease catalytic domain from the

present invention

Sequence 1142 BP; 235 A; 360 C; 303 G; 244 T; 0 U; 0 Other;

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2619

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Gaps

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81; Indels

DB 1;

Score 23.4; Di Pred. No. 50; 0; Mismatches

ch 0.7%; il Similarity 49.4%; 85; Conservative

Query Match Best Local Similarity

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blood disorders, AIDS, diabetes, obesity, asthma, IgA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activation construct; catalytic; fusion gene; expression vector; proteolysis; serine protease; zymogen precursor; characterisation; analysis; modulator; identification; ds.
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                                                                                                                                                                                                 DB 1; Length 882;
                                                                                                                                         Sequence 882 BP; 165 A; 303 C; 254 G; 160 T; 0 U; 0 Other;
                                                                                    wasting disorders associated with chronic diseases
                                                                                                                                                                                                                                                  0; Mismatches 81;
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                                                                                                                                                                                              Score 23.4;
Pred. No. 47
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                                                                                                                                                                                           0.7%;
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                                                                                                                   Expression vector; zymogen precursor; serine protease; prostasin; professe; inflammation; reproduction; epidermal tissue; skin care; neurological tissue; laundry detergent; stain-removing solution; protactin; protease Ek; ds.
                                                                                         Nucleotide sequence of catalytic domain in CFEK2-6XHIS-TAG.
                                                                                                                                                                                                                                                  /*tag= b
/note= "chymotrypsinogen presequence"
                                                                                                                                                                                                     Location/Qualifiers
13. .972
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                                                                                                                                                                                                                                                                        162. .951
/*tag= c
/note= "prostasin"
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RESULT 94
AAF55268/c
ID AAF55268 standard; DNA; 1142 BP.
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                                                                                                                                                                                                                                                                                                                                                                                             99US-00386642
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P-PSDB; AAB67541.
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                                                                       29-MAY-2001
                                                                                                                                                                                                                                        sig_peptide
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                                                                                                                                                                               Synthetic
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                                                AAF55268;
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The present invention describes an expression vector (I) comprising in frame and in order, a presequence, a prosequence, and a cloning site for the in frame insertion of catalyric domain cassette. (I) can be used as a modulator of proteins expressed from a zymogen activation construct. The recombinant catalytic domain of serine protease is useful for identifying compounds modulating the activation of proteases is expressed and activated from the zymogen activation construct. A method from the present invention comprises combining a modulator of the recombinant catalytic domain of a protease and measuring an effect of the modulator on the protein preferably inhibiting or enhancing its enzymatic activity or stimulation or inhibition of proteolysis mediated by the expressed catalytic domain. The present sequence represents a specifically claimed

Expression vector for producing recombinantly producing serine protease domains, comprising a presequence, a prosequence, and a cloning site for the insertion of catalytic domain cassette.

WPI; 2000-687533/67.

Claim 7; Page 40-41; 89pp; English.

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2679
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precursors of serine proteases (e.g. prostasin) in a highly controlled and reproducible fashion. The expression vector comprises, in frame and in order, a pre-sequence and a cloning site for in frame insertion of a catalytic domain cassette. The expression vectors of the invention are useful for the expression of heterologous inactive zymogen proteases that can subsequently be proteolytically processed to generate the active enzyme product. The active enzyme produce can be useful for directly treating diseases associated with inflammatory, reproductive, epidermal or neurological tissue or for identifying modulators of protease activity which can be used for treatment. The proteases can also be used in commercial products, e.g. laundry detergents stain-removing solutions and skin care products. The present sequence represents the encodes a prostasin protease sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; NOV14b; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiaethmatic; Deprocropic; Hepstortopic; Neuroprotective; Nootropic; Antibacterial; Nortopic; Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis; arthritis; AIDS; diabetes; chesity; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; prostasin-like protein; chromosome 16; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                               2620 GGCAGGAGAGAAGGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          477 recadedesecedaredesecedareradededadamentalidaererecidadricad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2680 G-----ACGIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAGGGAGG 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTGCAATGTCGCCCTGGGAGCCTCCTGGAGCTAGCTGGGGTGGGGATG 366
                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                     0.7%; Score 23.4; DB 1; Length 1142; 49.4%; Pred. No. 50; ive 0; Mismatches 81; Indels 6
                                                                                                                                                                                                                                                                                   Sequence 1142 BP; 235 A; 360 C; 303 G; 244 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NOV14b, prostasin-like protein, coding sequence.
                                                                                                                                                                                                                                                                                                                                                        81;
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1. .1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "NOV14b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN85393 standard; DNA; 1161 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0260417P.
2001US-0260831P.
2001US-0272338P.
2001US-0274876P.
2001US-0284704P.
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                                                                                                                                                                                                                                                                                                                                      Local Similarity 49.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2001;
28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001;
18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-0CT-2002
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                                                                                                                                                                                                                                                                                                                         Query Match
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The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-sessociated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IGA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOV14b is a prostasin-like protein, and the NOV14b coding sequence localises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619
                                                                                                                                                                                                    useful for preventing or
inflammation, or
tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678 rockodoadeckoardedeccodaroraccodadaaderoardardegercrocroadaderroard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 égéckacaridacéccadeccagnéacagnecagnegagecécconnegeaaggagegenridec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activation construct PFEK2-6XHIS-TAG fusion gene vector SEQ ID NO:7.
                                                                ¥.
                              Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM; Arglor S, Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K; Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G; Gunther E, Stone DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGG 2725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activation construct; catalytic; fusion gene; expression vector; proteolysis; serine protease; zymogen precursor; characterisation; analysis; modulator; identification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.4; DB 1; Length 1161;
Pred. No. 51;
0; Mismatches 81; Indels 6;
                           Shenoy S, Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1161 BP; 219 A; 349 C; 364 G; 229 T; 0 U; 0 Other;
                                                                                                                                                                                                    NOVX polypeptides and encoding polynucleotides, treating NOVX-associated disorders e.g. cancer, Alzheimer's disease, and in chromosome mapping,
                                                                                                                                                                                                                                                                                        Claim 9; Page 99; 358pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC87795 standard; DNA; 1169 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%;
ilarity 49.4%;
Conservative
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CURAGEN CORP
                                                                                                                                                   2.002-590674/63.
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                        pharmacogenomics.
                                                                                                                                                   WPI; 2.002-590674/
P-PSDB; ABB98416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 16
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13-APR-2000; 2000WO-US009973

WO200066709-A2

09-NOV-2000,

99US-00303162

30-APR-1999;

10664775-2.rng

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Expression vector for producing recombinantly producing serine protease domains, comprising a presequence, a prosequence, and a cloning site for the insertion of catalytic domain cassette.
                        Qi J, Andrade-Gordon P;
       (ORTH ) ORTHO-MCNEIL PHARM RES INC.
                                                                                         Claim 7; Page 39-40; 89pp; English
                                       WPI; 2000-687533/67
                        Darrow A,
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The present invention describes an expression vector (I) comprising in frame and in order, a presequence, a prosequence, and a cloning site for the in frame insertion of catalytic domain cassette. (I) can be used as a modulator of proteins expressed from a zymogen activation construct. The recombinant catalytic domain of serine protease is useful for identifying compounds modulating the activity of proteases is expressed and activated from the zymogen activation construct. A method from the present invention comprises combining a modulator of the recombinant catalytic domain of a protease and measuring an effect of the modulator on the strimulation or inhibiting or enhancing its enzymatic activity or stimulation or inhibition of proteolysis mediated by the expressed catalytic domain. The present sequence represents a specifically claimed fusion gene with a human serine protease catalytic domain from the

Sequence 1169 BP; 248 A; 358 C; 313 G; 250 T; 0 U; 0 Other;

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2679
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                                                                         564 GGCCACATGACCCCAGCCAGTGACAGTGCAGTGGAGGCCGTTGGGGAAGGAGGCGTTGGC
                                                                                                                                               2620 GGCAGGAGAGAAGGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG
                                                                                                                                                                                  504 TGCAGGGAGGCAGATGGGCCGGATGTAGCGGGAGAAGGTGATGAGGTCTGCTGAGTTGGAG
                                                                                                                                                                                                                    2680 G-----ACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGG 2725
                                                                                                                                                                                                                                          , 9
0.7%; Score 23.4; DB 1; Length 1169; 49.4%; Pred. No. 51;
                                    0; Mismatches
                                      85; Conservative
               Best Local Similarity
Matches 85; Conserv
 Query Match
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Nucleotide sequence of catalytic domain in PFEK2-6XHIS-TAG
5267/c
AAF55267 standard; DNA; 1169 BP.
                                                                                                 (first entry)
                                                                                               29-MAY-2001
                                                      AAF55267;
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Expression vector; zymogen precursor; serine protease; prostasin; protease; inflammation; reproduction; epidermal tissue; skin care; neurological tissue; laundry detergent; stain-removing solution; prolactin; protease EK; ds.

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/*tag= a
13..99
13..99 b
/note= "chymotrypsinogen presequence"
190..972
/note= "prostasin"
                                                                 Location/Qualifiers
13. .999
                                                                             sig_peptide
                                                                                         mat_peptide
                                                         Synthetic
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through limited proteolysis, the activation of expressed zymogen through limited proteolysis, the activation of expressed zymogen precursors of serine proteases (e.g. prostasin) in a highly controlled and reproducible fashion. The expression vector comprises, in frame and in order, a pre-sequence, a pro-sequence and a cloning site for in frame in order, a pre-sequence, a pro-sequence and a cloning site for in frame invention are useful for the expression of heterologous inactive zymogen proteases that can subsequently be proteolytically processed to generate the active enzyme product. The active enzyme produce can be useful for directly treating diseases associated with inflammatory, reproductive, epidermal or neurological tissue or for identifying modulators of protease activity which can be used for treatment. The proteases can also be used in commercial products, e.g. laundry detergents, stain-removing solutions and skin care products. The present sequence represents the construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 TGCAGGGAGGCAGATGGGCCGGATGTAGCGGGAGAAGGTGATGGGTCTGCTGAGTTGGAG 445
                                                                                                                                                                                                                                                                                                                                       An expression vector for the expression of inactive zymogen proteases useful for therapeutic or commercial products comprises a pre-sequence, pro-sequence and a cloning site for in frame insertion of a catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 geccacardacccaardacagrecadresandasecerresasaadaacecrrese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 GAGTGCAATGTCGCCCTGGGAGCCTCTGGAGGTAGCTGGGGTGGCGGATG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.7%; Score 23.4; DB 1; Length 1169;
19.4%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1169 BP; 248 A; 358 C; 313 G; 250 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encodes a prostasin protease sequence
                                                                                                                                                                                                                                  Qi J, Andrade-Gordon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 3A-D; 175pp; English.
                                                                                                                                                                                       (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                    14-AUG-2000; 2000WO-US022283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Conservative
                                                                                                                                                                                                                                                                           WPI; 2001-218523/22.
P-PSDB; AAB67540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            domain cassette.
                  WO200116289-A2
                                                             08-MAR-2001
                                                                                                                                                                                                                                     Darrow A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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임
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Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein; fusion protein; coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human; ds. AAA54031/c ID AAA54031 standard; DNA; 1507 BP Human factor X coding sequence. (first entry) AAA54031; 

10664775-2.rng

Homo sapiens.

21-SEP-2000

16-MAR-1999;

High KA,

UYNC-)

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The invention relates to a gene expression profile comprising one or more genes (AB234889-AB23692) and generated from a cell type. The cell type of a coronary artery endothelium, umbilical artery or vein endothelium, actic endothelium, dermal microvascular endothelium, pulmonary artery continued profile endothelium, prometrium microvascular endothelium, real endothelium, renal profile epithelium, renal epithelium, renal proximal tubule epithelium, renal cortical epithelium, renal profile epithelium, renal cortical epithelium, umbilical artery smooth muscle, small airway epithelium, renal epithelium, umbilical artery smooth muscle, commerce, mescle, mesangial cells, ocronary artery smooth muscle, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, actric smooth muscle, uncortinued smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profile may also be used for creating microarrays. The microarray is useful for may also be used for creating microarrays. The microarray is useful for may also be used for creating microarrays. The microarray is useful for medical diagnosis, genotyping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue confirming cell or tissue may income and in identifying promising antibiotics, antiviral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Farnesyl transferase inhibitor modulated leukemia associated gene #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; cytostatic; farnesyl transferase inhibitor; gene expression; quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.4; DB 1;
Pred. No. 54;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 580-581; 850pp; English.
                                                                                                                                                                                                                                                                                                                                                      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE84862/c
ID ADE84862 standard; DNA; 1507 BP.
                                                                                                                                                                                                                                    20-MAR-2002; 2002WO-US008456
                                                                                                                                                                                                                                                                                                20-MAR-2001; 2001US-0276947P
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ilarity 81.8%;
Conservative
gene expression; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-740862/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antifungal agents
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                                                                                                               40200274979-A2
                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Wan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Efficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence, formation of disculation of discussion of emino terminal glutemaic acid residues, to gamma-carboxyglutamic acid; modification of one aspartic acid in the first epidermal growth factor (BGF) domain to Beta-hydroxyaspartic acid in the first epidermal growth factor (BGF) domain to Beta-hydroxyaspartic acid; modification of N- and O-linked oligosaccharides to the activation peptide; cremoval of an internal tripeptide to these modifications do not appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gammacraboxylation are all steps which are important requisites for the production of biologically active factor X/FXa. Isolated chimeric polynucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin K-dependent protein (WXDP). The fusion proteins and recombinant call y gamma-carboxylation of a WXDP to produce a fully gamma-carboxylation of a WXDP to produce a fully gamma-carboxylated without a carboxylation of fully gamma-carboxylated mature wXDPs, which are biologically active. The invention encompasses all combinations of the propertied sequence (modified or not) and WXDPs, which are biologically active. The invention encompasses all combinations of the properties (modified or not) and wXDPs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, artery, endothelium, umbilical, vein; aorta, pulmonary artery,
bronchial epithelium, prostate, muscle, lung fibroblast, osteoblast,
tumour, microarray, genome mapping, antibiotic, antiviral, antifungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the signal, propeptide and mature protein sequence of human Factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.7%; Score 23.4; DB 1; Length 1507; Best Local Similarity 81.8%; Pred. No. 54; Matches 27; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene expression profile polynucleotide SEQ ID NO 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1501 TTTTTTTTTTTTTTTTTTTTGAGTGGGAT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTTTTAAAGAATGTCAT 3277
                                                                                                                                                                                                                                                                                                                                                                                                                      Stafford DW;
                                                                                                                                                                                                                                                                                                                             CHIL-) CHILDRENS HOSPITAL PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 6a, 60pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Camire RM, Larson PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ35322/c
ID ABZ35322 standard; cDNA; 1507 BP.
                                                                                                                                                                                                       16-MAR-2000; 2000WO-US006934
                                                                                                                                                                                                                                                                    99US-0124609P
                                                                                                                                                                                                                                                                                                                                                            UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-638152/61.
                                                                                     WO200054787-A1.
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Gaps

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Indels

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05-FEB-2003

ABZ35322;

RESULT 99

3245 TT

qq ò

Length 1507;

Jiang Y;

Raponi

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The invention relates to an isolated polymucleotide (I) comprising: (a)

any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

complements of (a); (d) sequences consisting of at least 20 contiguous

residues of (a); (d) sequences that hybridize to (a), under moderately

creditions; (e) sequences having at least 75% or 90% identity

co (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-

ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer

catibodies, fusion proteins; T cell populations and antigen presenting

calls expressing the polypeptide are useful in treating pancreatic cancer

can stimulating an immune response. The polymucleotides can be used as

probes or primers for nucleic acid hybridisation, in the design and

preparation of ribozyme molecules for inhibiting expression of the tumour

preparation of ribozyme molecules for inhibiting expression of the tumour

comprehence and proteins in the tumour cells, in vaccines and for gene

comparation of ribozyme molecules for inhibiting expression of the tumour

preparation of ribozyme molecules for inhibiting expression of the tumour

comparation of ribozyme molecules for inhibiting expression of the tumour

preparation of ribozyme and proteins in the tumour cells, in vaccines and for gene

comparation of ribozyme data for this patent did not form part of the

printed specification, but was obtained in electronic format directly

comparation of ribo.int/pub/published_pot_sequence
                                                                                                                                                                                                                                                                New isolated polynucleotide and pancreatic tumor polypeptides, useful idiagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; histocompatibility locus antigen; HLA; determination; allele; HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 375;
                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 3852; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histocompatibility locus antigen B intron 2 SEQ ID NO:342.
                                                                                                                                                                      Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 375 BP; 79 A; 94 C; 87 G; 107 T; 0 U; 8 Other;
                                                                                                                                                                      Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3245 TTTTTTTTTTTTTTTAAAGAATG 3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
0.6%; Score 23.2; D
Best Local Similarity 86.2%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
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                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186/c
AAX38186 standard; DNA; 244 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VISI-) VISIBLE GENETICS INC. (BLAS/) BLASCZYK R H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-CA000768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00909290
16-WAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333626P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leushner J;
                                                                                                                                                                         Kalos MD,
                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                     WPI; 2002-627435/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9907883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blasczyk RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX38186;
                                                                                                                                                                              Benson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 102
AAX38186/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (3)-6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl)-4-(3-chlorophenyl) in methyl-2-(if)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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0.7%; Score 23.4; DB 1; Length 1507;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 27; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pancreatic cancer expressed cDNA SEQ ID NO 3852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3245 TITITITITITITITITITIAAAGAAIGICAI 3277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1501 TTTTTTTTTTTTTTTTTTTGAGTAT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 81; 346pp; English
                                                                                                                                                                                                                                                                                                                           (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV98444 standard; cDNA; 375 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0265305P.
2001US-0265682P.
2001US-0267568P.
2001US-0278651P.
2001US-0287112P.
                                                                                                                                                                                                     30-OCT-2001; 2001US-0338997P.
30-OCT-2001; 2001US-03400B1P.
30-OCT-2001; 2001US-0341012P.
                                                                                                                                                       10-OCT-2002; 2002WO-US034784:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-513497/48.
                                                           WO2003038129-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200260317-A2.
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21-MAR-2001;
28-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001;
               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003
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                                                                                                              08-MAY-2003
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RESULT 101 ABV98444

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Gaps

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Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                         Substance P antisense oligonucleotide.
                                    Disclosure, Fig 13; 195pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 39; 71pp; English
                                                                                                                                                                                                                                                             AAT76438/c
ID AAT76438 standard, DNA, 250 BP.
                                                                                                                                                                                                                                                                                                                                                                               96WO-US009306
                                                                                                                                                                                                                                                                                                                                                                                           95US-00474497
                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                          Local Similarity 60.3
hes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Metzger WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-051871/05
                                                                                                                                                                                                                       CAC 2753
                                                                                                                                                                                                                                   CAC 5
                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                      WO9640162-A1
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                             16-SEP-1997
                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                       2751
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                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                AAT76438;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nyce JW,
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                       RESULT 103
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the substance P, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases han inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AACTAGTCAATCTAATCACACACGAGCCATGTCTAACTCAATGAAACTAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AACCAGAAACTCAGCACCCGCGGGGACVGVCGVCGCAAAAVCCAACAVGAAAAVCCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 23; DB 1; Length 250; Best Local Similarity 38.5%; Pred. No. 43; Matches 52; Conservative 26; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 250 BP; 1 A; 64 C; 70 G; 65 T; 0 U; 50 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || | :||: :|||
CAAVGAVGAVCVGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 CACTGGAGAAGGGAA 318
                                                                                                                                                                                                                                                                                                                                                                                                    hyper-reactive airways
g
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                                                                                                                                                                                                                                                                The present invention describes a method using novel primers involving the PR-based determination of histocompatibility locus antigen B (HLA-B) class I group type. Determining the HLA-B class I group type of a subject class I group type. Determining the HLA-B class I group type of a subject comprises: (i) combining a group-specific untranslated region primer pair with a target DNA sample from the subject under conditions such that primer based amplification of the target DNA may occur; and (ii) determining whether a nucleic acid product is produced by the amplification; where the ability of the primer pair to produce a nucleic amplification; where the ability of the primer pair to produce a nucleic can be used for HLA-B typing. In the method, the initial group specific amplification allows a PCR based separation of haplotypes in 95% of patient samples. It permits the resolution of cis/trans linkages of percentages. PAX37845 to AAX38286 respecsent DNA sequence used in the exemplification of the present invention
                                                                                             Determination of HiA class I group type of a subject - using group specific untranslated region primer pair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 244 BP; 31 A; 91 C; 90 G; 32 T; 0 U; 0 Other;
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243 179 303

0; Gaps

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AAX54759 standard; DNA; 250 BP.
                                                                                                                                                                                            05-JUL-1999
                                                  118
                                                                                                                                                             AAX54759
                                                                                                             AAX54759/
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                                                               2691 GGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGCGATTCATGGGGT 2750
                                                                                              Gaps
                                 .,
0.6%; Score 23; DB 1; Length 244; 60.3%; Pred. No. 42; tive 0; Mismatches 25; Indels
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Substance P antisense oligonucleotide fragment.

(first entry)

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Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
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Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary Mypertension; pulmonary vasconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                             hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides used in treatment of, vasoconstriction.
                                                                                                                                                                                                                                                                                                                  98WO-US019419
                                                                                                                                                                                                                                                                                                                                         97US-0059160P.
98US-00093972.
                                                                                                                                                                                                                                                                                                                                                                               EAST CAROLINA.
                                                                                                                                                                                                           prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-229400/19.
                                                                                                                                                                                                                                                              WO9913886-A1
                                                                                                                                                                                                                                                                                                                17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                         17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                       09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                               (UYEC-) UNIV
                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         Ayce JW;
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and non-coding targions of RNAs corresponding to target genes, coding and codons, genemic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX5572-74. These multiple target oligonucleotides may be derived sequences AAX55710-71 can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, distress syndrome, pain, cystic fibrosis, pulmonary hypertension, cucte asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary and cancers such as leuvemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lancer, melanoma, heptic metastases, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       well as all types of cancers which may metastasize or have metastasized
to the lungs, including breast and prostate cancer
Disclosure; Page 59; 120pp; English.
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Sequence 250 BP; 1 A; 64 C; 70 G; 65 T; 0 U; 50 Other;

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238 AACCAGAGAACTCAGCACCCCGCGGGACVGVCCGVCGCAAAAVCCAACAVGAAAAVCCV 179
                                                                                                                                                                                            244 TGCCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGATGTGGTC 303
                                                                                                                                                                                                                     184 AACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAGCCA
                                                0; Gaps
ch . 0.6%; Score 23; DB 1; Length 250; 1 Similarity 38.5%; Pred. No. 43; 52; Conservative 26; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                       304 CACTGGAGAAGGGAA 318
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     Query Match
Best Local (
                                                Matches
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Human adenosine receptor related polynucleotide SEQ ID NO:1895. AAA34206 standard; DNA; 250 BP 28-JUL-2000 (first entry) AAA34206; AAA34206 

antiallergic; antiasthmatic; cytostatic; analgesic; impaired airwäy; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome, pain, cytic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. Human, adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

Homo sapiens.

WO200009525-A2.

98US-0095212P. 3-AUG-1998;

99WO-US017712

3-AUG-1999;

(UYEC-) UNIV EAST CAROLINA.

WPI; 2000-205971/18. Nyce JW; 

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchlis, emphysema, respiratory distress syndrome, ischemia or

Disclosure; Page 503; 1343pp; English

The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 158), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiniflammatory, antialergic, and/or conflammation. The ON can have antiniflammatory, antialergic, antialergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation.

CC impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating of e.g. ischaemic conditions, pulmonary viscomitions, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic through the respiration, respiratory distress syndrome, pain, cystic throasis, pulmonary hypertension, emphysema, chronic obstructive conflowers, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the release of decoxyadenosine which may metastasise to the lungs, including breast and prostate cancer. The A-containing ONs break down with the release of decoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA33313 to AAA33312 represent the nucleidus sequences given in the sequences differ from the previously named sequences. SEQ ID NO:11 to 2815, and then the last 185 sequences are also called SEQ ID NO:10 to 185, but the sequence for match in the disclosure of the present invention, on the present invention. N. B. C. Up with their corresponding SEQ ID NO: sequences given in the sequence given in the sequence

Sequence 250 BP; 1 A; 64 C; 70 G; 65 T; 0 U; 50 Other;

243 238 AACCAGAGAACTCAGCACCCGCGGACVGVCGCCAAAAVCCAACAVGAAAAVCCV 179 244 TECCCGTGGGGGAACCCAAGATGGGCAGGTCATGTGGAGAGATCTGACAGAATGTGGTC 303 184 AACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAGCCA 0.6%; Score 23; DB 1; Length 250; 38.5%; Pred. No. 43; tive 26; Mismatches 57; Indels Conservative Local Similarity 52; Query Match Matches 셤 ò a

AAF20328 standard; DNA; 250 BP RESULT 106 AAF20328,

304 CACTGGAGAAGGGAA 318 

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14-MAR-2001 (first entry) AAF20328; 

Human substance P polynucleotide fragment #1895.

Low adenosine antisense oligonucleotide, phosphorothioate, allergy; human, alway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; astima; RDS; respiratory distress syndrone; pain; cystic fibrosis; allergic rhinitis;

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pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; pulmonary hypertension; Homo sapiens. cancer; ss.

40200062736-A2.

26-OCT-2000

24-MAR-2000; 2000WO-US008020. 99US-0127958P 16-APR-1999;

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Claim 14; Page 245; 1592pp; English.

The present invention describes low adenosine (A) content antisense cligonucleotides and compositions (I) comprising them. In the antisense cligonucleotides the A is replaced by a 'Universal' or alternative base. (C) ligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. Cr The antisense oligonucleotides and (I) can be used to down-regulate the ung/respiratory disorders and malignancies, such as stimulating and creativity of target polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide creeptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide antisense oligonucleotides may be used in this way to treat disorders creeptors, binding proteins and malignancy associated proteins The antisense oligonucleotides may be used in this way to treat disorders condition selected from pulmonary vasocoactive peptides and on and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasocoactive pulmonary disease (CNDS), pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary hypotections in malyeanes and condition, respiratory distrass syndrome conditions mandyon respiratory condition, pulmonary disease (CNDD), cullenger, invention antisense oligonucleotides used in the exemplification of the present invention 

Sequence 250 BP; 1 A; 64 C; 70 G; 65 T; 0 U; 50 Other;

the present invention

243 238 AACCAGAGAAACTCAGCACCGGGGGACVGVCCGVCGCAAAAVCCAACAVGAAAAVCCV 179 244 TGCCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGATCTGACAGAATGTGGTC 303 184 AACTAGTCAATCTAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAGCCA 0.6%; Score 23; DB 1; Length 250; 38.5%; Pred. No. 43; tive 26; Mismatches 57; Indels 57; Indels Conservative Best Local Similarity 52; Query Match Matches δ 엄 g à

118 CAAVGAVGAVCVGAA 104

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RESULT 107

ABZ96022 standard, DNA, 250 BP.

ABZ96022/

ABZ96022;

17-OCT-2003 (first entry)

Human substance P antisense fragment no.1882.

Human, antisense, lung dysfunction, nasal airway dysfunction, antinfiammatory steroid, ubiquinone, antiinflammatory, antiallergic, antiinfiammatiory, antiallergic, antiathmatic, hypotensive, immunosuppressive, cytostatic, gene therapy, antisense gene therapy, respiratory, lung, adenosine sensitivity, adenosine receptor, bronchodilation, bronchoconstriction, lung allergy, lung inflammation, respiratory disease, ds.

Homo sapiens.

WO200285308-A2.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Sandrasagra A, Ke 5, Shahabuddin S; Li Y, San Tang L, Nyce JW, Lu

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 11264; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the instantion coodon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antihiflammatory steroid and ubjquinone. A composition of the invention has antihiflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artiniflammatory steroid in a subject, for reducing levels of adenosine of or or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, stissue, or respiratory disease or condition, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed section, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 250 BP; 1 A; 64 C; 70 G; 65 T; 0 U; 50 Other;

; 0 0.6%; Score 23; DB 1; Length 250; 38.5%; Pred. No. 43; tive 26; Mismatches 57; Indels 52; Conservative Query Match Best Local Similarity Matches

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184 AACTAGTCAATCAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAGCCA

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CACTGGAGAAGGGAA 318

304

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, and as ABX34813-ABX49947, or complements of them. Also included are in the call having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non-translated sequence that acid linked to a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyademylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or itsue comprising; (3) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement of fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the complementary nucleic acid sequences or its complementary nucleic acid permits the detection of the complementary nucleic acid secured to a molecule in a bovine cell or tissue.

The action of the complementary nucleic acid is used for level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cartle breeding, preparation of constructs for use in cattle gene expression, or for genome intension is not be an expression, or for genetically improving cattle. The present sequence is one of the
238 AACCAGAGAAACTCAGCACCCCGCGGGACVGVCCGVCGCAAAAVCCAACAVGAAAAVCCV 179
                                           244 IGCCCGTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGGATCTGACAGAATGTGGTC 303
                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine, ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine EST associated with lactation/muscle/fat deposition #11540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 11540; 245pp; English.
                                                                                                                                                                                                                                                                                             ABX46375 standard; cDNA; 370 BP.
                                                                                                                                                              || | ::||:
118 CAAVGAVGAVCVGAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001US-00960352,
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11-JAN-2000; 2000US-00480902,
                                                                                                                                   304 CACTGGAGAAGGGAA 318
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-110599/10.
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(TAON/) TAO N.
(WARR/) WARREN W C.
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                                                                                                                                                                                                                                                   78 ATGAAAGGAAAATATATGGCATATATACCAAGGTGTCCCGGTATGTCAACTGGATTAAGGAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide (1) comprising; (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV9945); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABF68596-ABF66517) encoded by (1) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polymeticotides antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer
15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreas; cancer; gene therapy; vaccine; immunostimulant;
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                                                                                                                                 Query Match 0.6%; Score 23; DB 1; Length 370; Best Local Similarity 54.0%; Pred. No. 47; Matches 47; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3282; 300pp + Sequence Listing; English.
                                                                                              Sequence 370 BP; 126 A; 58 C; 77 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pancreatic cancer expressed cDNA SEQ ID NO 3282
                                                                                                                                                                                                                                                                                        1620 AAGTCAGAGGAACCAGAGACCAAATTG 1646
                                                                                                                                                                                                                                                                                                                           138 aaaacaaagcrcacaraaagaaaaa 164
                                                                                                                                                                                                                                                                                                                                                                                                                       ABV97874 standard; cDNA; 381 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-0278651F.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-0291631F.
12-ULL-2001; 2001US-0313999F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; tumour; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2002; 2002WO-US002781
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2001US-0267568P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benson DR, Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-627435/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200260317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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09-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 109
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probes or primers for nucleic acid hybridisation, in the design and preparation of riboxyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence dara for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   stimulating an immune response. The polynucleotides can be used as
                                                                                                                                                                                                                                                                                                        DB 1; Length 381;
                                                                                                                                                                                                                                           Sequence 381 BP; 81 A; 97 C; 93 G; 104 T; 0 U; 6 Other;
8833333333
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Gaps ; 0 Indels TTTTTTTTTT 3265 31 0; Mismatches 48; Trgracaagcririririririririririr Pred. No. Query Match Best Local Similarity 83.9%; Matches 26; Conservative 3235 TTTAATAAAGTT

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AAN60065 standard; DNA; 2438 (revised) (revised 25-MAR-2003 31-OCT-2002 23-MAY-1991 AAN60065; RESULT 110 

Factor VII; Factor IX; DNA construct Factor IX/Factor VII cDNA fusion (first entry) Unidentified

Location/Qualifiers 7. .1368 /*tag= a

10-DEC-1986 EP200421-A.

86EP-00302855 85US-00724311 .6-APR-1986; 17-APR-1985;

85US-00810002

16-DEC-1985;

(ZYMO ) ZYMOGENETICS INC.

Berkner KL, Murry MJ, Hagen FS,

Ę, Gray

Woodbury RG,

Insley MY,

WPI; 1986-326899/50. P-PSDB; AAP60057.

ruct used to transfect hosts - to produce protein which to give factor VIIa. DNA construct activates to c

Disclosure; Fig 7; 55pp; English.

The cDNA is a fusion of Factor IX and Factor VII. It is used to express Factor IX and Factor VII. CDNA encoding Factor VII can be used in DNA construct which contains a nuclectide sequence encoding a protein which, on activation, has the same biological activity for blood coagulation as Factor IIa. The nuclectide codes at least partially for Factor VII and comprises a sequence encoding a calcium binding domain joined to a sceond sequence downstream of this encoding a catalytic domain for the serine protease activity of Factor VIIa. The calcium binding domain comprises a gene encoding Factor VII. IX, X, Protein C, prothrombin or Protein S. The construct is used to transfect host cells to produce the protein which, on activation, yields Factor VIIa. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

ô 1661 ATCATGGAAAAGCAAGAGGTTCCAGAAAAACATCTATTTCTGCTTTATTGACTATGCA 1720 84 Human, differentially regulated gene, macrophage development, diagnosis, matrix metalloproteinase 19; MMP19; antiarthritic, antiinflammatory; destructive macrophage development inhibitor; arthritis; 25 Archideckakarckacadecercarckacarcraecritraseararcraereer Gaps 1721 AAAGCCTTTGACTGTGGGGGTCACAATAACTGTGGAAAATTCTGAAAGGG 1771 GAATGTACAGTTTTTCTTGATGAAACGCCAACAAAATTCTGAATCGG 135 ö Sequence 2438 BP; 658 A; 670 C; 666 G; 444 T; 0 U; 0 Other; 0.6%; Score 23; DB 1; Length 2438; 50.5%; Pred. No. 77; Ve 0; Mismatches 55; Indels Human differentially regulated gene from Fig 35. colorectal cancer; immune response; ss. (EOSB-) EOS BIOTECHNOLOGY INC. AAC55669 standard; cDNA; 231 15-MAR-2000; 2000WO-US006883 99US-0124530P 50.5%; (first entry) Conservative WPI; 2000'-628200/60. Local Similarity tes 56; Conserv WO200055373-A2. 15-MAR-1999; Homo sapiens 17-JAN-2001 21-SEP-2000 Query Match 82 AAC55669 Murray R; Matches 8 ద ò a

The present invention describes a method for screening drug candidates. The method comprises adding a drug to a cell that expresses an expression profile gene encoding a protein encoded by 5 sequences of defined base pairs as given in C5563, C5564, C55643, C55644 and C55653 or a sequence represented by Genbank accession number X92521, X62466, J04130, X62087 and X76534 (or a fragment) and determining the effect of the drug on the expression of the expression profile gene. An inhibitor of matrix metalloprocteinase 19 (MMP-19), preferably an antibody, is useful for treating destructive macrophage disorders (DMD) by inhibiting DM development in a cell of an individual having arthritis. Antibodies to WMP-19 are useful for localising a therapeutic moiety preferably composition comprising WMP-19 is useful for eliciting an immune response in an individual. C55635 to C55710 represent human differentially Example 2; Fig 35; 99pp; English. regulated genes of the invention

Screening drug candidates comprises adding a drug to a cell expressing an expression profile gene and determining the effect of the drug on the expression of the expression profile gene.

0.6%; Score 22.8; DB 1; Length 231; 79.4%; Pred. No. 47; ive 0; Mismatches 7; Indels 0 Sequence 231 BP; 66 A; 65 C; 61 G; 39 T; 0 U; 0 Other; Conservative Best Local Similarity Matches 27; Conserv Query Match

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Gaps

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The invention relates to diagnosing (M1) a destructive macrophage disorder (DMD) or determining (M2) the prognosis of an individual with DMD, by determining the expression of the gene encoding MMP-19. (M1) involves comparing the expression of the gene encoding MMP-19 in a first tissue type of a first individual, with expression of the gene from second normal tissue from the individual, with expression of the gene from second normal tissue from the individual, with expression of the determining level of MMP-19 in sample, where high level of MMP-19 in candidates (involves providing a cell that expression of fewer indicates poor prognosis. Also included are screening (M3) drug candidates (involves providing a cell that expresssion as expression profile gene which encodes a protein encoded by any one of 5 expression profile gene which encodes a protein encoded by any one of 5 expression profile gene which encodes a protein encoded by accession number X9221, X62466, J04130, X62078 and X76534, or its fragment; adding a drug candidate to the cell, and determining the effect of the drug candidate on the expression of the expression profile gene), screening (M4) for a bloactive agent capable of modulator protein (where the DM modulator protein (where the DM modulator protein (where the DM modulator protein (where the DM modulator protein or its fragment, screening for a bloactive agent capable of interfering with the binds of a DM modulator protein or its fragment and an antibody (II) which specifically binds to MMP-19, or its fragment, screening antisense molecules to MMP-19. The DM cell by administering antibody (II) which specifically binds the protein or its fragment and an antibody is useful for treating antibone protein or its fragment and antibody is Diagnosing destructive macrophage disorder (DMD) such as arthritis, aneurysms or atherosclerosis, or determining prognosis of individual with DMD, by determining expression or level of matrix metalloproteinase-19. Destructive macrophage disease; differential expression; ss; human; antiarthritic; antiinflammatory; antiatherosclerotic; DMD; MMP-19; arthritis; inflammatory bowel disease; vascular disease; chronic obstructive pulmonary disorder; arherosclerosis; aneurysm. 3245 TITITITITITITITITITIAAGAATGICATI 3278 225 Trrrrrrrrrrrrrrrrrrrr 192 Human destructive macrophage sequence, DM35. Murray R, Caras IW, Hevezi P, Wilson K; Example 2; Fig 35; 61pp; English. ACD81661 standard; cDNA; 231 BP 15-MAR-2000; 2000US-00525978. LS-MAR-1999; 99US-00124530. 18-SEP-2003 (first entry) (MURR/) MURRAY R. (CARA/) CARAS I W. (HEVE/) HEVEZI P. (WILS/) WILSON K. WPI; 2003-512353/48. JS2003049722-A1. Homo sapiens. 13-MAR-2003. ACD81661; RESULT 112 ACD81661/c 

The invention relates to novel proteins involved in the biosynthesis of polyketide dorrigocin (DORR) or lactimidomycin (LACT) biosynthesis by microorganisms. Sequences of the invention allow direct manipulation of dorrigocin, lactimidomycin and related chemical structures via chemical engineering of the enzymes involved in the biosynthesis of dorrigocin and lactimidomycin. They are useful for introducing chemical handles into normally inert positions that permit subsequence chemical modifications and facilitate the development of polyketides. The genes and proteins of the invention can also be used to generate a focused library of analogues around a polyketide lead candidate to fine-tune the compound for optimal properties. They are useful for generating antibodies specific for the Novel isolated or purified polypeptide involved in biosynthesis of polyketide dorrigocin or polyketide lactimidomycin, useful for preparing dorrigocin or lactimidomycin. modulator protein is useful for eliciting an immune response in an individual. The methods and compositions are useful for treating a DWD such as arthritis, inflammatory bowel disease, chronic obstructive pulmonary disorder and vascular disease, including atherosclerosis and aneurysms. The present sequence is a cDNA fragment from a gene differentially expressed in the development path of destructive Polyketide biosynthesis; dorrigocin; DORR; lactimidomycin; LACT; gene; Gaps ò DB 1; Length 231; Indels Sequence 231 BP; 66 A; 65 C; 61 G; 39 T; 0 U; 0 Other; Streptomyces amphibiosporus lactimidomycin ORF2 DNA. 3245 TITITITITITITITITITIAAAGAATGICAIL 3278 225 triririririririririririscaaaaccccrrr 192 /product= "LACT ORF2 protein" /note= "No start codon" /partial Farnet CM, Zazopoulos E, Staffa A, Yang X; Query Match
0.6%; Score 22.8; D
Best Local Similarity 79.4%; Pred. No. 47;
Matches 27; Conservative 0; Mismatches Score 22.8; I Pred. No. 47; Claim 6; Page 232-235; 312pp; English. Location/Qualifiers (ECOP-) ECOPIA BIOSCIENCES INC. AAD54232 standard; DNA; 255 BP. 26-APR-2002; 2002WO-CA000591. 26-APR-2001; 2001US-0286346P. Streptomyces amphibiosporus. 17-JUN-2003 (first entry) /*tag= a WPI; 2003-201222/19. P-PSDB; AAE35496. WO200288176-A2. 07-NOV-2002. macrophages AAD54232; RESULT 113 AAD54232 88888888888 g 

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                                                                                                                                                             981 AGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTTGGAATACGGAATGA 1040
                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                             5 AGCAGGAACTCAAGCAGTACATGGAAGAGCAGTTCATGTTCGAGTTCGAGTTCA
                                                                                                                                 Gaps
polyketide biosynthesis. The present sequence is S. amphibiosporus lactimidomycin ORF2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine EST associated with lactation/muscle/fat deposition #2042.
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                                                                                           DB 1; Length 255;
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                                                       84 G; 45 T; 0 U; 0 Other;
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                                                                                                                           0; Mismatches
                                                                                         0.6%; Score 22.8; I
6.8%; Pred. No. 49;
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                                                 Sequence 255 BP; 51 A; 75 C;
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                                                                                                          56.8%;
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                                                                      Query Match
Best Local Similarity 56.0.
Best A2; Conservative
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                                                                                                                                                                                                                                                                   CCGAGGACACCGAC
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(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
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detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in
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66.8%; Pred. No. 53;
ve 0; Mismatches 32; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 356 BP; 76 A; 107 C; 106 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     electronic format from the USPTO web site;
segdata.uspto.gov/seguence.html?DocID=20020137139
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Best Local Similarity 56.0%
Thes 42; Conservative
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(MATH/) MATHIALAGAN N.
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(WARR/) WARREN W C.
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Claim 25; SEQ ID NO 1540; 487pp; English
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acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of pulyadenylated ribonucleotides to a 3' end of the makin molecule; and (2) determining a level or pattern of a molecule in a bovine cell or issue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is used for level or pattern of the molecule in a bovine cell or tissue. The LMFD nucleic acid is used for certaining a level or pattern of a molecule in a bovine cell or tissue. The correction of the molecule in a bovine cell or tissue. The correction of the molecule is acid is used for a testing, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in the constructs for a site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #1540 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2651 GATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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56.8%; Pred. No. 55;
ive 0; Mismatches
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26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0263366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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                                                                                                                                                                                                                                                                                                                                                                                                                    42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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04-OCT-2000;
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Matches
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

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2608 GGAGGGATTGGGGGCAGGAGAGAGGGGACGACAGAGGATGAGATGGCTGGATGGCATC 2667
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                                                                                                                                                                                                                                                                                                                                                                                              79 dakadakaradadadakakaracadadagachakaratarakarakararakadaka 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                        Length 468;
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                                                                                                                                                                                                                                   Sequence 468 BP; 122 A; 106 C; 129 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                  24; Indels
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                                                                                                                                                                                                                                                                    Score 22.6; DB 1;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                             0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA53297 standard; DNA; 468
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                                                                                                                                                                                                                                                                                                                        37; Conservative
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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79. GGAGGGAGTGGGGGCAGCAGAATGCAGGGGGCAAACATGCTAAACTGGGTATTGAGCACC 138
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                                   2668 A 2668
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                                                                  139 A 139
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                        cancer; ss.
                                                                                                                                                                            ABA42875;
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                                                                                                                  RESULT 119
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                                                                                                                                                       2608 GGAGGGATTGGGGGCCAGGAGAGAGGACGACGACAGGATGAGATGGCTGGATGCATC 2667
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                     79 GGAGGGAGTGGGGGCAGAATGCAGGGGCAAACATGCTAAACTGGGTATTGAGCACC
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #1586 used to measure gene expression in human placenta sample.
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0
                                                                                              DB 1; Length 468;
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                                                               Sequence 468 BP; 122 A; 106 C; 129 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 468 BP; 122 A; 106 C; 129 G; 111 T; 0 U; 0 Other;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
                                                                                                                            24;
                                                                                                             Pred. No. 65;
0; Mismatches
                                                                                             0.6%; Score 22.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 1586; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                               BP.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                          60.7%;
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30-JUN-2000; 2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                           Best Local Similarity 60.7
Matches 37; Conservative
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Best Local Similarity
Matches 37; Conserv
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                                                                                             Query Match
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involuse contracting the probes with a collection of detectably labelled nucleic acids derived from expression of the microarray. The probes are useful for verifying the probes of the microarray. The probes are useful for verifying the corporation of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or proposing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring sessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                            Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 22.6; DB 1; Length 468; 60.7%; Pred. No. 65; ive 0; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1570; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 468 BP; 122 A; 106 C; 129 G; 111 T; 0 U; 0 Other;
                                                                                                                   Human breast cell single exon nucleic acid probe #1570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
ABA42875 standard; DNA; 468 BP.
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2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                             (first entry)
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Best Local Similarity 60.7
Matches 37; Conservative
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2667 ö

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2608 GGAGGGATTGGGGGCAGGAGAGGGGACGACGACGAGGATGAGATGGCTGGATGGCATC

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RESULT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived probe thuman heart via microarrays. By measuring gene expression, the probes are useful for predicting, dispnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease, Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic
                              79 GGAGGGAGTGGGGGCCAGAATGCAGGGGGCAAACATGCTAAACTGGGTATTGAGCACC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGGGAGTGGGGGGAGAATGCAGGGGGGAACATGCTAAACTGGGTATTGAGCACC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                Probe #1536 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                Human, gene expression, heart, microarray, vascular system, probe, cardiovascular disease, hypertension, cardiac arrhythmia, congenital heart disease, ss.
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Pred. No. 65;
0; Mismatches 24; Indels
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                                                                                                                                                                                 ABA23070 standard; DNA; 468 BP.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 60.7°
Matches 37; Conservative
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21-SEP-2000;
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2608 GGAGGGATTGGGGGCAGGAGAAGGGGACGACGACAGAGGATGAGATGGCTGGATGGCATC 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes which are derived from genomic sequences expressed in the human brain. They can be used from genomic sequences expressed in the human which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GGAĞGGAGTGGGGGCAĞCAGAATGCAĞGGGGCAAACATGCTAAACTGGGTATTGAĞCACC 138
                                                                                                                                           Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                             Human brain expressed single exon probe SEQ ID NO: 1548
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            AAK01557 standard; DNA; 468 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
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26-MAY-2000; 2000US-0207456P.
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                                                                           05-NOV-2001 (first entry)
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Best Local Similarity
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                                             AAK01557;
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AAK0155
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Location/Qualifiers

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DNA construct used to transfect hosts - to produce protein which activates to give factor VIIa.
                               Factor VII; Factor VIIa; DNA construct.
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                                                                                                                                                                                                                                   86EP-00302855.
                                                                                                                                                                                                                                                                     85US-00724311
85US-00810002
                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC
 Partial Factor VII cDNA.
                                                                                                                                                                                                                                                                                                                                                     Hagen FS, Murry MJ,
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1986-326899/50.
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                                                                   Homo sapiens
                                                                                                                                                                                                                                     16-APR-1986;
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16-DEC-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes are useful for a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, saging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocyptic changes, proliferative breast disease and noncarcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2608 GGAGGGATTGGGGGCCAGGAGGAGGGACGACAGAGGATGAGATGGCTGGATGGCATC 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel single exon nucleic acid probe used to measuring gene expression in
                                                                        Probe, human; breast disease, breast cancer; development disorder; ss, inflammatory disease; proliferative breast disease, non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GGAGGGAGTGGGGGGGAGGAGGAGGGGGGAAACAAGGTAAACTGGGGTATTGAGCACC
                                       Probe #1524 used to measure gene expression in human breast sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 468 BP; 122 A; 106 C; 129 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 1524; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                            2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                            27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                          29-JAN-2001; 2001WO-US000661
        (first entry)
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                          WO200157270-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a human breast
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                          Homo sapiens
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26-MAY-2000;
        09-OCT-2001
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31-OCT-2002
23-MAY-1991
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ij

Gray

Berkner KL, Insley MY, Woodbury RG,

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2245
The partial factor VII cDNA sequence is produced by joining portions of cDNA clones lambda VII2115 and lambda VII1923. It is used in a DNA construct which contains a nucleotide sequence encoding a protein which, on activation, has the same blological activity for blood coagulation as Factor IIa. The nucleotide codes at least partially for Factor VII and comprises a sequence encoding a calcium binding domain joined to a sceond sequence downstream of this encoding a catalytic domain for the serine protease activity of Factor VIIa. The calcium binding domain comprises a gene encoding Factor VII. IX, X, Protein C, prothrombin or Protein S. The construct is used to transfect host cells to produce the protein which, on activation, yields Factor VIIa. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2186 IGTCAGACTITATITITGGGGGCTCCCAAAATCACTGCAGATGGTGACTGCAGCCATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 2177;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2177 BP; 569 A; 624 C; 605 G; 379 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 22.6; D
48.8%; Pred. No. 94;
live 0; Mismatches
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ID ABN76724 standard; cDNA; 186 BP.
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Matches 61; Conservative
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RESULT 123
AAN60063
XX
XX
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AC
AC
DT
25-MAR
DT
31-OCT
XX

Matches

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Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopolesis regulation; tissue growth, angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cancer; proliferative disorder; neurological disorder; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; hypothyroid; antipsoriatic; antidiabetic; cytostatic; montropic; antidiatherosclerotic; antioadialan; hypotensive; antichyroid; antinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss. 

Homo sapiens.

29-NOV-2001.

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. P-PSDB; ABP32698. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 1; Page 1094; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054.

Gesignated ORF (open reading frame) 1-4534, and sequences ABN75054.

ABN79587 represent DNAs encoding them. The invention also encompasses polypeptides at least 88 identical to referred to as ORFX) proteins, polynucleotides at least 88 identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX to polynucleotides. The recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of screening for modulators of ORFX sepression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide control of the order of biological activities, such as ovioxine, cell proliferation, cell differentiation, immune modulation, mematopoists regulation, cell differentiation, immune modulation, mematopoists regulation, cell differentiation, immune modulation, thrombolytic activity, chemotatic, chemokinetic activity, has mostatic activity, thrombolytic activity, chemotatic, cell differentiation, immune modulation, has manipulation activity, chemotatic, and antihined activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, other proliferative disorders such as psoriasis and bonign tumours, corporation activity, and antibodies may be used in Alzheimer of sacrae, and infectious associated by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a sequence, in genetic dispense, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a sequence, in genetic dispense, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as sequences, in genetic dispense, and infectious of primers and probes; and the detection of ORFX genomic acids may additionally be use

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                                                                                                       2670 IGACTCGAIGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTG 2729
                                                                                                                                         148 redecceerreagicacecradarearcadececedeserececederececederes
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0
                                 DB 1; Length 186;
                                                                    Indels
Sequence 186 BP; 37 A; 66 C; 51 G; 32 T; 0 U; 0 Other;
                                                                  0; Mismatches
                                 Score 22.4; I
Pred. No. 57;
                                                                                                                                                                              2730 TCCTGCGGCGATTCATGGGGTCACAAAG 2757
                                                                                                                                                                                                                 88 GCAGGCGGCCTTGATGTGCTCAGGTAG 61
                                 0.6%;
                                                53.4%;
                                                                    47; Conservative
                                 Query Match
Best Local Similarity
                                                                    Matches
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Human, pancreas, cancer; gene therapy; vaccine; immunostimulant; cytostatic; tumour; gene; ss. Human pancreatic cancer expressed cDNA SEQ ID NO 3367. ABV97959 standard; cDNA; 317 BP. 14-JAN-2003 (first entry) ABV97959; RESULT 125 

WO200260317-A2.

08-AUG-2002.

30-JAN-2002; 2002WO-US002781

31-JAN-2001; 2001US-0265682P. 09-FEB-2001; 2001US-0267568P. 30-JAN-2001; 2001US-0265305P

21-MAR-2001; 2001US-0278651P 28-APR-2001; 2001US-0287112P

12-JUL-2001; 2001US-0313999P. 16-MAY-2001; 2001US-0291631P

27-NOV-2001; 2001US-0333626P

(CORI-) CORIXA CORP.

WPI; 2002-627435/67.

Hepler WT, Jiang Y; Lodes MJ, Persing DH, Benson DR, Kalos MD, New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic

Claim 1; SEQ ID NO 3367; 300pp + Sequence Listing; English.

The invention relates to an isolated polynuclectide (I) comprising: (a) any of a group of over 4000 nuclectide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-C) ABP66637) encoded by (I) and oligonuclectide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and polypeptides and proteins in the immune for gene to polypeptides and proteins in the immune for gene therapy. Note: The sequence data for this patent did not form part of the

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Gaps

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Indels Length

21;

DB 1;

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The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases. Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                         3245 TITITITITITITITITAAAGAATGTCATTCTTTGTGAAGTTTTTGACAATGC 3300
printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                             311 Trrrrrrrrrrrrrrrrrrrrrrangagagagagacacacrrracrracraragagacrec 256
                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism containing sequence #258.
                                                       Sequence 317 BP; 95 A; 79 C; 76 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 253 BP; 92 A; 41 C; 58 G; 61 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cargill M, Daley GQ, Ireland JS,
Patil N, Sklar P;
                                                                                                                            0; Mismatches
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                                                                                         Score 22.4; I
Pred. No. 66;
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                                                                                          Score
                                                                                                                                                                                                                                                                                      BP.
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                                                                                         0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0127248P
                                                                                                                                                                                                                                                                                  AAC70944 standard; DNA; 253
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                                                                                                                            Conservative
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                                                                                                       Local Similarity
les 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altshuler D,
Lipshutz RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000.
                                                                                                                                                                                                                                                                                                                   AAC70944;
                                                                                          Query Match
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Matches
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Lander ES

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3250
176 CTTCCCTCCTTCCCTGTAGCCGGCACAGATCATCTTATGGGTTATTTTATGTCCTCTGTA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
                    TCTTTAAATTCATTATTCTTTGATAACAGCTTCAGTTCTATGGCTTTAATAAAGTTTTTT
                                      116 refrencescacientespecare -- craasserateroscrines assassari
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                                                                                                                                                                                                      cancer; gene therapy; vaccine; immunostimulant;
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                                                                                                                                                                                   Human pancreatic cancer expressed cDNA SEQ ID NO 3117.
                                                           TTTTTTTTTTTAAAGAATGTCATTCTTT 3282
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                                                                             TIGIATITIGICIGAAAAAATITITITIGGIT
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                                                                                                                           BP.
                                                                                                                          ABV97709 standard; cDNA; 397
                                                                                                                                                                                                    Human; pancreas; cancer; gene
cytostatic; tumour; gene; ss.
                                                                                                                                                                                                                                                                                                                                                         16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
27-NOV-2001; 2001US-0333658P.
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                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Kalos MD,
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                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
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31-JAN-2001; 2
09-FEB-2001; 2
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The invention relates to an isolated polynuclectide (I) comprising: (a) any of a group of over 4000 nuclectide sequences (ABV94628-ABV93145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-C) at least 20 contiguous (b) sequences having at least 75% or 90% identity. (b) appearate on compositions on antigen presenting on a patient and compositions comprising polypeptides, polymucleotides, or nucleotides (all polypeptides or be used as probes or primers for nucleic acid hybridisation, in the design and propertiens and proteins of athe tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at feb. wipo.int/pub/published_pot_sequences Claim 1; SEQ ID NO 3117; 300pp + Sequence Listing; English.

Sequence 397 BP; 84 A; 97 C; 89 G; 112 T; 0 U; 15 Other;

1;

Gaps

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72; Indels

Local Similarity 50.7 les 77; Conservative

Matches

Length 253;

DB 1;

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Gaps
                                   ö
   DB 1; Length 397;
                                 9; Indels
ch 0.6%; Score 22.2; D
1 Similarity 75.0%; Pred. No. 79;
27; Conservative 0; Mismatches
 Ouery Match
Best Local 9
                               Matches
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3235 TITAATAAAGTITITITITITITITITAAAGA 3270 ABV98476 standard; cDNA; 234 (first entry) 14-JAN-2003 ABV98476; 

Human; pancreas; cancer; gene therapy; vaccine; immunostimulant; Human pancreatic cancer expressed cDNA SEQ ID NO 3884.

Homo sapiens.

cytostatic; tumour; gene; ss.

MO200260317-A2.

30-JAN-2002; 2002WO-US002781.

31-JAN-2001; 2001US-0265682P. 09-FEB-2001; 2001US-0267568P. 21-MAR-2001; 2001US-0278651P. 28-APR-2001; 2001US-0291631P. 12-JUL-2001; 2001US-0305484P. 20-AUG-2001; 2001US-0313999P. 27-NOV-2001; 2001US-0333626P. 30-JAN-2001; 2001US-0265305P.

(CORI-) CORIXA CORP.

Hepler WT, Jiang Y; Persing DH, Lodes MJ, Benson DR, Kalos MD, WPI; 2002-627435/67. New isolated polynucleotide and pancreatic tumor polypeptides, useful diagnosing, preventing and/or treating cancer, particularly pancreatic

Claim 1; SEQ ID NO 3884; 300pp + Sequence Listing; English.

The invention relates to an isolated polymucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (BN94628-AN99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridiac to (a), under moderately crimpent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-CC ABP6863) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions of polypeptides (ABP68596-CC ABP6863) encoded by (I) and oligonucleotide can be used to not in degenerate polypeptides are useful in treating pancreatic cancer in a patient and compositions. T cell populations and antigen presenting calls expressing the polypeptide are useful in treating pancreatic cancer of simulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of tibozyme molecules for inhibiting expression of the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly come with the polyment of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community of the community o

Seguence 234 BP; 41 A; 70 C; 62 G; 61 T; 0 U; 0 Other;

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                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                 Gaps
                             921 CCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA 974
                                         88 CCTCACAGATGTAGCCCCCAACGATCTTGTCATCATCATCAAAGGGGCAGCAA 35
0.6%; Score 22; DB 1; Length 234; 63.0%; Pred. No. 77; 77; Pred. 0; Mismatches 20; Indels
                                                                                                                              Human prostate expression marker cDNA 8812.
                                                                                 ABV08821 standard; cDNA; 397 BP.
                                                                                                             13-SEP-2002 (first entry)
Query Match
Best Local Similarity 63.0°
Matches 34; Conservative
                                                                                                ABV08821;
                                                                  RESULT 129
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 13-DEC-2000; 2000US-0255281P.

; 2000US-0189862P. ; 2000US-0207454P. ; 2000US-0211314P. ; 2000US-0219007P.

25-MAY-2000; 17-FEB-2000;

18-JUL-2000;

2000US-0183319P

20-FEB-2001; 2001WO-US005171.

WO200160860-A2. Homo sapiens.

23-AUG-2001.

Monahan JE;

WPI; 2001-662795/76.

Schlegel R, Endege WO,

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 1389; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker

Sequence 397 BP; 85 A; 89 C; 82 G; 141 T; 0 U; 0 Other;

0; Gaps . Match 0.6%; Score 22; DB 1; Length 397; Local Similarity 47.8%; Pred. No. 89; Pred. No. 89; 0; Mismatches 70; Indels 64; Conservative Query Match Matches

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1203 TATACAGTCAGCAAAACAAGACCAGGAGCTTACTGTGGCTCAGATCATGAACTCCTTAT 1262 370 TATACCATCCAGACATTGAAAACTAAGGCCATTCTGTGAGTTATTTTAAAAACTTGGTGT 311 셤

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1263 IGCCAAATTCAGACTTAAATTGAAGAAAGTAGGGAAAACCACTAGATCACTCAGGTAAGA 1322

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10664775-2.rng

seqdata.uspto.gov/sequence.html?DocID=20020137139

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX99947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is useful for general for pattern of a molecule in a bovine cell or tissue.

The is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs. For use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in celectronic format from the USPTO web site:
310 TITGCACATAATGATCTTAAAAAAAAATGAATTACCAAAAACCAAGATTCTCTTCTAAAA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping; gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine EST associated with lactation/muscle/fat deposition #14612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Byatt JC, Mathialagan N, Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 14612; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX49447 standard; cDNA; 432 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-1999; 99US-0115707P.
                                                                                                                                1323 CCTAAATCCAATCC 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                      250 TGAAATTTAATGC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-110599/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2002137139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAO N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX49447;
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The present invention relates to the isolation of cDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host cell that expresses these polynucleotides is useful for determining the protein experience of cancer in a patient. A composition comprising the polynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosis, prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the development of cancer in a patient, or as market for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays.

ABNA44061-ABNA4209 represent cDNA sequences encoding for human pancreatic
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                                                                                                                         2919 TACTTATTTAATTTTGGGATTTTTAACTATTCTTCAATGACTTGTATTTCTAATATTTAC 2978
                                                                                                                                                                 267 TGCTTCCAAAATTCAGTAGTTTTCTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotide encoding pancreatic tumor polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; pancreatic tumour protein; immune response; pancreatic cancer;
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development of cancer; cancer progression; cytostatic; gene; ss.
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                                      Score 22, DB 1; Length 432;
Pred. No. 91;
0; Mismatches 40; Indels
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Sequence 432 BP; 140 A; 69 C; 107 G; 116 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA #97 encoding human pancreatic tumour protein.
                                                                                                                                                                                                          2979 TIATICIATITIACITIAATIGCACT 3004
                                                                                                                                                                                                                                   207 CTACATTTTTCTTCTTTACATTCTCT 182
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                                                                                                                                                                                                                                                                                                                                                       ABK44157 standard; cDNA; 534 BP.
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30-JAN-2001; 2001US-0265447P.
15-MAY-2001; 2001US-0291201P.
                                        Query Match
Best Local Similarity 53.5%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-241741/29.
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RESULT 132 AAN81633/c

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AAT03999-T04001 are all human cDNA sequences which code for pancreatic trypsin III (AAR87203), the sequences differ only in their stop codons. The cDNA molecules can be used in the recombinant production of trypsin which can be used as a drug to treat diseases wherein trypsin production is impaired. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCITITAGAACIAACACCCCAAAAAGAIGICCTICCICATTATAGGGGACTGGAA 974
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                                                                                                                                                                                                                                                                                                                                                                                                                - can be easily produced by
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Pred. No. 1e+02;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pancreatic trypsin III; trypsinogen; human; hydrolysis; ds
                                                                                 Pancreatic trypsin III; trypsinogen; human; hydrolysis; ds.
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/product= "pancreatic_trypsin_III"
                                                                                                                                                                                              "pancreatic_trypsin_III"
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                                                                                                                                                 Location/Qualifiers
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                                                        Human pancreatic trypsin III cDNA.
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ilarity 63.0%;
Conservative
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(first entry)
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/product=
           (revised)
(first entry)
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Best Local Similarity
Matches 34; Conservat
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-287966/38.
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19-MAR-1996
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUL-1995
           25-MAR-2003
19-MAR-1996
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                               Gaps
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                                                                                         cercaeaargradececeaacarerrerearcareareaaggggggggagaa 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human spleen trypsin - used to treat lesions or trauma, without hypersensitive allergic side effects.
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Best Local Similarity 63.0%; Pred. No. 1e+02;
Matches 34; Conservative 0; Mismatches 20; Indels
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DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                        "human spleen plasminogen III."
                               20; Indels
                                                                                                                                                                                                                                                                                                                Human spleen plasminogen; trauma lesions; ss.
Score 22; DB 1
Pred. No. 96;
0; Mismatches
                                                                                                                                                                                                                                                                                Human spleen trypsin III (trysinogen III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT04001 standard; cDNA to mRNA; 744 BP.
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                        BP.
   0.6%;
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(first entry)
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/product=
                                 Conservative
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   Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-DEC-1986;
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                                                                                                                                                                                                                                                                                                                                                 sapiens
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07-NOV-1990
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RESULT 133
AAT04001/c
ID AAT040
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AC AAT040

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Gaps

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DNA encoding trypsinogen-like protein - used for recombinant production of the protein.
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                                                                                                                                                                                                                                               921 CCTTTTAGAACTAACACCCAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA
                                                                                                                                                                                                                                                                                                         ccrcacacereracccccaacaarcricrcarcercaaaeeeeacae
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                                                                                                                      0.6%; Score 22; DB 1; Length 744; ilarity 63.0%; Pred. No. 1e+02; Conservative 0; Mismatches 20; Indels
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                                                                   Sequence 744 BP; 162 A; 214 C; 200 G; 168 T; 0 U; 0 Other;
      is impaired. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 790;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "trypsinogen-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 0.6%; Score 22; DB 1; 1
1. Similarity 63.0%; Pred. No. 1.1e+02;
34; Conservative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypsinogen-like protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV24548 standard; cDNA; 790 BP
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Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-289873/26.
                                                                                                                   Query Match
Best Local Similarity
Matches 34; Conserv
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AAV24548/C
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAT03999-T04001 are all human cDNA sequences which code for pancreatic trypsin III (AAR87203), the sequences differ only in their stop codons. The cDNA molecules can be used in the recombinant production of trypsin which can be used as a drug to treat diseases wherein trypsin production is impaired. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT03999-T04001 are all human cDNA sequences which code for pancreatic trypsin III (AAR87203), the sequences differ only in their stop codons. The CDNA molecules can be used in the recombinant production of trypsin which can be used as a drug to treat diseases wherein trypsin production
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                                                                                                                                                                                                                                                                  Novel human pancreatic trypsin III - can be easily produced by recombinant methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 744 BP; 161 A; 214 C; 201 G; 168 T; 0 U; 0 Other;
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/*tag= a
/product= "pancreatic_trypsin_III"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 7-8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pancreatic trypsin III cDNA.
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                                                         86JP-00307770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-00311512.
94JP-00311512
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(first entry)
                                                                                                                      SANY ) SANKYO CO LID
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                                                                                                                                                                            WPI; 1995-287966/38.
P-PSDB; AAR82703.
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25-DEC-1986;
                                                      25-DEC-1986;
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19-MAR-1996
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Gaps 974 20

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Human, artery, endothelium, umbilical, vein; aorta, pulmonary artery,
bronchial epithelium, prostate, muscle, lung fibroblast, osteoblast,
tumour, microarray, genome mapping, antibiotic, antiviral; antifungal;
                                                                                                                                                                                                 New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer.
                                                                                                                                             (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                       Claim 5; Page 405; 850pp; English
                                                                                                          20-MAR-2002; 2002WO-US008456.
                                                                                                                            20-MAR-2001; 2001US-0276947P.
                                   gene expression; gene; ss.
                                                                                                                                                                                  WPI; 2002-740862/80.
                                                                                                                                                                Wang Y;
                                                                      WO200274979-A2.
                                                      Homo sapiens.
                                                                                                                                                                Иап J,
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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery vendothelium, unbilical artery or vein andothelium, cortic endothelium, dermal microvascular endothelium, prostate epithelium, bronchial epithelium, renal proximal tubule epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, prostate epithelium, renal proximal tubule epithelium, muscle, camal airway epithelium, renal epithelium, renal proximal tubule epithelium, contic smooth muscle, neoratal dermal fibroblast, pancorary artery smooth muscle, carrier, muscle, mesangial cells, coronary artery smooth muscle, carrier smooth muscle, lung fibroblast, coronary artery smooth muscle, cortic smooth muscle, uterine smooth muscle, lung fibroblast, coronary artery smooth muscle, corrected stromal cell. The gene expression profile is used for determining the phenotype of a cell and distinguishing cell types. The gene or a protein phenotype of a cell and distinguishing cell types. The gene or a protein alterations of gene expression profile is useful in identifying disease pathologies involving alterations of gene expression with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antivixal or antifungal agents

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                                                 0; Gaps
                                                                                              921 CCTTTTAGAACTAACACCCAAAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA 974
                                                                                                                                           137 cercacadergradecécéaacaarerrerererereseaaagegaeaeaa 84
0.6%; Score 22; DB 1; Length 853;
53.0%; Pred. No. 1.1e+02;
Ive 0; Mismatches 20; Indels
                           ilarity 63.0%;
Conservative
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                                                 Matches
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Seguence 853 BP; 192 A; 253 C; 231 G; 177 T; 0 U; 0 Other;

Query Match

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Factor IX mutation correcting oligonucleotide SEQ ID NO: 2445.
                     ABA79599 standard; DNA; 121 BP.
                                                                                                                     (first entry)
                                                                                                                     24-JAN-2002
ABA79599,
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Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin, retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDRV2A, melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia, alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucurcnosyltransferase; amyloid precursor protein; presentlin-1; Altheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss.

Homo sapiens.

WO200173002-A2.

04-OCT-2001.

27-MAR-2001; 2001WO-US009761.

27-MAR-2000; 2000US-0192176P.

27-MAR-2000; 2000US-0192179P. 01-JUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P.

(UYDE ) UNIV DELAWARE.

Gamper HB, Rice MC; Kmiec EB,

WPI; 2001-639230/73.

Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.

Claim 7; Page 183; 294pp; English.

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Pactor V, Factor VIII, Pactor IX, haemoglobin alpha locus (HBA21), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APCB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentlin-2 (BERN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanowa, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention

Sequence 121 BP; 29 A; 28 C; 16 G; 48 T; 0 U; 0 Other;

0; Gaps DB 1; Length 121; Query Match 0.6%; Score 21.8; DB 1; Length 121 Best Local Similarity 58.5%; Pred. No. 72; Matches 38; Conservative 0; Mismatches 27; Indels

845 CAGTA 849 ò

12 GAGCA 8

RESULT 139

ABA79602 standard; DNA; 121 BP.

ABA79602 ID ABA7 XX

Factor IX mutation correcting oligonucleotide SEQ ID NO: 2449.

(first entry)

24-JAN-2002

ABA79603;

ABA79603 standard; DNA; 121 BP.

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Claim 7; Page 183; 294pp; English.
                                                                                                                                                                                                                                                                               oligonucleotides of the invention
                                                                                                                                                         Rice MC;
                                                                                                                      27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
                                                                                                             27-MAR-2001; 2001WO-US009761
          (first entry)
                                                                                                                                                        Gamper HB,
                                                                                                                                               (UYDE ) UNIV DELAWARE
                                                                                                                                                                  WPI; 2001-639230/73.
                                                                        antilipemic; ss
                                                                                          WO200173002-A2.
          24-JAN-2002
                                                                                                                                                                                     modification.
                                                                                                    04-OCT-2001
ABA79602;
                                                                                                                                                         Kmiec EB,
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Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2, CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HaBA1; HBBA2; dadenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOS; mismatch repair; MSH5; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; FSBN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentilin-1; ALAPAREME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-0192179P.
01-UUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-024899P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kmiec EB, Gamper HB,
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ABA79603,
                      Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; metanoma; APC; HaRA1; HBA2, adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercholesterolaemia; UGTI; syndrome, APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; althinimatic factors amyloid precursor protein; presentlin-1; althinimatic factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and factors and fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical
                                    Factor IX mutation correcting oligonucleotide SEQ ID NO: 2448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.8; D
Pred. No. 72;
0; Mismatches
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Best Local Similarity :
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27-MAR-2001; 2001WO-US009761

antilipemic; ss.

WO200173002-A2 Homo sapiens.

04-OCT-2001

Rice MC;

UYDE ) UNIV DELAWARE.

```
The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblascoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus apolipoprotein E (APDE), IDL receptor (LDLR), WDP-glucuronosyltransferase (UGTI), amyloid precursor protein (ARC), presentilin-1 (PSEN1) and presentilin-2 (SSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, although the deaminase deficiency, cystic fibrosis, although the deaminase deficiency, cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deam of the deaminase deficiency cystic fibrosis, although the deam of the deaminase deficiency cystic fibrosis, although the deaminase deficiency cystic fibrosis, although the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of the deam of deam of the deam of the deam of the deam of the deam of the deam of deam of the deam of the deam of the deam of the deam of the deam of t
Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 183; 294pp; English.
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0; Gaps

27; Indels

Length 121;

DB 1;

Score 21.8; DE Pred. No. 72; 0; Mismatches

Query Match
Best Local Similarity 58.5%;
Matches 38; Conservative

844

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27; Indels

Conservative

8 Dp ò

GAAGTTTTTGAAAACACTGAAAGAACAGTGATATTTCCACATAATACCCTTCAGATGCA 111

CAGTA 849 112 GAGCA 116

845 52

785 GCAGICICAAAAACGACAGAAIGAICICIGIIIGIIICCAAGGCAAACCAIICAAIAICA

11

785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGCTTTCCAAGGCAAACCATTCAATATCA 844

GAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCA

70

8

845 CAGTA 849 10 GAGCA 6 ò

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Matches

ABA79598 standard; DNA; 121 BP

ABA79598;

24-JAN-2002 (first entry)

Factor IX mutation correcting oligonucleotide SEQ ID NO: 2444.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDRV2A, melanoma, APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDRA; familial hypercholesterolaemia; UGT1; syndrome, APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss.

WO200173002-A2

27-MAR-2001; 2001WO-US009761.

27-MAR-2000; 2000US-0192179P. 01-JUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P. 27-MAR-2000; 2000US-0192176P.

(UYDE ) UNIV DELAWARE.

Rice MC; Gamper HB, Kmiec EB,

WPI; 2001-639230/73.

Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.

Claim 7; Page 183; 294pp; English.

The present invention provides single-stranded oligonuclectides which can be used for the targeted alteration of genomic sequences, where the oligonuclectide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTK, Cyclin-dependent Kinase inhibitor 2A retinoblastoma, BRCA1, BRCA2, CFTK, Cyclin-dependent Kinase inhibitor 2A (HBA1), haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolicoprotein E (APOS), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentiln-1 (PSEN1) and presentiln-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, had anomalia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention 

Sequence 121 BP; 48 A; 16 C; 28 G; 29 T; 0 U; 0 Other;

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Query Match 0.6%; Score 21.8; DB 1; Length 121; Best Local Similarity 58.5%; Pred. No. 72;
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2655 GCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGAT 2714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                  785 GCAGICTCAAAAACGACAGAATGAICICIGIIIGIIICCAAGGCAAACCAIICAAIAICA 844
                                                                    50 GAAGITTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithehial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the crvix, notably cervical cancer. Note: The sequence data for this patent did not form patr of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                      Probe #14645 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 GCTGAACGAGAGAGAGAGACCCGGGAGGAGGCAGTGCGAGAGCTGCAGGAGATGGTGCA 71
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell;
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51.5%; Pred. No. 86;
stive 0; Mismatches 47; Indels
27; Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 14645; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00623366.
27-SEP-2000; 2000US-023468FP.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GS-00024263;
                                                                                                                                                                                                                               AAI24712 standard; DNA; 224 BP.
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                                                                                                                                                                                                                                                                                                   12-OCT-2001 (first entry)
38; Conservative
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Les 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer; ss.
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                                                                                                       845 CAGTA 849
                                                                                                                                          110 GAGCA 114
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17-OCT-2001 (first entry)
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                                                                                                                                                              WO200157272-A2.
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ABA36799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GCTGAACGAGAGAGAGCCCGGGAGGAGGCAGGGAGGCTGCAGGAGATGGTGCA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 21.8; DB 1; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 18267; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 47; Indels
                                                                                                                                                                                                                  Human foetal liver single exon nucleic acid probe #18267
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GCCCCAGCCGCCTCGGGGGAGCAGCTGGCGGTGGCC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MX-2200; 2000US-0201456P.
30-UDN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SFP-2000; 2000US-023468P.
21-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000GB-00034263.
                                                                                                          BP.
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                                                                                                         ABA69962 standard; DNA; 224
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les 50; Conservative
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                                                                                                                                                                                                                                                                                                                       WO200157277-A2.
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                                                                                                                                             ABA69962;
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                                                                        RESULT 143
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                                                                                         ABA69962
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AAI50074 standard; DNA; 224 BP

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AAI50074

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2655 GCTGGAIGGCAICACTGGACTCGAIGGACGIGAGTCTGGGTGAACTCCTGGAGTTGGTGAT 2714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #18760 used to measure gene expression in human placenta sample.
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                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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2655 GCTGGAIGGCATCACTGGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGAT 2714
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                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 18621; 658pp + Sequence Listing; English.
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Pred. No. 86;
0; Mismatches
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30-JUN-2000; 2000US-0068408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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                         03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02365359P.
04-OCI-2000; 2000GB-00024263.
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1 Similarity 51.5%;
50; Conservative (
30-JUN-2000; 2000US-00608408
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and e.g. cardiovascular disease. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
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30-JUN-2000; 2000US-00608408.
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                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheiner's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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                                             Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                 Example 4; SEQ ID NO 18163; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 224 BP; 46 A; 50 C; 97 G; 31 T; 0 U; 0 Other;
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30-JUN-2000; 2000US-00608408.
03-AGG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488898/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2003
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                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS43718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                      brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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2655 GCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGAT 2714
liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioletomyomtosis; Karagener syndrome; pulmonary hyeolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hypaliasy ciliary dyskinesis; pulmonary hypertension; hypaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon probe ORF from lung SEQ ID No 18288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224 BP; 46 A; 50 C; 97 G; 31 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 GGCGCAGGCGGCCTCGGGGGAGGAGCTGGCGGTGGCC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21.8; DB; Pred. No. 86; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%;
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26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABS18297 standard; DNA; 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 51.59
Watches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 149
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ID ABS1
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24-SEP-2001; 2001US-00960352.

26-SEP-2002.

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The invention relates to a spatially addressable set of single exon nucleic acid probes having one of from the nucleic acid probes to a measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung and the specification, or their complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements or the probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (b) detecting at least one exon from genomic sequences of the array; identifying exons in a eukaryote lung mRNA, to a single exon probe, the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) measuring the expression of each of the exons in several in the above mentioned microarray; assigning exons to a single exon probe a included above and (b) measuring the expression of each of the exons in the tissues and/or cell types undicates that tissues and/or cell types undicates that tissues and/or cell types undicates that tissues and/or cell types which the exons in the tissues and/or cell types which the exons in a gene, particularly using mman or probes/open reading frames (ORF). The probes for the exons in the tissues and/or cell types which the study of lung diseases (ILD), familial idiopathic pulmonary diseases (ILD), familial idiopathic pulmonary dispasses (ILD), familial idiopathic pulmonary dispasses, humonary and expense tendence is a s
                                                  The invention relates to a spatially-addressable set of single
Claim 4; SEQ ID NO 18288; 634pp; English.
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2655 GCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGAT 2714 0; Gaps Score 21.8; DB 1; Length 224; Pred. No. 86; 0; Mismatches 47; Indels C Sequence 224 BP; 46 A; 50 C; 97 G; 31 T; 0 U; 0 Other; 2715 GGACAGGGAGGCCTGTCCTGCGCGCGATTCATGGGGTC 2751 72 édececadecédecitedesedades de dececedo de 108 Local Similarity 51.5%; nes 50, Conservative Query Match Matches S 셤 ò

Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Bovine EST associated with lactation/muscle/fat deposition #7535. ABX42370 standard; cDNA; 361 BP 20-FEB-2003 (first entry) ABX42370; RESULT 150 ABX42370 

Bos Taurus.

JS2002137139-A1

The invention relates to a purified nucleic acid molecule associated with catcation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing as ABX34886-ABX4947, or complements of them. Also included are caid linked to a promoter and a 3' non- translated sequence that caid linked to a promoter and a 3' non- translated sequence that caid linked to a promoter and a 3' non- translated sequence that corporations in the cell to cause termination of transcription and addition of the comprising a level or pattern of a molecule in a bovine cell or cassue comprising a level or pattern of a molecule in a bovine cell or tissue comprising a level or pattern of a molecule in a bovine cell or complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid pattern of the complementary nucleic acid sequences or its complementary nucleic acid molecule. The LMFD nucleic acid, is used for the detection of the complementary nucleic acid is predictive of the acterning a level or pattern of the complementary nucleic acid is used for the molecule. The LMFD nucleic acid, is used for the molecule. The LMFD nucleic acid is used for the sequence mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the constant sequence was not shown in the specification but was obtained in plantary in the present sequence is not shown in the specification but was obtained in New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, ô Score 21.8; DB 1; Length 361; Pred. No. 98; 0; Mismatches 27; Indels 0 Sequence 361 BP; 117 A; 62 C; 83 G; 99 T; 0 U; 0 Other; deposition, useful for genome mapping, gene identific cattle breeding, or for genetically improving cattle. segdata.uspto.gov/sequence.html?DocID=20020137139 Tao N, Warren WC; present sequence was not shown in the specelectronic format from the USPTO web site: Claim 2; SEQ ID NO 7535; 245pp; English. 12-JAN-1999; 99US-0115707P. o.6%; Similarity 58.5%; Byatt JC, Mathialagan N, Ouery Match Best Local Similarity 58.5: Matches 38; Conservative (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. WPI; 2003-110599/10. (MATH/) MATHIALAGAN (TAON/) TAO N. (WARR/) WARREN W C. 

1461 CATGGAAAAGAAATGCAAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAATAGCTGT 1520

ВР. ABK44151 standard; cDNA; 522 1521 GAAAA 1525 228 AAACA 232 ABK44151; RESULT 151 ABK44151/c В ò

(first entry)

21-MAY-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention relates to the isolation of cDNA sequences encoding human pancreatic tumour proteins. The polynucleotide sequences encoding human pancreatic tumour proteins are useful for stimulating an immune response in a patient and treating pancreatic cancer in a patient. A host presence of cancer in a patient. A composition comprising the polynucleotide, its encoded protein, or an antibody that binds to the protein may be used in the diagnosis, prevention and/or treatment of diseases, particularly pancreatic cancer. The sequences of the invention are also useful in pharmaceutical compositions, e.g. vaccines, for the diagnosis and treatment of pancreatic cancer. Such compositions may be useful for inhibiting the development of cancer in a patient, or as markers for the progression of cancer. The polynucleotide sequences may also be used as probes or primers for nucleic acid hybridisation assays. The markets for the progression of cancer acid hybridisation assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding pancreatic tumor polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
                                                Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         921 CCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTG 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21.8; DB 1; Length 522; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 522 BP; 110 A; 162 C; 132 G; 116 T; 0 U; 2 Other;
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cDNA #91 encoding human pancreatic tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 142; 167pp; English.
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                                                                                                                                                                                                                                                                                             07-AUG-2000; 2000US-0223130P.
30-JAN-2001; 2001US-0265447P.
15-MAY-2001; 2001US-0291201P.
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Best Local Similarity 62.7%;
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour proteins
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                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyle RA,
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Homo sapiens

RESULT 152 AAL48492

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Transmembrane serine protease MP493 for diagnosis of and developing drugs for cancer, kidney diseases and lung diseases e.g. asthma, allergy, bronchitis, pneumonectasis, pancreatitis and nephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ACTAGTCAATCACACTAGGACCACAGCCTTGTCTAACTCAATGAAACTAAGCCAT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a thuman serine procease designated MR493. The sequences can be used in the diagnosis of and development of drugs for treating cancer, kidney and lung diseases, for example asthma, allergy, bronchitis, pneumonectasis, viral diseases, shock, multiple organ failure, pancreatitis and nephritis. The present sequence is a coding sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deletion; cistron; expression; human insulin; interferon; interleukin; tissue plasminogen activator; growth hormone releasing factor; translational activating sequence; HPI; human proinsulin; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 711 BP; 149 A; 205 C; 212 G; 145 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        Okawa K;
                                                                                                                                                                                                                                                                                                                                                                        Okamoto A,
                                                                                     /partial
/note= "no start or stop codon"
                                           /*tag= a
/product= "unknown protein"
                                                                                                                                                                                                                                                                                                                                                                        e,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                  23-JAN-2001; 2001JP-00014963.
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                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y, Sugano S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GCCCGTGGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-566849/60.
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                                                                                                                                                   WO200259295-A1
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                                                                                                                                                                                             01-AUG-2002
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Key
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AAQ3831
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forms.
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                                                                                                                                                                                                                                                                        Example 3 describes the construction of plasmid pHDM121. The gene encoding MetTyr human proinsulin was produced from synthesised oligonucleotides, which, when annealed, comprise both complementary strands of the MetTyr human proinsulin gene with Ndel-BamHI cohesive ends. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proinsulin gene; human insulin analogues; ds; sticky ends.
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 268 BP; 49 A; 75 C; 87 G; 57 T; 0 U; 0 Other;
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| Similarity 53.6%;
45; Conservative (
                        91US-00811045
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(first entry)
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Best Local Similarity
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04-AUG-1989;
                        18-DEC-1991;
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04-JAN-1991
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Expression of this gene lead to the inclusion of an extra amino acid (Arg) in the second position from the N-terminal of mature hpl. The extra amino acid chost provides increased expression levels of the protein acid then cleaved off to avoid undesirable immuno-logical effects when used in humans. (Updated on 25-MAR-2003 to correct PN field.)
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was, together with other components, used in the construction of plasmid pRB145. See also AAQ05662-3, AAR06443-4 and AAR07658-60. (Updated on 25-MAR-2003 to correct PA field.)
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Pred. No. 1e+02;
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Local Similarity 53.6%;
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P-PSDB; AAR33855.
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19-JUL-1993
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                                                                                                                         cerdenace de de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia de la constancia del constancia del constancia del constancia de la constancia del constancia d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
                                                                        2550 CCAGTACTTTGGCCACCTGATCAGAAGAGCTGACTCACTGGAAAAGACCCTGATGCTGGG
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Pred. No. 1e+02;
0; Mismatches 39; Indels
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16-JAN-2002; 2002US-0349738P.
16-JAN-2002; 2002US-0349793P.
16-JAN-2002; 2002US-0349979P.
53.6%;
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                                                                                                                                                      GACACCAACCAGAAGACCGAGCTGCAGGCCATCCACCTGGCCCTG
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50.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV p15RnaseH.opt.SF2 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 26; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX37095
ID ABX37095 standard; cDNA; 372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2002; 2002WO-US021342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349728P.
                                                                                                                                                                                                                                                                                                      ACC78504 standard; DNA; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnett
                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003020876-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2003
18-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                      ACC78504;
                                                                                            2662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91
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2602 ATGCTGGGAGGGATTGGGGGCAGGAGAGAAGGGGACGACAGAGGATGAGATGAGATGGCTGGAT 2661

0.6%; Score 21.6; DB 1; Length 360; 50.0%; Pred. No. 1.1e+02; Live 0; Mismatches 54; Indels (

54; Conservative

Matches

Query Match Best Local Similarity

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26-SEP-2002.
      Bos Taurus.
ABX37095;
               (TAON/)
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ABX14193;
                                                                                                                                                                                                                                              AAK53749;
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                                                                                                                                                                  AAK537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                    g
                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a purified nucleic acid molecule associated with catcation or muscle and fat deposition (designated LMFD), derived from catcation or muscle acid can specifically hybridise to a second nucleic acid molecule cacid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are compressed to a promoter and a3 'non-translated sequence that cacid linked to a promoter and a3 'non-translated sequence that comprising a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid septemble obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the molecule. The LMFD uncleic acid is used for the detection of the molecule. The LMFD nucleic acid, subset for the acterning a level or pattern of the molecule. The LMFD mucleic acid, subset for the complementary nucleic acid is used for the substructs for use in catle gene expression, or for generically improving cattle. The Present sequence is one of the complement sequence was not shown in the specification but was obtained in a laboration in a laboration of constructs for use in catle and analysis, acitle of present sequence was not shown in the specification but was obtained in a laboration of the complement expension of the sequence was not shown in the specification but was obtained in a laboration of the complement expension of the sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACTIGIATITICIAATATITIACTITATICIATITITIACTITIAATITGCACTIATITITATIGA 3016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 GACTAITITITCCAATACGAACTAIGAAAATICTICIGAGGCIGAAATAATTIGGGATAA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                          Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                           Bovine EST associated with lactation/muscle/fat deposition #2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=20020137139
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0.6%; Score 21.6; DB 1;
Best Local Similarity 53.6%; Pred. No. 1.1e+02;
Matches 45; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tao N, Warren WC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 2260; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence was not sh
electronic format from the
                                                          20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                  US2002137139-A1.
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3457 TGGCTTTAAAAAGTATTTGCTGCTATTAAACATGAATTAAGTCTTATTTGGACTATAAGTG 3516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3' -end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53416-AAK54275 represent fragments of the gene library described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 idecingcacacacaterretreceaeaceacatrerreardacerecedeaetearrie 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine transport and binding associated protein encoding cDNA SEQ ID 314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine, liver, gene library, amino acid synthesis, binding protein, cell metabolism, energy metabolism, fatty acid metabolism, synthesis, phospholipid metabolism, purine, pyrimidine, nucleoside, nucleotide, replication, transcription, transcription, transcription, transcription,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 427 BP; 95 A; 126 C; 101 G; 105 T; 0 U; 0 Other;
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3017 ITTTTCTAATAAATCCAGTCCTT 3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 GAGCAACCAAAGGGATGCGGATGA 409
                                                              329 cgicacicaaagcaaccaaicair 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 106; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2001; 2001DE-02003510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2001; 2001DE-02003510.
                                                                                                                                                                                                                                                          AAK53749 standard; cDNA; 427
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-2001
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2957

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Homo sapiens.
Unidentified.
          Synthetic.
 Human;
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fibrin clot; haemostatic; tissue factor; zymogen; Factor IX; Factor X; prothrombin; thrombin; Factor V; Factor VIII; fibrinogen; fibrin; plasma factor; bleeding episode; haemophilia A; haemophilia B; thrombus; intimal hyperplasia; restenosis; cardiogenic embolism; stroke; platelet deposition; percutaneous transdermal coronary angiogenesis; ischaemia; reperfusion; thrombolysis; rhumour; angiogenesis; ischaemia; reperfusion; thrombolysis; hypotension; adult respiratory distress syndrome; ARDS; myocardial infarction; vasotropic; cerebroprotective; antibacterial; immunosuppressive; cardiant; gene therapy; ds; plN174.
                                                                                                         coagulation; Factor VII; Factor VIIa; blood coagulation;
Plasmid pLN174 for expressing human coagulation Factor VII.
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/notes= "No start codon shown. Xaa = gamma carboxylated glutamic acid" (pos:324. .326, aa.Xaa) (pos:330. .332, aa.Xaa) (pos:339. .344, aa.Xaa-Xaa) (pos:357. .362, aa.Xaa-Xaa) /partial /transl_except= (pos:300. 305.aa:Xaa-Xaa /transl_except= (pos:324. 326.aa:Xaa) /transl_except= (pos:330. 332.aa:Xaa) /transl_except= (pos:357. 362.aa:Xaa) /transl_except= (pos:357. 362.aa:Xaa-Xaa /transl_except= (pos:369. 371.aa:Xaa) /transl_except= (pos:369. 371.aa:Xaa) /transl_except= (pos:369. 371.aa:Xaa) 'product= "Coagulation Factor VII" Location/Qualifiers .1505 ď

WO200277218-A1

03-OCT-2002

21-MAR-2002; 2002WO-DK000189.

22-MAR-2001; 2001DK-00000477.

(NOVO ) NOVO NORDISK AS

Persson E:

WPI; 2003-058374/05. P-PSDB; ABG73119 Novel factor VII polypeptide, its derivatives useful for preparing medicament for treating bleeding episodes, or for enhancing normal hemostatic system, especially for treating hemophilia.

Disclosure; Page 82-85; 96pp; English.

The invention discloses a human factor VII polypeptide, or a variant or derivative of it, where an amino acid has been modified. This change results in a polypeptide with the same or an increased activity when compared to recombinant wild type human factor VIIa. Blood coagulation compared to recombinant wild type human factor VIIa. Blood coagulation consists of a complex interaction of various blood components that consists of a complex to a fibrin clot. Initiation of the hamostatic process is mediated by the formation of a complex between tissue factor or and Factor VIIa (the active form of the Factor VII zymogen). This complex activates Factors V and VIII leading to a full thrombin burst. The activates Factor VII zymogen, or its derivative, can be modified in its clot. The Factor VII zymogen, or its derivative, can be modified to activate plasma factor X or IX. The factor VII deplypeptide to activate plasma factor X or IX. The factor VII delivative is useful for preparing a medicament for the treatment of bleeding episodes, for the preparing a medicament for the treatment of bleeding chrombus formation. The inactivated factor VII derivatives are useful for treatment of the mormal hamostatics are useful for treating intimal

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                                                                                                                                                                                                                                                                                                                                                                             2690 GAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAAT 2749
                         (PTCA), stroke,
                     disorders, percutaneous transdermal coronary angioplasty (FTCA), stroke, cancer, tumour metastesis, angiogenesis, ischeemia/reperfusion, trheumatoid archritis, thrombolysis, arteriosclerosis, acute and cindications, such as inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS) and myocardial infarction. The sequence presented is the plasmid, pLNN74, which expresses the inactivated human coagulation Factor VII polypeptide
                                                                                                                                                                                                                                                                                          0; Gaps
hyperplasia, restenosis, cardiogenic emboli, platelet deposition
                                                                                                                                                                                                   Sequence 6098 BP; 1413 A; 1587 C; 1623 G; 1475 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           21.6; DB 1; Length 6098;
No. 1.6e+02;
                                                                                                                                                                                                                                                                                        34; Indels
                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                           0.6%; Score 21.6;
55.3%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                   3000 GCACTTATTTTATTGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                          3060 AAAATTATTAATTTCT 3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2750 AACCCTGATAAATGCT 2765
                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.39
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ADB81477 standard; DNA; 144 BP. ADB81477; ADB81477/ 

04-DEC-2003 (first entry)

Human oestrogen receptor alpha splice variant 7 (ESR-alpha VII) DNA.

human; ds; oestrogen receptor alpha; ESR-alpha VII; oestrogen receptor 1; SSR1; NRSA1; bone maintenance; cardiovascular system; cancer; gene therapy; hyperproliferative disease; inflammation; tumour formation; infection; cytostatic; antiinflammatory; antimicrobial.

Homo sapiens.

WO2003052072-A2.

26-JUN-2003

13-DEC-2002; 2002WO-US040083.

18-DEC-2001; 2001US-00027983.

(ISIS-) ISIS PHARM INC.

Dobie KW, Roach MP;

WPI; 2003-577322/54.

New antisense compound targeted to nucleic acid encoding estrogen receptor alpha and inhibiting expression of estrogen receptor alpha, useful for treating a disease or condition e.g. a hyperproliferative disease.

Claim 20; Page 232; 232pp; English.

This invention relates to human oestrogen receptor alpha (ESR-alpha), and the novel antisense oligonuclectides that modulate its expression. The ostrogen receptor alpha protein is also known as oestrogen receptor 1, ESR1, and NR3A1. Oestrogen, the steroid hormone ligand of ESR-alpha, is important for bone maintenance and plays a protective role in the cardiovascular system, as well as being required for normal sexual maturation through promoting growth and differentiation. Splice variants of ESR-alpha, however, have been associated with various cancers oligonuclectides that inhibit the expression of ESR-alpha in cells or tissues can be used in gene therapy to treat conditions such as

10664775-2.rng

126 GTGGTGGGGACCGCTGGC 144

243

standard; DNA;

AAA49060 AAA49060;

RESULT 163

AAA49060

HIV; human immunodeficiency virus; vaccine; AIDS; snut; silent nucleotide substitution; ds.

Human immunodeficiency virus 1.

WO200029561-A2.

25-MAY-2000.

27-MAR-2000; 2000WO-DK000144.

99DK-00000427.

29-MAR-1999; 09-APR-1999;

(STAT-) STATENS SERUM INST

Snut O-N-Lang DNA used in HIV DNA vaccine.

(first entry)

(revised)

15-SEP-2003 16-NOV-2000

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125

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(TSP) polypeptide, comprising a protease domain of a type-II membrane-
type serine protease or its biologically active portion. The invention is
useful for cleaving a TSP substrate protein by contacting TSP with a
substrate protein under serine protease activity permissive conditions.
The invention is useful as an immunogen to generate antibodies that bind
TSP or TSP1-TSP43 proteins, useful for treating disease e.g. cancer and
autoimmune disease. The present sequence is human TSP1-TSP34 gene exon
hyperproliferative disease, inflammation, tumour formation and to prevent or delay infection. As such, the present invention describes these antience oligos as having cytostatic, antiinflammatory and antimicrobial activities. This polymucleotide is the DNA of the human oestrogen receptor alpha splice variant designated ESR-alpha VII of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New purified transmembrane serine protease polypeptides (TSP1-TSP34) comprising a protease domain or its biologically active portion, useful for identifying modulators of proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; transmembrane serine protease; TSP; therapy; immunogen; cancer; autoimmune disease; immunomodulatory; immunosuppressive; enzyme; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to purified human transmembrane serine protease
                                                                                                                                                                                                                          2680 GACGIGAGICIGGGIGAACICCIGGAGIIGGAIGGACAGGGAGGCCIGICCIG 2734
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                gaggaggagcriggccagccgcrigcrigcrigcrigcagggarcaggccrigccrrig 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human transmembrane serine protease (TSP1-TSP34) gene exon 11.
                                                                                                                                                     DB 1; Length 144;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 172 BP; 26 A; 51 C; 66 G; 29 T; 0 U; 0 Other;
                                                                                                                 Sequence 144 BP; 38 A; 48 C; 40 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                        21;
                                                                                                                                                   0.6%; Score 21.4; Dl
61.8%; Pred. No. 97;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 232; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                               AAD58758 standard; DNA; 172 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2002; 2002US-0352806P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L, Niknejad A,
                                                                                                                                                                                            34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENEPROT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-627608/59.
                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                    106
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                                                                                                                                                       Query Match
                                                                                                                                                                              Local
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                         RESULT 162
                                                                                                                                                                                                                                                                                                                                               AAD58758
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The present invention relates to a nucleotide construct with optimised codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The construct uses codons from highly expressed mammalian proteins to code for each derivative of an early, primary HIV envelope gene. The first stage in the production of the construct was the cloning of an HIV envelope gene. A nucleotide sequence encoding this gene was then created using codons from highly expressed mammalian genes. The present sequence is one of the snuts (AAA49060-A49079) that were created by redesigning this nucleotide construct so that restriction enzyme sites surrounded functional regions of the sequence. The snuts were then assembled into pieces (AAA49080-A49092). Each derivative of the envelope gene (AAA49083-A49097) was then built using the pieces. The HIV DNA vaccine may be used as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patients. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing nucleotide sequence construct with optimized codons for human immunodeficiency virus (HIV) genetic vaccine involves obtaining a first nucleotide sequence from a HIV patient, redesigning and assembling it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1423 CATGACATTGTACAGGAGACAGGGATCGAGACCATCCCCATGGAAAAGAAATGCA 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 21.4; DB 1; Length 243; 11.8%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 243 BP; 53 A; 81 C; 77 G; 32 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV98158 standard; cDNA; 380 BP.
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Best Local Similarity
Matches 34; Conserv
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GTAAAGAGATACCCCACGC 99

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GGAGAGGTACCTACCCTCGTCCAAGGTAAGGAGCAGTAGCTGCGCTTTGCTGGAGCAGCC 80

0.6%; Score 21.4; DB 1; Length 172; 4.4%; Pred. No. 1e+02; ve 0; Mismatches 36; Indels

0; Mismatches

ilarity 54.4%; Conservative

Local Similarity tes 43; Conserv

Best Loc Matches

Query Match

(first entry)

12-JUL-2002

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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99165); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a) Polypeptides (ABF6856 to ABF68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polymelectides, and patient and compositions comprising polypeptides, polymelectides, and intibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymulacides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour perparation of ribozyme molecules for inhibiting expression of the tumour the tumour cells, in vaccines and for gene therapy. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21.4; DB 1; Length 380;
Pred. No. 1.3e+02;
0; Mismatches 22; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 3566; 300pp + Sequence Listing; English.
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                                                          Human pancreatic cancer expressed cDNA SEQ ID NO 3566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001US-0265305P.
31-JAN-2001; 2001US-026582P.
09-FEB-2001; 2001US-026768P.
21-MAR-2001; 2001US-0287112P.
                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2001; 2001US-0291631P.
12-JUL-2001; 2001US-0305484P.
20-AUG-2001; 2001US-0313999P.
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                                                                                                                      cytostatic; tumour; gene; ss
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Matches 34; Conservative
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                                                                                                pancreas;
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Jiang Y;

Hepler WT,

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert or cytosine (C) but not methylated C, to uracil, then part of the genomic supplicant in the contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognesis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastroinestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP'S); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultanceusly. ABOJAHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic DNA sequences used to illustrate the method e degree of cytosine methylation described in the
                                                                              Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                     Oligonucleotide for detecting cytosine methylation SEQ ID NO 34557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guetig D;
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from chemically treated DNA.
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Best Local Similarity 54.4%;
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
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ABQ47967 standard; DNA; 612 BP.

RESULT 166 ABQ47967,

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à 셤 ABQ47966 standard; DNA; 612 BP.

RESULT 165

ABQ47966;

ABQ47966 ID ABQ4 XX AC ABQ4 XX

ABQ47967;

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert octosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes oligomers, the degree of methylation is calculated. The method is used: if for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-
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                                                                                                                                                                     Human, cytosine methylation, S'-CpG-3', uracil; cytosine; diagnosis, drug, side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
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                                                                                                        Oligonuclectide for detecting cytosine methylation SEQ ID NO 34558.
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Pred. No. 1.48+02;
0; Mismatches 36; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; 56pp + Sequence Listing; 56pp; German.
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1 Similarity 54.4%;
43; Conservative (
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                                12-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200218632-A2.
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 167
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2764 ACACGACTGAGCAACTGAACTGAACTGTACTGAACCTTAGTAGTTTATATTACT 2823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                         Human, foetal liver, gene expression, single exon nucleic acid probe, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #23734 used to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 22872; 639pp + Sequence Listing; English.
                                                                      Human foetal liver single exon nucleic acid probe #22872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 177 BP; 44 A; 45 C; 44 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR,
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                                                                                                                                                                                                                                                                                                               26-MAY-2000, 2000US-0207456P.
30-UTM-2000; 2000US-00608408.
33-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
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                                  01-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
                                                                                                                                                                                    WO200157277-A2.
                                                                                                                                                   Homo sapiens.
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGACTCTCTTGAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                       2764 ACACGACTGAGCAACTGAACTGAACTGTACTGAAACCTTAGTAGTTTATATTACT
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                      Example 4; SEQ ID NO 23770; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 21.2; DB 1; Length 177; Best Local Similarity 53.7%; Pred. No. 1.2e+02; Matches 44; Conservative 0; Mismatches 38; Indels (
                                                                                                                                                                                                                                                                                                                            Sequence 177 BP; 44 A; 45 C; 44 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver single exon probe, SEQ ID No 23846.
                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR;
                                                                                                                                                           gene expression in human bone marrow.
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                                                  (MOLE-) MOLECULAR DYNAMICS INC
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      27-SEP-2000; 2000US-0236359P 04-OCT-2000; 2000GB-00024263
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                  Hanzel DK,
                                                                                                             WPI; 2001-488900/53
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                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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Pred. No. 1.2e+02;
0; Mismatches 38; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 177 BP; 44 A; 45 C; 44 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 23734; 654pp; English.
                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                               Rank
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                                                                                                                                                                                                                                                                                                                                      gene expression in human placenta.
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                                                                                                     04-FEB-2000; 2000US-0180312P.
26-WAY-2000; 2000US-0207456P.
30-UVN-2000; 2000US-00608408.
31-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                        30-JAN-2001; 2001WO-US000663
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                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53
            WO200157272-A2
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                           09-AUG-2001
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult ther. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements, fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABSISOII-ABSISOS represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2764 ACACGACTGAGCAACTGAACTGAACTGAACTGAAACCTTAGTAGTAGTTTATATACT 2823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AGACCACTGGGAACAATGAGAAGGAGAGATTCTACTGGTCACAGACAAGACTCTCTTGAT 63
                                                                                                                                                                                                                                                                                                                                                                           ; DB 1; Length 177; 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus licheniformis genomic sequence tag (GST) #3901.
                                                                                                                                                                                                                                                                                                                                       Sequence 177 BP; 44 A; 45 C; 44 G; 44 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Score 21.2;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                  Claim 4; SEQ ID NO 23846; 658pp; English
gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2824 CAGAAATAGTAATTTCATATG 2845
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                                                                                                                                                                                                                                                                                                                                                                           0.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001; 2001US-0279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000US-00680598
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                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus licheniformis.
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                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   fatches
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1D ABK
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Claim 4; SEQ ID NO 3901; 200pp; English

Gaps ö

38; Indels

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The invention describes a method of monitoring differential expression of content in a first Bacillus cell relative to expression of the genes in other than a calls, comprising hybridasing labelled nucleic acid probes isolated from Bacillus cells, comprising hybridasing labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for menauring the expression of genes in a first Bacillus cell relative to expression of the same genes in or more second Bacillus cells. The method is useful for monitoring genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring che way in which Bacillus cells adapt to changes in culture conditions, in which Bacillus cells adapt to changes in culture conditions, on the confinence represents a genomic sequence information is available. This sequence represents a genomic sequence information is available. This sequence represents a genomic sequence information is available. This sequence represents a genomic sequence information is available. This sequence expenses of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human polypeptides and polymuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2589 ggapangaCcCTGATGCTGGGAGGATTGGGGGCAGGAGAGAGGGGAC 2638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GCCATCGGCCGGGGTGCGGTGGAGGGCAGGAGCAGGAGCAGGAGGC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 231; .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 231 BP; 55 A; 41 C; 131 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX polynucleotide sequence SEQ ID NO:15045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 21.2; DE
4.0%; Pred. No. 1.2e-
.ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN23284 standard; cDNA; 273 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2001; 2001WO-US010836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myasthenia gravis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 64.0
les 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14.
P-PSDB; ABP07532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                       The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 or 1 the specification). ABM15762 to ABM27222 encode the human ORFX proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, or sociated with ORFX-associated disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ cramplantation, cardiovascular disorders, disorders, infectious corage disease, various immune deficiencies and disorders, infectious croage disease, autoimmune disorders such as multiple sclerosis, rheumatorid arbitis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, ulcers, for treating obsectorosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, competcion or regeneration and treatment of lung or liver fibrosis, creperitation injury in various tissues and conditions resulting observation cytokine damage. NuB. The sequence data for this patent did not corm part of the printed specification, but was obtained in electronic corm part of the printed specification, but was obtained in electronic corm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%; Score 21.2; DB 1; Length 273; Best Local Similarity 69.0%; Pred. No. 1.38+02; Matches 29; Conservative 0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1395 AGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACA 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AGGAGCTAATGACCTGTGCCAAGAGTGTGAGGATATTGTCCA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 273 BP; 67 A; 78 C; 75 G; 53 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer expressed polynucleotide 14742,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; breast cancer; cell marker; cytostatic; ss.
                   Disclosure; SEQ ID NO 15045; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL22285 standard; cDNA; 280 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0176077P.
2000US-0189167P.
2000US-0192099P.
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2000US-0205230P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0211315P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-451856/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200151628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL22285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynuclectides encoding protease homologs of the G-protein-coupled protease family, useful in identifying agonists and antagonists for diagnosis and treatment of protease mediated disorders.
                                                                                The invention relates to human breast cancer expressed polynucleotides (AALO7544-AALS6789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                             2764 ACACGACTGAGCAACTGAACTGAACTGAACTGTACTGAAACCTTAGTAGTTTATATTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AGACCACTGGAACAATGAGAAGGAGAGATTCTACTGGTCACAGACAAGACTCTTGAT
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                             Length 280;
                                                                                                                                                                                                                                                                                                                                                                                   38; Indels
                                                                                                                                                                                                                                                                                                  Sequence 280 BP; 69 A; 70 C; 74 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; gene; G-protein-coupled protease; gene the protease mediated disorder; proliferative disorder; differentiative disorder; haematcopoietic disorder; haematcopoietic disorder.
                                                                                                                                                                                                                                                                                                                                        Score 21.2; DB 1;
Pred. No. 1.3e+02;
0; Mismatches 38;
                                          Claim 1; Page 2657-2658; 3695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 95-98; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein-coupled protease #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2824 CAGAAATAGTAATTTCATATG 2845
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                                                                                                                                                                                                                                                                                                                                           0.68;
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK30273;
                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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The present sequence

Sequence 609 BP; 139 A; 153 C; 156 G; 161 T; 0 U; 0 Other;

disease or condition associated with a protease. represents a protease gene of the invention.

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treminity and agents that annow to the pivotesh and identification of a complement (i.e. gene that modulates the expression of the mucleic acid can be used to its complement (i.e. gene that modulates the expression or activity of the complement of an explaint modulates the expression or activity of the concleic acid, and can be used to isolate the protein. The mucleic acid can be used in diagnostic assays for determining nucleic acid expression or activity in the connext of a biological sample (e.g., blood, serum, cells, tissue) to determine whether an individual has a disease or disorder, or is at risk of developing a disease or disorder, associated of with aberrant expression or activity of the mucleic acid. The nucleic acid can be used to detect mutations in protease genes and gene expression probes to detect naturally-occurring genetic mutations in a protease gene. The nucleic acid can be used as the protease mediated disorders that can be used to diagnose and treat or identify agonists and antagonists that can be used to diagnose and treat as probes, primers, in biological assays, to determine patterns of gene expression, to design ribozymes and to construct transgenic animals. The presents sequence represents one of the 268 disclosed human G-proteinidentifying agents that bind to the protein and identification of a

Sequence 505 BP; 95 A; 135 C; 170 G; 105 T; 0 U; 0 Other;

Gaps ö DB 1; Length 505; 13; Indels TITITITITITITAAAGAAIGICATICITIGIGAAGITITIGA 3294 TITITITITITICIAACAGAIGCAITIAAIGGGAAAICTIAA 42 0.6%; Score 21.2; DB 1; 69.0%; Pred. No. 1.5e+02; live 0; Mismatches 13 29; Conservative Local Similarity 3253 Query Match Matches ò 엄

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ADA50533 standard; DNA; 609 BP ADA50533 

20-NOV-2003 (first entry) ADA50533;

Human protease gene SEQ ID NO:37,

ds; enzyme; gene; human; protease.

Homo sapiens.

WO2003040393-A2.

15-MAY-2003.

04-NOV-2002; 2002WO-IB004615

06-NOV-2001; 2001US-0332633P.

Martinez RAM, Sigurdsson GT;

(DECO-) DECODE GENETICS

WPI; 2003-441582/41. P-PSDB; ADA50486.

Novel isolated protease polypeptide and polynucleotide encoding the polypeptide useful for diagnosing and treating diseases or conditions associated with a protease.

Claim 4; Page 80-81; 160pp; English.

The invention relates to a novel isolated polypeptide comprising an amino acid sequence that has greater than 95 % identity to any one of 47 150-850 residue protease polypeptide sequences, given in the specification. The nucleic acids, probes, primers, polypeptides and antibodies of the invention can be used in methods of diagnosis of a susceptibility to a

ö The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and astmma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rethritis and psorials); central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention Human, protease, cancer; immune-related disorder; cardiovascular disease, neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; gene; ds. 143 inaitreccararatiasarcareciersecertrreritrecaartricircait 202 203 ggalioggaldatriadecaataedicidaetidearitgiridetaeagaatgetagaa 262 Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory 2908 IGATITITCICIACITATITAATITITGGGATITITAACIATITCAATGACTIGIATIT Gaps .. O Caenepeel S; ch 0.6%; Score 21.2; DB 1; Length 609; Similarity 47.1%; Pred. No. 1.6e+02; 65; Conservative 0; Mismatches 73; Indels useful for Sudarsanam S, Manning G, DNA encoding novel human protease #26. Claim 26; Fig 1AA-BB; 313pp; English. 3028 AAATCCAGTCCTTGTTT 3045 263 TTTGTAGGATCATGTTGT 280 26-JUN-2001; 2001WO-US020171. 26-JUN-2000; 2000US-0214047P ABK31769 standard; DNA; 888 (first entry) Whyte D, WPI; 2002-139913/18. P-PSDB; AAU82727. (SUGE-) SUGEN INC. WO200200860-A2 Plowman G, Wł Charydczak G; Homo sapiens 23-APR-2002 03-JAN-2002. disorders. ABK31769; Query Match Local Matches **5** ò g ò ò

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2742
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disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. ABK31744-ABK31802 represent DNA sequences encoding for the novel human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide hormone; antidiabetic; anorectic; antianorectic; antiasthmatic; antidepressant; nootropic; neuroprotectant; hypotensive; hypertensive; cytostatic; cerebroprotective; vasotropic; human; ds.
                                                                                                                                                                                       2683 GIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAGGGAGGCCIGICCIGCGGCGAII
                                                                                                                                                                                                                  620 GGGATTCCATGTTTTGTGCTGCTGAGGATGGCAGTGTAGACACCTGCAAAGGTGACT
                                                                                                                                                               Gaps
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                                                                                                                                  0.6%; Score 21.2; DB 1; Length 888; 2.2%; Pred. No. 1.8e+02; ve 0; Mismatches 43; Indels
                                                                                                           Sequence 888 BP; 163 A; 268 C; 269 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            2743 CATGGGGTCACAAAGAGTTGGACACGACTG 2772
                                                                                                                                                                                                                                                                     680 cácicarcerracicirardacard 709
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of GSK gene Id 15037.
                                                                                                                                                                                                                                                                                                                                     AAI67198 standard; DNA; 918 BP
                                                                                                                                                52.2%;
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                Local Similarity 52.2
es 47; Conservative
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                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                              2742
                                                                                          system including those leading to stroke. The polynucleotides may be used as diagnostic reagents through detecting mutations in the associated gene and for chromosome localization and for tissue expression studies. The polypeptides and polynucleotides may also be used as vaccines
                                                                                                                                                                                                                                                                                                                                706
as diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, astima, manic depression, dementia, delirium, mental retardation, huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New serine protease termed protease T, useful for treating and preventing skin flaking or imbalance of desquamation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a protease T fusion protein. Protease T is useful for treating a condition mediated by protease T. It is useful for treating an imbalance of desquamation, by topical application of a pharmaceutical composition containing the protease. The composition is useful as a topical skin care composition. It is useful as a laundry detergent, shampoo, hard surface cleaning composition, and dish care cleaning composition, and dish care cleaning composition. Protease T protein is useful for treating and and it provides skin flaking. It is less immunogenic to sensitive individuals environment
                                                                                                                                                                                                                                                                                            2683 GIGAGICIGGGIGAACICCIGGAGITGGTGAIGGACAGGGAGGCCIGICCIGCGGCGAIT
                                                                                                                                                                                                                                                                                                                                647 GGGATTCCATGTTTTGTGCTGCTGTGAGGATGGCAGTGTAGACACCTGCAAAGGTGACT
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, protease T; serine protease, dermatological, desquamation, skin care, laundry; detergent; shampoo; skin flaking; fusion;
                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                       ; DB 1; Length 918;
1.8e+02;
                                                                                                                                                                                    Sequence 918 BP; 170 A; 272 C; 282 G; 194 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion gene of protease T in a zymogen activation vector.
                                                                                                                                                                                                                                                         43; Indels
                                                                                                                                                                                                                       Score 21.2; DB
Pred. No. 1.8e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     2743 CATGGGGTCACAAAGAGTTGGACACGACTG 2772
                                                                                                                                                                                                                                                                                                                                                                                                     707 cagerecacerrecrereacaaceare 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qi J, Andrade-Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF77000 standard; cDNA; 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 4; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zymogen activation vector; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-2000; 2000WO-US023823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00386653
                                                                                                                                                                                                                       0.6%;
                                                                                                                                                                                                   Ouery Match
Best Local Similarity 52.2.
Best 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB73946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200116293-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Darrow AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF77000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 178
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The invention provides polypeptides (AAG65886-65918) which may be peptide hormones (including insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, Halikreins, lamins, melanins, naturitetic hormones, neuropepsin, pituitary hormones, pleiotrophins, prostaglandins, seretogranins, selectins, thromboglobulins, thymosins) identified by high throughput genome-based biology and polymoleotides (AAI67176-67208) encoding them. The polypeptides can be expressed by standard recombinant methodology. The polypeptides are useful in the treatment of disease such

Isolated polypeptides, which may be peptide hormones, which are identified by high throughput genome-based biology which identifies and gene products as therapeutic targets for treatment of diseases s

Claim 2; Page 52; 99pp; English.

as diabetes and cancer.

Kabnick KS;

2 Xiang

Smith RF,

Rizvi SK,

Agarwal P, Murdoch PR,

WPI; 2001-639223/73. P-PSDB; AAG65908.

BEECHAM CORP.
BEECHAM PLC.

(SMIK ) SMITHKLINE (SMIK ) SMITHKLINE

28-MAR-2000; 2000US-0192668P. 27-APR-2000; 2000US-0200166P.

22-MAR-2001; 2001WO-US009226. 24-MAR-2000; 2000US-0192158P.

WO200172961-A2

04-OCT-2001

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cleaning composition, dish care cleaning composition, skin care composition and hair care composition. Protease C-E is useful for treating and preventing skin flaking, neurodegenerative disorders and dermatological pathologies. It is less immunogenic to sensitive individuals and it provides efficient proteolytic activity in a nonnatural environment. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 180
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ12680
              8888888888
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                                                                                                                               ö
                                                                                                                                                                                                                                       1110 TTATAATGGTTACAATAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTC 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; serine protease; protease C-E; therapy; desquamation; skin care; laundry detergent; shampoo; cleaning agent; hair care; skin flaking; neurodegenerative disorder; dermatological; immunogenic; proteolytic; bowine; zymogen activation construct; PFEK2-C-E-HIS ERI-HCII; fusion protein; chromosome 16p13.3; ds.
                                                                                                                                                                                     2860 TCATAATGTTGGTTAAGATAATAAGATTTTCAAATTGATTTTTATCTTTGATTTTTCTCT
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel serine protease termed protease C-E_{\nu}, useful for treating and preventing skin flaking or imbalance of desquamation.
                                                                                                                               ö
                                                                    Score 21.2; DB 1; Length 1130; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                   2920 ACTIATITAATITIGGGATITITAACTATITCTICAATGACTIGIAT 2965
                                                                                                                                                                                                                                                                                                                                                     1050 Achecarreraerierestrirerecaacrearearierareriar 1005
           A; 329 C; 327 G; 225 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zymogen activation construct, PFEK2-C-E-HIS ERI-HCII DNA.
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "PFEK-C-E-HIS fusion protein"
                                                                                                                               53;
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qi J, Andrade-Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD02991/c
ID AAD02991 standard; DNA; 1166 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig 4; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2000; 2000WO-US022117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00386629.
                                                                          0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                     Query Match
Best Local Similarity 50.v.
Local Sinconservative
Si Conservative
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/*tag= a
                       Sequence 1130 BP; 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY72891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200116288-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos sp.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2003
31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Darrow A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD02991;
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                                                                               2919
                                                                                                        1146 itaitaaidoitacaaataaagcaatagcaicacaaatricacaaataaagcairiritic 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The fusion was constructed using site-directed mutagenesis to fuse PAP-I encoding amino acid 1-136 with a protein C DNA sequence at the codon for amino acid 46. A plasmid contey this construct was transfected into BHK cells which were then cultured to produce PAP-I-protein C fusions which were activated to a form fully active in both amidolytic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
                                                                              2860 TCATAATGTTGGTTAAGATAATAAGATTTTCAAATTGATTTTTATCTTTGATTTTTCTCT
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                         Phopholipid; binding protein; lipocortin; domain; vitamin K; PBP; gla-domain; VKDP; ss.
                                                     ö
                             Length 1166;
                                                                                                                                     2920 ACTIATITAATITIGGGAJTITAACTATITCTICAATGACTIGTAT 2965
                                                                                                                                                               1086 Acrecarreragricresririerceaacrearcarerarierari 1041
Sequence 1166 BP; 232 A; 335 C; 349 G; 250 T; 0 U; 0 Other;
                                                       Indels
                          Score 21.2; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /labbl= PAP-I
/note= "amino acids 1-136"
409. .1529
/*tag= b
/labbl= protein_C
/note= "amino acids 46-136"
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                  PAP-I-protein C fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00459082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-00459082
                                                                                                                                                                                                                                     AAQ12680 standard; DNA; 1529
                               0.6%;
                                           50.0%;
                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-222905/30.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR13083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9109953-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-1991.
                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                          53;
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10664775-2.rng

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P-PSDB; ABG73119.
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ABL28111/c
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                                                                                                    ò
                                                                                                                         2134 GCATCTGGTCCCATCACTTCATGGGAAATAGATGGGGAAACAGTGGAAACAGTGTCAGAC 2193
anticoagulant assays. The sequence may encode amino acids 46-49 or 46-419 of protein C. See also AAQ12678-81. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                       Human; coagulation; Factor VII; Factor VIIa; blood coagulation; fibrin clot; haemostatic; tissue factor; zymogen; Factor IX; Factor X; prothrombin; thrombin; Factor V; Factor VIII; fibrinogen; fibrin; plasma factor; bleeding episode; haemophilia A; haemophilia B; thrombus; lintimal hyperplasia; restencesis; cardiogenic embolism; stroke; platelet deposition; percutaneous transdermal coronary angioplasty; PTCA; cancer; tumour; angiogenesis; ischaemia; reperfusion; thrombolysis; rheumatoid arthritis; arteriosclerosis; inflammation; septic shock; hypotension; adult respiratory discress syndrome, ARDS; myocardial infarction; vasotrophic; cerebroprotective; antibacterial; immunosuppressive; cardiant; gene therapy; ds; pIN174.
                                                                                                                                               274 derraridaaergaaeargeerreaaggaderiggaaeaargaaaaggaeraegaeagaa 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_except= (pos:300. .305,aa:Xaa)
/transl_except= (pos:324. .326,aa:Xaa)
/transl_except= (pos:330. .332,aa:Xaa)
/transl_except= (pos:339. .344,aa:Xaa)
/transl_except= (pos:357. .366,aa:Xaa-Xaa)
/transl_except= (pos:369. .371,aa:Xaa)
/transl_except= (pos:369. .371,aa:Xaa)
/transl_except= (pos:387. .389,aa:Xaa)
/transl_except= (pos:387. .389,aa:Xaa)
/transl_except= (pos:387. .389,aa:Xaa)
/transl_except= (pos:387. .389,aa:Xaa)
                                                                                                  ;
0
                                                                        Query Match 0.6%; Score 21.2; DB 1; Length 1529; Best Local Similarity 52.2%; Pred. No. 1.9e+02; Matches 47; Conservative 0; Mismatches 43; Indels 0.
                                                Sequence 1529 BP; 357 A; 420 C; 467 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Plasmid pLN174 for expressing human coagulation Factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= a
product= "Coagulation Factor VII"
                                                                                                                                                                         2194 TITATITITGGGGGCTCCAAAATCACTG 2223
                                                                                                                                                                                                  334 ATTATIGCTICAAGGACACCIGAAGAACIG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                            ABX14193 standard; DNA; 6098 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-2001; 2001DK-00000477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-DK000189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1505
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
Unidentified.
Synthetic.
                                                                                                                                                                                                                                                                                                           11-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2002
                                                                                                                                                                                                                                                                                    ABX14193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Persson
                                                                                                                                                                                                                                   RESULT 181
ABX14193/c
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The invention discloses a human factor VII polypeptide, or a variant or derivative of it, where an amino acid has been modified. This change results in a polypeptide with the same or an increased activity when compared to recombinant wild type human Factor VIIa. Blood coagulation consists of a complex interaction of various blood components that eventually give rise to a fibrin clot. Initiation of the haemostatic process is mediated by the formation of a complex between tissue factor and factor VII (the active form of the Factor VII zymogen). This complex activates Factors V and VII leading to a full thrombin burst. The cutivates Factor VII leading to a full thrombin burst. The thrombin converts fibrinogen to fibrin resulting in formation of a fibrin clot. The Factor VII zymogen, or its derivative, can be modified in its catalytic centre to inhibit the ability of the Factor VII polypeptide to preparing a medicament for the treatment of bleeding episodes, for the chancement of the normal haemostatic system, especially for the chancement of the normal haemostatic system, especially for the treatment of haemosphilia A or B and for inhibiting thrombus formation. The inactivated factor VII derivatives are useful for treatment of haemosphilia A or B and for inhibiting thrombus formation. The inactivated factor VII derivatives are useful for treating intimal hyperplasia, restences: a randocent conners and opposition and context of an anchor metaster and cornary and opposition and context and cornary and opposition and context which anchors are useful for treating intimal and cornary and context and some and context of an anchor metasters.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alsorders, percutaneous transdermal coronary angioplasty (PTCA), stroke, cancer, tumour metastastis, angiogenesis, ischaemia/reperfusion, rhemmatoid archritis, thrombafsis, arteriosclerosis, acute and chronic indications, such as inflammation, septic shock, hypotension, adult respiratory distress syndrome (ARDS) and myocardial infarction. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Novel factor VII polypeptide, its derivatives useful for preparing medicament for treating bleeding episodes, or for enhancing normal hemostatic system, especially for treating hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6098 BP; 1413 A; 1587 C; 1623 G; 1475 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence presented is the plasmid, pLN174, which expresses the inactivated human coagulation Factor VII polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6%; Score 21.2; DB 1; Length 6098; Best Local Similarity 50.0%; Pred. No. 1.8e+02; Matches 53; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2920 ACTIATITAATITIGGGATITITAACTATITCTICAATGACTIGIAT 2965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4896 Acricarircraciriristica a acricarcia retriari 4851
                                                                                                                                                                                                            Disclosure; Page 82-85; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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10664775-2.rng

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967 GACTGGAATGCAAAAGTAGGAAGCAAAGAAACACCTGGAGTAACAGGCAAATTTGGCCTT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907 GAAGACCTACAAGACCTTTTAGAACTAACACCCAAAAAAAGATGTCCTTCTCATTATAGGG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 GTÄGGAGTAGTAGTAGTAGCÄGGAGTÄGTÄGGAGTÄGTÄGTÄGTAGTAGTÄGTÄGTÄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryores for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA construct comprising a modified nucleic acid molecule having at
                                                                                                                      ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungicide; virucide; ds.
                                                                                                                                                                                         Claim 1; SEQ ID NO 35806; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 21; DB 1; Length 237;
46.3%; Pred. No. 1.4e+02;
tive 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum chalcone synthase CHS5 DNA sequence. SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 237 BP; 66 A; 75 C; 20 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA construct, transgenic plant; antibacterial; insecticide; gene therapy; genetic trait; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1027 GGAATACGGAATGAAGCAGGCCAAAGACT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGTACGAGTAGTAGGGCGAGGAAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ72491 standard; DNA; 291 BP
                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fermin-Munoz GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2002; 2002WO-US013377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 46.3
les 69; Conservative
                                                                                                                        New isolated nucleic
                                                   Venter JC, Adams M,
                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-093146/08.
                  (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200286146-A2.
                                                                                                                                                           .nteractions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2003
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                                                                                                                                         genes from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ72491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention describes a DNA construct (I) comprising a modified nucleic acid molecule having a nucleotide sequence which is at least 80%, but less than 100%, homologous to two or more desired trait DNA molecules and which imparts the desired trait to plants transformed with the DNA construct. Each of the desired trait DNA molecules relative to the construct. Each of the desired trait DNA molecules relative to the construct. Each of the desired trait DNA molecules relative to the construct. Each of the desired by no more than 3 percentage points. Also described: (1) a DNA expression vector comprising the DNA construct above; (2) a construct above; (3) a transgenic construct above; (4) imparting a trait to plant transformed with the DNA construct above; (4) imparting a transgenic plant seed and propagating a plant from the planted construct above; (5) preparing a molecule cold molecule cold molecule cold molecule cold molecule cold molecule suitable to impart multiple traits to a plant; and (6) determining confined multiple desired traits can be imparted to plants by a single confined and insecticide activities, and can be used in gene therapy. The modified nucleic acid molecule. (1) can have antibacterial, fungicide, variety of pathogens including viruses, bacteria, fungi, virolds, construct may also be used colding to impart a desired genetic trait to the plant, such as desired colour, construct may also and insects. The DNA construct may also be used to impart a desired genetic trait to the plant, such as desired colour, construct invention of enzyme production), and plant the colour, construct invention and invention invention invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2755 AAGAGTIGGACACGACTGAACTGAACTGAACTGAACTGTACTGAAACCTTAGTAGTT 2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2695 GAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGCGATTCATGGGGTCACA 2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GACATCGTGGTGGTGGTGCCCAAGCTAGGCAAGGCCGCGCGCATAAGGCGATCAAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 gadridesescadoceaarrocaagarcacircaccircircrecaccaccircesceic 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; panceneas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
least 80% homology to a desired trait DNA, useful for imparting resistance to plants against a variety of pathogens, e.g. viruses, bacteria, fungi or viroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 21; DB 1; Length 291;
48.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 291 BP; 69 A; 87 C; 93 G; 42 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pancreas specific cDNA sequence SEQ ID NO:166.
                                                                                                   Example 16; Fig 15; 191pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH57326 standard; cDNA; 292 BP.
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Best Local Similarity 48.0
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2815 TATAT 2819
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AAH57326/c
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17-MAY-2001; 2001US-0291849P. 19-UUN-2001; 2001US-0299776F. 20-UUN-2001; 2001US-0300001P.

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RESULT 186
ABL65438/C
ID ABL654
XX
AC ABL654
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH57161 to AAH57576 represent cell and tissue specific polynuclectide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimentos, peptides, proteins, agonists, antagonists, antibodies or their ragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                          New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 292 BP; 66 A; 76 C; 75 G; 58 T; 0 U; 17 Other;
                                                                                                                                Watson GA;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 127; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC46452 standard; cDNA; 631 BP
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2001US-0280067P.
2001US-0280068P.
2001US-0291280P.
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99US-0163508P
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                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                    WPI; 2001-291057/30.
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les 33; Conserv
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29-MAR-2001;
16-MAY-2001;
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04-NOV-1999;
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                                                                                                                                    Sornasse T,
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The invention relates to novel human diagnostic and therapeutic polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (ITITHP, ABR4136-1812). The invention also relates to proteins (ITITHP, ABR4136-1812). The invention also relates to polymucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transfering a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins and protein sequences; methods of detecting dithp nucleic acid sequences; methods of sessessing the toxicity of test compounds using a dithp hybridisation of text compounds using a dithp hybridisation proliferative disorders; and protein sequences and DITHP proteins may be used in the proliferative disorders; autoimmume or inflammatory disorders; bacterial, proliferative disorders; autoimmume or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; transport disorders; and connective tissue disorders; methodies or secen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dith mucleic acids are additionally useful in somatic or germline gene therapy of the disorders additionally useful in somatic or germline gene therapy of the disorders continuents above, as a source of antisense sequences, as a source of additionally useful in somatic or germline gene therapy of the disorders in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a dithp cDNA encoding a DITHP protein which is involved in protein modification, and disease or knock in which is protein which mas obtained in e
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                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
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                                                                                                                                                  Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin St, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;
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54.5%; Pred. No. 1.8e+02;
ve 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 2; SEQ ID NO 373; 591pp; English.
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Conservative
                                                                                                               (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                    Dario ...
Dufour GE, Hillman ...
Daughtery SC, Dam TC,
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les 42; Conserv
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                                                                                                                                                                                                                                  Peralta ČH,
Flores V,
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Matches
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ABL65438 standard; DNA; 850 BP

ABL65438

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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                             Human; cancer; colon; breast; ovary; ossophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                           Lung cancer related gene sequence SEQ ID NO:3775
                                                                                                                                                                                                                                    20-SEP-2000; 2000US-0234052P.
22-SEP-2000; 2000US-0234509P.
22-SEP-2000; 2000US-0234923P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235977P.
25-SEP-2000; 2000US-0235097P.
25-SEP-2000; 2000US-0235134P.
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2000US-0235638P
2000US-023571DP
2000US-0235840P
2000US-0235863P
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2000US-0234009P.
2000US-0234034P.
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                                                                                                                                                          30-MAY-2001; 2001WO-US010838
         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AVAL-) AVALON PHARM.
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                                                                                                                   WO200194629-A2
                                                                                                 Homo sapiens.
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27-SEP-2000;
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28-SEP-2000;
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Soppet DR, 1
         15-MAY-2002
                                                                              gene; ds.
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 447 sequences (given in Abl61664 to Abl70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidarey, prostate or pencreatic cancer, adenocarinoma, carcinoma, carcinoma, cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease(s) and kinase involved in regulating cell activity and viability - particularly the testis-specific protease HELA2 used for modulation of fertility and as tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 CITITAGAACTAACACCCAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA 974
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 850;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 850 BP; 191 A; 253 C; 229 G; 177 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Match 0.6%; Score 21; DB 1; Length 850 Local Similarity 62.3%; Préd. No. 1.96+02; es 33; Conservative 0; Mismatches 20; Indels
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97AU-00000422.
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Example 15; Fig 20B; 167pp; English.

Claim 1; SEQ ID NO 3775; 44pp; English.

Horrigan S;

Endress G,

Ebner R,

Carter KC,

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AAV59134-36 represent HELA2 homologues. The genes are found in a cluster on chromosome 16p13.3 HELA2 was isolated from HeLa cells, and has homology to serine proteases. The protein is involved in or associated with regulation of cell activity and/or viability. Administration of cell activity and/or viability. Administration of cell activity and/or viability. Administration of Extension of HeLA2 calcos fertility. HellA2 is also a suppressor of testicular germ cell cancers (seminoma) and is also expressor of testicular cancers (of colon, pancreas, prostate and ovary), so is a marker/potential therapeuic target for cancer. The promoter from the CHELA2 gene is useful for testis-specific expression of other genes, e.g. for gene therapy or modulation of fertility. Drugs that block activity of HELA2 should have antitumour activity (other than in testis) while in testis recombinant HELA2 can be used for orchidectomy). Identification of mutant forms of HELA2 can be used to diagnose infertility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 933 BP; 166 A; 294 C; 284 G; 189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 21; DB 1; Length 933; 54.5%; Pred. No. 2e+02;
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/product= "NOV25a"
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2001US-0327917P.
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les 42, Conservative
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2001US-0328849P. 2001US-0329414P. 2001US-0330142P.

2001US-0330309P

2001US-0328044P

09-OCT-2001; 09-OCT-2001; 12-OCT-2001; 15-0CT-2001; 17-0CT-2001; 18-0CT-2001;

2001US-0328029P

09-OCT-2001;

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The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated mucleic acid described above; (3) an isolated mucleic acid comprising the above processed above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically by the prosence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a cell compression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aborrant physiological interactions of the polypeptide for identifying a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide is useful in a method for polypeptide described above polypeptide in a method for polypeptide described above polypeptide. Novx a pathology associated with the polypeptide; (12) a method of the polypeptide described above polypeptide in a mannal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide in a mannal; and (14) a method for producing the above polypeptide in a sequences have antidiabetic, anoretic; antibacterial, virucide, polypeptide is useful in manniacturing a medicament for treating a sequence associated with a human disorders and was disorders such as Alzielemer's disease or pervent metabolic acid molecule may be used to diagnose, infections, eachexia, cancer, informance disorders, when a human disorders and various disorders whener invention.

Compared planamaccent invention.

Compared planama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malyankar UM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shenoy SG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 191; 586pp; English.
                                                                                                                                                                                    2002US-0373884P.
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2002US-0383656P.
2002US-0383831P.
                                        001US-0343629P.
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P-PSDB; ADA05758.
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                                                                                   01-NOV-2001;
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immune disorders such as immune complex

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                                                                                                       845 retertegesececedagesecechagateceaereageaectecheareeche
                                                                                                                                                                                                                                                                                                                              granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour artigen PS3; cyclin-dependent kinase inhibitor 1C; ds; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
                                                                                   TGTTTGTTTCCAAGGCAAACCATTCAATATCACAGTAATCCAAGTCTATGCCCCAACCAG
                                                           Gaps
                                                                                                                                                                                                                                                                                                                    converting enzyme splice variant; ACEV; interleukin 6;
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0
                                                                                                                                                                                                                                                                                            converting enzyme (ACEV) splice variant DNA #59.
              BP; 156 A; 310 C; 292 G; 193 T; 0 U; 0 Other;
                                    Length 951;
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                                                             35;
                                   DB 1;
                                                2e+02;
                                   Score 21; DB 1; Pred. No. 2e+020; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 358; 519pp; English.
                                                                                                                                                                                                                       BP.
                                                                                                                                     TAATGCTGAAGAAGCTG 889
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                                                                                                                                                                                                                       AAS06059 standard; DNA; 1551
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                                     0.6%;
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                                                 Local Similarity
nes 42; Conserv
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               Sequence 951
                                                                                                                                                                                                                                                                        12-SEP-2001
                                                                                                                                                                                                                                                                                                 Angiotensin
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                                                              Matches
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1390 GACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGAGACAGGGATC 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ80296 shows the cDNA encoding human Factor VII. Factor VII is a trace plasma glycoprotein that circulates in blood as a single-chain zymogen. The zymogen is catalytically inactive, and is converted into a two-chain active mol. by cleavage of an internal peptide bond located approx. In the middle of the mol. Factor VIIa rapidly activates Factor X or Factor IX by limited proteolysis. Modified Factor VII has anticoagulant properties, for preventing the coagulation cascade. The modified factor VII has an active site modified by at least one amino acid substitution, and in its modified form is capable of binding tissue factor and
                                                                                                                                                                                                                                                                                                                                                                                                                        Factor VII, plasma glycoprotein, derivative, tissue factor, TF; inhibition, vascular restenosis, platelet deposition, catalytic centre, factor IX; factor X; inactivation, thrombosis, embolism; stroke, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1450 GAGACCATCCCCATGGAAAAGAAATGCAAAAAAGCAAAATGGCTCTCTGGGGAGGCC 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 redececeretrelegadadadadetecaareadadadeareceretrieadadeee 224
                                                                                                                                                                                                                                                                                                      Gaps
diseases such as hypertrophy, immune disorders such as immune complentitis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein
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                                                                                                                                                                                                                                                Length 1551;
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                                                                                                                                                                                                                                             Score 21; DB 1;
Pred. No. 2.2e+02;
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/note= "wild type Factor VII"
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                                                                                                                                                                                                                                             ch 0.6%;
1 Similarity 48.7%;
57; Conservative
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17-JUL-1995
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inhibiting its action. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                      Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;
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ö Gaps ö DB 1; Length 2422; 2.2e+02; hes 0; Indels Query Match 0.6%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 21; Conservative 0; Mismatches TTTT 3265 2422 Trititritritritritri 2402 3245 TTTTTTTTTTT δ g

RESULT 191

AAV02230/c ID AAV02230 standard; cDNA; 2422

AAV02230;

(first entry) 08-JUN-1998

sapiens cDNA encoding Ser344Ala modified factor VII.

Factor VII; modified; Ser344Ala mutant; vascular patency; prevention; myocardial injury; blood flow; angioplasty; trauma; intimal hyperplasia; restenosis; deep vein thrombosis; treatment; pulmonary embolism; stroke; disseminated intravascular coagulation; fibrin deposition; endotoxaemia; myocardial infarction; anticoagulant; ss.

Homo sapiens.

Location/Qualifiers 41. .1375 /*tag= a

/product= "Ser344Ala modified factor VII"

WO9747651-A1

18-DEC-1997

06-JUN-1997;

96US-00660289 07-JUN-1996;

(NOVO ) NOVO-NORDISK AS. (ZYMO ) ZYMOGENETICS.

Rasmussen ME; Hedner U, Hart CE, Petersen LC,

Inhibiting thrombus formation by topical administration of modified factor VII - also used to maintain vascular patency, prevent myocardial injury and improve regional myocardial blood flow. WPI; 1998-052245/05. P-PSDB; AAW31687.

Example 1; Page 69-73; 97pp; English

The sequence is that encoding a Ser144Ala modified factor VII which can be used as part of a method for inhibiting thrombus formation. The method is used to maintain or improve vascular patency, to prevent or minimise myocardial injury associated with post-ischaemic reperfusion and to improve regional myocardial blood flow during post-ischaemic reperfusion. The method is particularly used where the site of thrombus or reduced patency is associated with (micro) surgery, angioplasty or trauma or where the myocardial injury is myocardial necrosis. Particular applications are in treatment or prevention of intimal hyperplasia or restenosis caused by stroke; disseminated intravacular coagulation; fibrin deposition associated with endotoxaemia and myocardial infarction 

Sequence 2422 BP: 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;

ö The present invention describes a method for the inhibition or minimisation of myocardial injury associated with post-ischaemic reperfusion by administering factor VII, which has at least 1 modification in its catalytic triad (therefore inhibiting the ability of factor VII to activate plasma factor X or IX). The method can be used for inhibiting or minimising myocardial injury and for imparting regional myocardial blood flow associated with post-ischaemic reperfusion. It can also be used for inhibiting blood coagulation, platelet deposition, thrombus formation and maintaining or improving vascular potency. Factor VII can be administered at relatively low doses and does not produce undesirable side effects. Further it acts specifically at sites of injury. The present sequence encodes Factor VII Factor VII; catalytic active site; blood coagulation; plasma; Factor X; Factor IX; vasotropic; antiischaemic; anticoagulant; myocardial injury; post-ischaemic reperfusion; platelet deposition; thrombus formation; Gaps Inhibition or minimization of myocardial injury associated with post-ischemic reperfusion. ö Length 2422; DB 1; Le 2.2e+02; Rasmussen ME; 0.6%; Score 21; DB 100.0%; Pred. No. 2.2 :ive 0; Mismatches /*tag= a /product= "Factor VII" Factor VII encoding cDNA SEQ ID NO:1. Disclosure; Col 43-48; 34pp; English. Location/Qualifiers 28. .1375 Hedner U, 2422 rrrrrrrrrrrrrrrrrrrrr AAZ57385 standard; cDNA; 2422 91US-00662920. 93US-00065725. 94WO-US005779. 94US-00475845. 96US-00660289. 97US-00871003 (first entry) Conservative (NOVO ) NOVO-NORDISK AS. (ZYMO ) ZYMOGENETICS INC Petersen LC, vascular potency; ss. WPI; 2000-104599/09. Query Match Best Local Similarity Matches 21; Conserv P-PSDB; AAY67967 3245 TTTTTT Unidentified , 1997; 24-OCT-1994; 07-JUN-1995; 05-APR-2000 28-FEB-1991; 21-MAY-1993; US5997864-A 23-MAY-1994 07-JUN-1996 07-DEC-1999 AAZ57385; Hart CE, AAZ57385/ Key ò 셤

Sequence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other; DB 1; Length 2422; Score 21; 0.6%;

Query Match

10664775-2.rng

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                Gaps
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0
               0; Indels
  100.0%; Pred. No. 2.2e+02;
               Mismatches
               ó
               21; Conservative
Best Local Similarity
Matches 21; Conserv
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2422 TITITITITITITITITI 2402 3245 TTTTTTTTTTTTTTTTTTTT ద ò

RESULT 193 AAF57099/

AAF57099 standard; cDNA; 2422 BP

AAF57099;

(first entry) 14-MAY-2001

Human Factor VII polypeptide encoding cDNA.

Factor VIIa; thrombus; vascular patency; blood coagulation; Factor X; plasma factor; Factor IX; myocardial injury; human; Factor VII; ss.

Homo sapiens

Location/Qualifiers 41. .1375 /*tag= a 41. .154 /*tag= b 155. .1372 /*tag= c sig_peptide

JS6183743-B1

mat_peptide

06-FEB-2001,

99US-00378907 20-AUG-1999;

91US-00662920. 92WO-US001636. 93US-00065725. 94WO-US005779. 94US-00327690. 95US-00475845. 96US-00660289. 97US-00871003. 28-FEB-1991; 28-FEB-1992; 21-MAY-1993; 23-MAY-1994; 24-OCT-1994; 07-JUN-1995; 06-JUN-1997 

(ZYMO ) ZYMOGENETICS INC. (NOVO ) NOVO NORDISK AS.

Rasmussen ME; Hart CE, Petersen LC, Hedner U,

WPI; 2001-201993/20. P-PSDB; AAB61992 Use of modified human factor VIIa with a covalent modification in its catalytic center, to inhibit thrombus formation or to maintain vascular patency.

Example; Col 43-48; 34pp; English.

inhibiting thrombus formation, or maintaining or improving vascular patency in a patient. The modified factor VIIa comprises a covalent modification in its catalytic center which effectively interrupts the blood coagulation cascade. The modifications render Factor VIIa substantially unable to activate plasma factor IX or X. The modified Factor VIIa associated with post-ischemic reperfusion, for improving regional myocardial blood flow during reperfusion, for improving regional vascular patency in a patient. The present sequence represents the cDNA encoding a human Factor VII polypeptide invention relates to the use of modified human Factor VIIa for

Seguence 2422 BP; 596 A; 712 C; 692 G; 422 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                         human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic; dermatological; anorectic; immunosuppressive; cytostatic; antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory; neuroprotective; anabolic; noorcopic; antiparkinsonian; gene therapy; cardiomyopathy; atherosclerosis; hypertension; congenital heart defect; pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AIDS; bronchial asthma; Crohn's disease; multiple sclerosis; infectious disease; anorexia; neurodegenerative disorder;
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease, Parkinson's disease; immune disorder;
haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.
                          · :
Query Match 0.6%; Score 21; DB 1; Length 2422; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Human NOV8a encoding cDNA SEQ ID NO:33.
                                                      3245 TITITITITITITITI 3265
                                                                                  2422 ritiritiritiritiri 2402
                                                                                                                                                    ADC24226 standard; cDNA; 2422
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                        18-DEC-2003
                                                                                                                                                                              ADC24226;
                                                                                                                         RESULT 194
                                                                                                                                       ADC24226/c
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Location/Qualifiers /product= "NOV8a" 41. .1375 /*tag= a

Homo sapiens

18-SEP-2003,

WO2003076584-A2

06-MAR-2003; 2003WO-US006951

; 2002US-0361974P. ; 2002US-0365477P. ; 2002US-0366928P. ; 2002US-0401661P. ; 2003US-00401661. 06-AUG-2002; 05-MAR-2003; 06-MAR-2002; 19-MAR-2002; 22-MAR-2002;

(CURA-) CURAGEN CORP.

Kekuda R; Pena CEA; Stone DJ; CE, Edinger SR, Gerlach VL, Ji W, Miller CE, Millet I, Patturajan M, Shenoy SG, Smithson G, Spytek KA, Alsobrook JP, Burgess Li L, Macdougall JR, Rieger DK, Sciore P, Voss EZ, Zhong M;

2003-722330/68. WPI; 2003-722330/ P-PSDB; ADC24227. New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or multiple sclerosis.

Claim 20; SEQ ID NO 33; 229pp; English.

The present invention describes novel human proteins, designated NOVX proteins. The NOVX sequences have cardiant, antiarteriosclerotic, hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,

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cytostatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic, antiinflammatory, neuroprotective, anabolic, nootropic and antiinflammatory, neuroprotective, and can be used in gene therapy. The NOVX caquences can be used as a therapettic in the manufacture of a medicament for treating a syndrome associated with a human disease, such as a pathology associated with NOVX. The NOVX proteins and nucleic acids or conditions associated with NOVX. The NOVX proteins and nucleic acids or conditions associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, pulmonary stenosis, scleroderma, obesity, metabolic disturbances associated with obesity, transplantation, adrenleukodystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, adenomarcinoma, fertility, haemophilia, graft versus host disease, also conceria, neurodegenerative disorders (e.g. Alzheimer's disease, disease, and wasting disorders (e.g. Alzheimer's disease, or parkinson's disease), immune disorders associated with chronic diseases. The proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunogens to produce antibodies and as the content of the proteins can also be used as immunosed manaled the content of the proteins can also be used as immunosed can be content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the 
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Gaps · 0 0.6%; Score 21; DB 1; Length 2422; 00.0%; Pred. No. 2.2e+02; ve 0; Mismatches 0; Indels 100.0%; Pred. ... 3245 TITITITITITITITI 3265 Conservative Best Local Similarity 21; Query Match Matches ð

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2422 Trrrrrrrrrrrrrrrrrrr 2402 셤

AAN60064 standard; DNA; 2483 BP 25-MAR-2003 31-OCT-2002 23-MAY-1991 AAN60064; AAN60064/c 

(first entry) (revised)

Factor VII cDNA of lambda VII2463.

VII; Factor VIIa; DNA construct. Factor

Unidentified

Location/Qualifiers 36. .1436 /*tag= a Key

EP200421-A.

10-DEC-1986

86EP-00302855. 16-APR-1986;

85US-00724311. 85US-00810002. 17-APR-1985; 16-DEC-1985;

(ZYMO ) ZYMOGENETICS INC.

Gray CL; Woodbury RG, Insley MY, Ϋ́, Berkner Hagen FS, Murry MJ,

WPI; 1986-326899/50. P-PSDB; AAP60056. DNA construct used to transfect hosts - to produce protein which activates to give factor VIIa.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34895-ABX49947, or complements of them. Also included are ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that

Claim 2; SEQ ID NO 14612; 245pp; English.

ö The partial factor VII cDNA sequence is from cDNA clon1 lambda VII2463. It is used in a DNA construct which contains a nucleotide sequence encoding a protein which, on activation, has the same biological activity for blood coagulation as Factor IIa. The nucleotide codes at least partially for Factor VII and comprises sequence encoding a calcium catalytic domain joined to a sceond sequence downstream of this encoding a catalytic domain for the serine protease activity of Factor VIIa. The calcium binding domain comprises a gene encoding Factor VII. IX, X, protein. C, prothrombin on Protein S. The construct is used to transfect host cells to produce the protein which, on activation, yields Factor VIIA. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Gaps Bovine EST associated with lactation/muscle/fat deposition #14612 . 0 0.6%; Score 21; DB 1; Length 2483; 00.0%; Pred. No. 2.2e+02; ve 0; Mismatches 0; Indels Sequence 2483 BP; 611 A; 725 C; 720 G; 427 T; 0 U; 0 Other; Warren WC; 100.0%; Preu. ... 3245 TITITITITITITITI 3265 2483 TTTTTTTTTTTTTTTTT 2463 Disclosure; Fig 1B; 55pp; English. Tao N, ABX49447 standard; cDNA; 432 BP. MAR-2003 to correct PA field.) 12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902. 24-SEP-2001; 2001US-00960352. (first entry) Byatt JC, Mathialagan N, 21; Conservative (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. (TAON/) TAO N. WPI; 2003-110599/10. (TAON/) TAO N. (WARR/) WARREN W C. Best Local Similarity US2002137139-A1. 26-SEP-2002. 21-FEB-2003 Bos Taurus. ABX49447; Query Match RESULT 196 Matches ABX49447 \$X0000000000000X8 g ò

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tingclust in the certain to cause termination of the mRNA molecule; and complete the complete the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid; is predictive of the level or pattern of the complementary nucleic acid; is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2800 GAAACCTTAGTAGTTTATATTTACTCAGAAAATAGTAATTTCATATGTATTC-AAAATTAT 2858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICATAATGITGGITAAGATAAAAGATTITCAAATTGATTITTATCTTTGATTTTTCTC 2918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2919 TACTIATITAATITIGGGATTITAACTATITICTTCAATGACTIGTATITICTAATATITAC 2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 TTGAAAACACTGAGAAACTACTGAATTTTGGAAGCAATATGTTGATGGAGATCAGTGTG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AATCCAATCCATGTTTAAATGGCGGCATGTGCAAGGATGACATTAATTCCTATGAATGTT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 dgaaccrigagagaargraaagaagaaaaargragrirrgaagaagcacgagaagrrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20.9; DB 1; Length 43
Pred. No. 1.8e+02;
0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 432 BP; 140 A; 69 C; 107 G; 116 T; 0 U; 0 Other;
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2001US-0267568P.
2001US-0278651P.
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st Local Similarity 46.3%;
tches 101; Conservative
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2001US-0291631P
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2001US-0333626P
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Best Local Similarity
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16-MAY-2001;
12-JUL-2001;
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09-FEB-2001;
21-MAR-2001;
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27-NOV-2001;
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99165); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences consisting of at least 75% or 90% identicy stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a); Polypeptides (ABP68596-C) ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as corbes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene polypeptides and was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from MIPO at fip. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psociasis; behign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                      New isolated polynuclectide and pancreatic tumor polypeptides, useful idiagnosing, preventing and/or treating cancer, particularly pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                        Jiang Y;
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                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2891; 300pp + Sequence Listing; English.
                                                        Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 197 BP; 59 A; 43 C; 65 G; 30 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1943 GAAACGCTGGCTGGAAGAAGCACAAGCTGGA 1974
                                                        Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 chgacrcrcccacacacacacaccrcaaccrcci
                                                          Lodes MJ,
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ID ABN18436 standard; cDNA; 252 BP.
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2000US-0228716P.
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                                                        Kalos MD,
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                   (CORI-) CORIXA CORP.
                                                                                                 WPI; 2002-627435/67
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29-AUG-2000;
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                                                            Benson DR,
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The specification describes subscintainy putting in the specification). ABN15762 to ABN2752 encode the human ORFX or treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a synchome associated with ORFX-associated disorder. ORFX polynuclectide synchome associated with ORFX-associated disorder. ORFX polynuclectide synchome associated with ORFX-associated disorder. ORFX polynuclectide synchome associated with ORFX-associated disorder. ORFX polynuclectide synchome associated with ORFX-associated disorder. ORFX polynuclectide correlations being trumours, kelodd, degenerative disorders, and in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic correspondant disorders influenced systemic storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune influences such as multiple sclerosis, rheumatoid arthritis, autoimmune influenced organic gravis, graft-versus-host disease and autoimmune influenced organic gravis, graft-versus-host disease and autoimmune influenced organic gravis, graft-versus-host confice and autoimmune influenced organic gravis, graft-versus-host useful for treating burns, incisions, ulcers, for treating organic protection or regeneration and treatment of ling or liver fibrosis, reperfusion injury in various tissues and conditions resulting from part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from MIPO at fibro, int/published_pct_sequences
                                                                                                                                                                                                                                                                                  present invention describes substantially purified human proteins
                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing
                                                                                                                                                              preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn tassel-derived polynucleotide (cdps) SEQ ID NO:4082.
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                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 5349; 1037pp; English.
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Best Local Similarity 51.0
Matches 49; Conservative
                      Shimkets RA, Leach MD;
                                                                   2002-106308/14.
                                                                                             P-PSDB; ABP02684
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The present sequence describes a purified corn tassel-derived polynuclectide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL7683. The cdps sequences canced corn tassel-derived polypeptides (CDPs). The cdps sequences can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid becading programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid sequences from DNA libraries, in nucleic acid sequences from the presence of and/or to be not hybridisation, and to identify the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to be not because the presence of and/or to t
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                                                                                                                                                                                                                                                                                                                   Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 GCGAGGAGTATTTGGCGTCGGAGGTGAGTCGGCGCACCAGGAGAGGCAGACAGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 281 BP; 49 A; 114 C; 79 G; 38 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 20.8; DB 1;
57.8%; Pred. No: 1.7e+02;
tive 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST SEQ ID No: 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 4082; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX40441 standard; cDNA; 323 BP.
99US-00294093
                                                   98US-0082567P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                 Lalgudi RV, Ito LY,
                                                                                                 LALGUDIRV.
                                                                                                    (LALG/) LALGUDI R V. (ITOL/) ITO L Y. (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                     WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2664 CATC 2667
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16-APR-1999;
                                                   21-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                               programs
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AAX40441/C
Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 ATTIGGAGATGGCAGACAAGCIGGGAIGACATTATCIGIGAIGGTGGCTGGGCGCCTTAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corn, corn tassel-derived polymucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 20.8; DB 1; Length 252; 51.0%; Pred. No. 1.6e+02; ive 0; Mismatches 47; Indels 0
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0; Gaps

Length 281; Indels 96

Human, secreted protein, EST, expressed sequence tag; diagnosis, forensic, gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation, tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.

Homo sapiens

JS2001051335-A1 13-DEC-2001

Zea mays

Pot D, Kassam A; n M, Drmanac S, Labat I; Stache-Crain B;

Sudduth-Klinger J;

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3189 GCTCTTTAAATTCATTATTCTTTGATAACAGCTTCAGTTCTATGGCTTTAATAAAGTTTT 3248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3249 ITITITITITITITITITAAAGAATGICATICITIGIGAAGITITIGACAATGCTITGAGGCA 3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide comprising a nucleotide sequence which hybridises to a sequence selected from one of 316 fully defined sequences given in the specification, antisense molecules complimentary to the sequences, the polypeptides encoded by the sequences and antibodies raised against the proteins. The nucleic acids are useful for detecting differentially expressed genes which correlate with a cancerous state of a mammalian cell i.e. diagnosing cancer (especially lung cancer, colon cancer, breast cancer, prostate cancer and adenocarionma). Modifying the gene products of of the nucleic acids results in inhibition of tumour growth. The nucleic acids are also useful in gene mapping and tissue profiling. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AGCTCTGCAAGAGAAATATCATAGTCATGTGATGGGGTGTTTGTATTTTTTCATGGACAATT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ATTCTCCGGAGACCCCGTTTCATTTTCGAAGGTTTTATTGTTACTCCAAAGGAAGCAGTC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 CATCTGGCAGGGTTCTTATATGTTGTAAAACAGTGAGCAGCACTCACAAGCCATGTGGCA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human polynucleotides useful for the treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine EST associated with lactation/muscle/fat deposition #10052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 380 BP; 106 A; 81 C; 92 G; 101 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    Williams LT, Escobedo J, Innis MA, Garcia PD, Reinhard C, He Z, Randazzo F, Kennedy GC, Pot Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Lebkkowitz D, Kita D, Garcia V, Jones LW, Stac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 20.8; DB 1; 44.3%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 216-217; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 cancer related cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВЪ.
                                                                                                                           27-MAR-2001; 2001WO-US009952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX44887 standard; cDNA; 396
                                                                                                                                                                             28-MAR-2000; 2000US-0192583P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3309 ATAATTTAGGAT 3320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Conservative
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                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-626251/72.
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                      WO200172781-A2.
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                                                                          04-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human secreted proteins expressed sequence tags (ESTS) for human secreted proteins expressed in prostate, and encode the proteins given in AAY11716 to AAY1993 respectively. The proteins given represent the signal peptide and aN 1-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene nucleic acid sequences can be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proteins obtained may have cytokine activity, cell critisis growth regulating activity, haemstopoiesis regulating activity, themostatic/chemokinetic activity, haemstatic and thrombolytic activity, receptor/ligand activity, and recent inhibition activity or other activity, haemstatic and crivity can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 GTGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGTGGTCCACTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 GAGAAGGGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTATGAA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GAGGCTTGCACTCGAACCCCTTGATGATCCTGGTCTCTCCCCTACAAGCCCTGTTGCCA 148
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 écércéceccadasagnacécecéretrieresandasecirécenéceaseser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20.8; DB 1;
Pred. No. 1.7e+02;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                   Lacroix B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 AAGGCAAAATGATAGGATACTGAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 174-175; 675pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 GAGCAAGCAGATTAACTGCAGAA 124
                                                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASS9116 standard; cDNA; 380 BP
                                                                                                                           98WO-IB001232
                                                                                                                                                                          97US-00905144
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Local Similarity 46.5%;
les 67; Conservative
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                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                  WPI; 1999-153780/13
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY11719
                                                                                                                                                                                                                               GEST ) GENSET
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                      WO9906550-A2
                                                                                                                         31-JUL-1998;
                                                                                                                                                                             01-AUG-1997;
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                                                                       11-FEB-1999
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AAS59116/
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DP à g 8

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Gaps

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Length 380;

(first entry)

10664775-2.rng

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New human polynucleotides useful for the treatment and diagnosis of
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Reinhard C, He Z, Randazzo F, Kennedy GC, Pot D, Kassem A;
Lamson G, Drmanac R, Crkvenyakov R, Dickson M, Drmanac S, I
Leshkowitz D, Kita D, García V, Jones LW, Stache-Crain B;
                                                                                                                                          Human, ss, lung cancer, adenocarcinoma, breast cancer, colon ca
prostate cancer, benign prostatic hypertrophy, BHP, cytostatic.
                                                                                          Human cancer related cDNA sequence #230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 215-216; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2000; 2000US-0192583P.
                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001; 2001WO-US009952.
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                                                                                                                                                                                                                                                                         WO200172781-A2.
                                                                                                                                                                                                                         Homo sapiens
                                             16-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically Mybridise to a second nucleic acid molecule comprising any of 15:112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (i) a transformed call having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) includating a marker nucleic acid (comprising any of the milecule; acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, to a pattern of the molecule obtained from the bovine cell or complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for complementary nucleic acid permits the molecule in a bovine cell or tissue. The suseful for genome mapping, gene identification and analysis, cattle of suseful for genome mapping, gene identification and analysis, cattle of spreash tayens to sequence as not shown in the sequence is one of the complement sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 cacadaargcagcaarrircaccardcaaaaggaccrgccaagggaarrgaccrcriricag 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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0.6%; Score 20.8; DB 1; Length 396;
Best Local Similarity 57.8%; Pred. No. 1.8e+02;
Matches 37; Conservative 0; Mismatches 27; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 10052; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Tao N,
                                                                                                                                                                    24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                         12-JAN-1999; 99US-0115707P
11-JAN-2000; 2000US-00480902
                                                                                                                                                                                                                                                                                                                                                                                                                                Mathialagan N,
                                                                                                                                                                                                                                                                                                 BYATT J C.
MATHIALAGAN N.
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                                                                                                                                                                                                                                                                                                                                                                           WARREN W C.
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                                                                          US2002137139-A1.
                                                                                                                            26-SEP-2002
                             Bos Taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1108
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(WARR/)
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Labat I;

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The invention relates to an isolated polynucleotide comprising a nucleotide sequence which hybridises to a sequence selected from one of sile fully defined sequences given in the specification, antisens on molecules complimentary to the sequences, the polypeptides encoded by the sequences and antibodies raised against the proteins. The nucleic acids are useful for detecting differentially expressed genes which correlate with a cancerous state of a mammalian cell i.e. diagnosing concer (especially lung cancer, colon cancer, breast cancer, prostate cancer adenocarcinoma). Modifying the gene products of of the nucleic acids results in inhibition of tumour growth. The nucleic acids are also useful in gene mapping and tissue profiling. The present sequence is one of the 316 cancer related cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3189 GCTCTTTAAATTCATTATTCTTTGATAACAGCTTCAGTTCTATGGCTTTAATAAAGTTTT 3248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3249 TITITITITITITITIAAAGAAIGICATICITIGIGAAGITITIGACAATGCTITGAGCA 3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 AGCICTGCAAGAAATATCATAGTCATGTGATGGGTGTTTGTATTTTTCATGGACAATT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 ATTCTCCGGAGACCCCGTTTCATTTTCGAAGGTTTTATTGTTACTCCAAAGGAAGCAGTC 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 carcriegcaggerrerrararerreraaaacagreaecaecreacaageccargeeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 20.8; DB 1; 14.3%; Pred. No. 1.8e+02; ve 0; Mismatches 107;
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Best Local Similarity 44.3
Matches 85; Conservative
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7855/c ABA67855 standard; DNA; 545 BP.

RESULT 204 ABA67855/ ID ABA6

AASS9112 standard; cDNA; 400 BP.

RESULT 203 AAS5911

CATC 29

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 16602; 658pp; English.
                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                    Chen W,
                                                                                                                               26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
                                                                                       30-JAN-2001; 2001WO-US000664
                                                                                                                2000US-0180312P
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2000GB-00024263
                                                                                                                                                                                                                                                    Hanzel DK,
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                                      WO200157273-A2
                                                                                                                                                                                 27-SEP-2000;
              Homo sapiens.
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                                                               09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AGAAGGGCAATGTCATGGTTGTACTTATTAATAGCTGCATTGTAGTTGTGGGGAATA 59
                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 16160; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 545 BP; 175 A; 108 C; 122 G; 140 T; 0 U; 0 Other;
                                                                  Human foetal liver single exon nucleic acid probe #16160.
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0.6%; Score 20.8; Dl
Best Local Similarity 51.0%; Pred. No. 2e+0<sup>o</sup>
Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                             2000US-0180312P
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ID ABS41612 standard; DNA; 545
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                                                                                                                                                 WO200157277-A2
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                                        01-FEB-2002
                                                                                                                         Homo sapiens
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               ABA67855;
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Rank DR;

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2827 AAAATAGTAATTICATATGTATTCAAAATTATTTCATAATGTTGGTTAAGATAATAAAA 2886
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measured in the human adult liver. (I) may be used for predicting and all liver. The genes identified may be in rowlved in genetic liver diseases such as cirrhosis, hyperlipidaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 AGAAGGCCAATGTCATGGGTTGTACTTATAATAGCTGCATTGTAGTTGTGGTGAGGAATA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 0.6%; Score 20.8; DB 1; Length 545; Local Similarity 51.0%; Pred. No. 2e+02; hes 49; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 545 BP; 175 A; 108 C; 122 G; 140 T; 0 U; 0 Other;
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Human, oxidoreductase enzyme, transferase, hydrolase, lyase, isomerase, ligase, hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder, neurological disorder, metabolic disorder; inflammatory disorder, reardovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                                                                                                                                                                                                      2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
                                                                                                                                                                         17-JAN-2001; 2001WO-US001239
                                                                                                                                                                                                                             2000US-0184664P
2000US-0186350P
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2000US-0216647P.
2000US-0216880P.
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2000US-0230437P.
2000US-0230438P.
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                                                                                                                       WO200155301-A2.
                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2-SEP-2000;
                                                                                                                                               02-AUG-2001
 The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIa (AAM5171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIa conjugates have haemostatic, thrombolyvic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIa/TF-related diseases or disorders such as haemophilia, liver disease, myocandial infarction, thrombotic stroke and deep-vain thrombosis. The conjugates have increased bioavailability and or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates have increased bioavailability and or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates has number of advantages over currently available such as longer duration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1443 AGGGATCGAGACCATCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGA 1502
                                                                                                                                                                                                                                                                                                                                    New conjugate, useful for treating Factor VIIa related diseases or disorders such as hemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AGAGCTCCGCCCTGGCTCCCTGGAACGCGAATGCAAAGAGGAACAGTGCAGCTTTGAGGA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1338 BP; 245 A; 427 C; 410 G; 256 T; 0 U; 0 Other;
                                                                                           'note= "CDS lacks an initiation codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding novel human enzyme polypeptide #301.
                                                                                                                                                                                                                                                                     Bornaes C;
                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 83-85; 89pp; English.
                         Location/Qualifiers
                                                   /*tag= a
/product= "FVII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS41085 standard; cDNA; 1352 BP.
                                                                                                                                                                         12-FEB-2001; 2001WO-DK000094.
                                                                                                                                                                                                  11-FEB-2000; 2000DK-00000218, 18-OCT-2000; 2000DK-00001558,
                                                                                                                                                                                                                                                                  Andersen KV, Pedersen AH,
                                       15. .1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 57.8
les 37; Conservative
                                                                               partial
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P-PSDB; AAM52171.
                                                                                                                                                                                                                                                                                                                                                                               polypeptide group
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Homo sapiens
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14-SEP-2000; 2000US-0233064P.
21-SEP-2000; 2000US-02333065P.
21-SEP-2000; 2000US-02333065P.
22-SEP-2000; 2000US-023499PP.
22-SEP-2000; 2000US-023499PP.
23-SEP-2000; 2000US-023499PP.
23-SEP-2000; 2000US-023499PP.
24-SEP-2000; 2000US-023499PP.
25-SEP-2000; 2000US-023499PP.
25-SEP-2000; 2000US-023499PP.
26-SEP-2000; 2000US-023499PP.
27-SEP-2000; 2000US-023499PP.
28-SEP-2000; 2000US-023499PP.
29-SEP-2000; 2000US-023499PP.
29-SEP-2000; 2000US-023499PP.
29-SEP-2000; 2000US-023499PP.
29-SEP-2000; 2000US-023499PP.
29-SEP-2000; 2000US-02349PP.
29-SEP-2000; 2000US-02349PP.
29-SEP-2000; 2000US-02349PP.
29-SEP-2000; 2000US-02349PP.
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29-SEP-2000; 2000US-02349PP.
20-OCT-2000; 2000US-02349PP.
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20-OCT-2000; 2000US-02349P
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08-DEC-2000;
08-DEC-2000;
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. altherosclerosis), blood-related disorders (e.g. paemophilas), reproductive disorders (e.g. altherosclerosis), blood-related disorders infectious disorders (e.g. influenca). The polynucleotides of the infectious disorders (e.g. Influenca). The polynucleotides of the invention can also be used in gene therapy. AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; ardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; coular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive;
                                                                                                                                                                                                                                                                                        Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 311; 1180pp; English
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                                                                                                                                                                                Ruben SM;
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08-DEC-2000, 2000US-0251869P.
08-DEC-2000, 2000US-0251999P.
08-DEC-2000, 2000US-0251990P.
11-DEC-2000, 2000US-0254097P.
05-JAN-2001, 2001US-0259678P.
                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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les 28; Conservative
                                                                                                                                                                              Rosen CA, Barash SC,
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P-PSDB; AAU23215.
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2000US-0180662BP.
2000US-0180626P.
2000US-01806350P.
2000US-01808350P.
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2000US-0209461P.
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2000US-021818P.
           17-JAN-2001; 2001WO-US001320
02-AUG-2001
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Ruben SM; 2000US-02363689 2000US-02363299 2000US-023436802P 2000US-02370399 2000US-02370399 2000US-02370399 2000US-02370399 2000US-02370399 2000US-02370399 2000US-02370399 2000US-02370399 2000US-0239917P 2000US-0239917P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249219P 2000US-0249299P 2000US-0249299P 2000US-0249299P 2000US-0249299P 2000US-0249299P 2000US-0249299P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P 2000US-0251888P Rosen CA, Barash SC, 29-58P-2000;
29-58P-2000;
20-0CT-2000;
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20-0CT-2000;
20-0C 05-JAN-2001; (HUMA-) 

WPI; 2001-476222/51

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P-PSDB; AAU17037.
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a labella condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, orber disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and any other disorders e.g. Alzheimer, to maintain organs before to prevent skin aging due to subburn, to maintain organs before crashes considered tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage and inherals, cofactors and other nutritional components. The present capabilities, capabilities, deformed by an order and other nutritional components. The present Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia. Claim 1; SEQ ID NO 134; 601pp; English

ö 0; Gaps Length 1352; Score 20.8; DB 1; Length 1: Pred. No. 2.4e+02; 0; Mismatches 12; Indels 3251 TITITITITITIAAAGAATGTCATTCTTTGTGAAGTT 3290 1352 riririririririsGAGAArAAATAATriATriGAAATT 1313 0.6%; Query Match Best Local Similarity 70.0 Matches 28; Conservative ò g

Human cDNA encoding ovarian antigen #46. ABK72087 standard; cDNA; 1352 BP 13-AUG-2002 (first entry) ABK72087; RESULT 209 ABK72087/c 

Human; ss; ovarian antigen; gene; ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; hyperproliferative disorder; hair loss; urinary system disorder; cardiovascular disorder; hair loss; respiratory disorder; cardiovascular disorder; arrhythmia; neural activity disorder; neurological disorder; endocrine disorder; gastrointestinal disorder; liver disorder; panoreatic disorder; gall bladder disorder; large intestine disorder; developmental disorder; inherited disorder; wound healing; skin aging; food additive; preservative

Homo sapiens.

02-AUG-2001.

40200155329-A2.

17-JAN-2001; 2001WO-US001360.

31-JAN-2000; 2000US-0179065P

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The invention relates to isolated ovarian related polypeptide (ovarian antigen) comprising a sequence at least 90% identical to a sequence selected from a polypeptide fragment, domain, epitope or full length protein of a sequence (51) appearing as ABG60139-ABG60296 having contein of a sequence (51) appearing as ABG60139-ABG60296 having contein of a sequence (51) appearing as ABG60139-ABG60296 having contein of a sequence (51) appearing as ABG60139-ABG60296 having contein of an enti-S1 antibody and the CDNA clones encoding the proteins of S1. S1, conteining or ameliorating a medical condition in mammalian subject conteining and the CDNA clones encoding the proteins of S1. S1, conteining or ameliorating and edited condition in mammalian subject consolated disorders (61) ansitions of the ovary and/or breast such as infectious diseases (e.g., mastitis), inflammatory diseases (e.g., abscesses), reproductive system disorders (haseases), reproductive system disorders (astendated disorders (sickle cell anaemia), hood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders are conteined isorders (halson's disease and parkinson's disease), conforders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver cirrhosis), conformental and inherited disorders (biliary liver also useful to prevent skin aging, for preventing hair loss, to maintain organs conformed additive or preservative. The present sequence is a condulate anammalian metabolism, to change a mammal's metabolism, to change a me
                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1352 BP; 238 A; 446 C; 407 G; 261 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 56; 524pp; English.
                                                                                                                                                                                                                                                               Barash SC, Ruben SM;
                07-UUN-2000; 2000US-0209467P.
14-SEP-2000; 2000US-023398P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025160P.
08-DEC-2000; 2000US-0251688P.
08-DEC-2000; 2000US-025190P.
                                                                                                                                                                                                       HUMA-) HUMAN GENOME SCI INC.
2000US-0180628P
                                                                                                                                                                                                                                                                                                              WPI; 2001-476195/51.
P-PSDB; ABG60284.
                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
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3251 TTTTTTTTTTTAAAGAATGTCATTCTTTGTGAAGTT 3290 1352 TTTTTTTTTTTTTGGAGAATAAATAATTTATTGAAATT 1313 ABK91679 standard; cDNA; 1352 ABK91679; RESULT 210 ABK91679/c g ******** à

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Gaps

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Query Match
0.6%; Score 20.8; DB 1; Length 1352;
Best Local Similarity 70.0%; Pred. No. 2.46+02;
Matches 28; Conservative 0; Mismatches 12; Indels 0;

cDNA encoding novel ovarian related polypeptide #46.

(first entry)

26-AUG-2002

200005-0232399P 200005-0232400P 200005-0232400P 200005-0233064P 200005-0233064P 200005-0233065P 200005-0234234P 200005-0234234P 200005-0234234P

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000;

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

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Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; tuberculosis; arthritis; immune system disorder; chediak-Higashi's syndrome; neonatal neutropenia autoimmune disorder; Chediak-Higashi's syndrome; neonatal neutropenia eptic shock; multiple solerosis; central nervous system disorder; neurological disorder; allergy; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atheroselerosis; blood related disorder; respiratory disorder; atheroselerosis; blood related disorder; respiratory disorder; anthary system disorder; musculoskeletal disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative;
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17-MAR-2000;
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08-SEP-2000;
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                                                                                                          Homo sapiens,
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20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000;

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08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

08-NOV-2000;

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2000US-0226868P.
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          Homo sapiens
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Pred. No. 2.4e+02;
0; Mismatches 12; Indels
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05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
06-DEC-2000; 2000US-0251988P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
11-DEC-2000; 2000US-0251869P.
11-DEC-2000; 2000US-0251869P.
11-DEC-2000; 2000US-0251868P.
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11-DAN-2001; 2001US-00764864.
17-JAN-2001; 2001US-00764869.
17-JAN-2001; 2001US-00764869.
17-JAN-2001; 2001US-00764889.
17-JAN-2001; 2001US-00764889.
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Best Local Similarity 70.0
Matches 28; Conservative
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(RUBI/) RUBIN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-2001
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XX AAS4
AC AAS4
XX AAS4
DE CDNA
XX Huma
KW Huma
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2000US-0249297P.
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                     2000US-0236370P.
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(HUMA-) HUMAN GENOME SCI INC.

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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences colophoptides (AAU22915-AAU23814), and the cDNA and genomic sequences cancing them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or lygases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. ander), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. ancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. archina), cardiovascular disorders (e.g. AIDS) autoimmune disorders (e.g. archina), cardiovascular disorders (e.g. althorous), inflammatory disorders (e.g. aschma), cardiovascular disorders (e.g. althorous). The polymucleotides of the invention can also be used in gene therapy. AAS40785-AA41684 represent invention and also be used in gene therapy. AAS40785-AA41684 represent clowed invention. Note: The sequence data for this patent did not form part of invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WiPo int/Published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrousscular disorder; angiogenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; corneal infection; wound healing; epithalial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                              Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 847; 1180pp; English.
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                                 Rosen CA, Barash SC, Ruben SM;
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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
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                                                                                                             WPI; 2001-465566/50.
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(HUMA-) HUMAN GENOME SCI INC

Ruben sc, Barash G, Rosen

SM;

WPI; 2001-476222/51 P-PSDB; AAU17038.

t t Novel polypeptides and polynucleotides useful as diagnostic reagents the diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

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                   The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnoshing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radicimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune of seases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiorers, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to preservative to increase or decrease storage crasplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, ocfactors and other nutritional components. The present cencedes a novel secreted protein, etc. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiant; hepatotrophic; cerebroprotective; haemophilia; liver dise
myocardial infarction; thrombotic stroke; deep-vein thrombosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pactor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                             ;
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0.6%; Score 20.8; DB 1; Length 1352;
Best Local Similarity 70.0%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 12; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /partial
/note= "CDS lacks an initiation codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                         3251 ITTITITITITIAAAGAATGICATICTITGIGAAGTI 3290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rrrrrrrrrrrragadahnaanaarrranraharr 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human FVII expression cassette SEQ ID NO 4.
   Claim 1; SEQ ID NO 135; 601pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI99983 standard; cDNA; 1357 BP.
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/product= "FVII"
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18-OCT-2000; 2000DK-00001558.
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                                                                                                                                                                                                                                                    The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIa (AAMS2171) in that least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIa conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIa/Frelated diseases or disorders such as haemophila; liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates have increased functional in vivo half life and/or increased plasma half
New conjugate, useful for treating Factor VIIa related diseases or disorders such as hemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   life, increased bicavailability and or reduced sensitivity to protectly degradation. Consequently medical treatment using the conjugates has a number of advantages over currently available such as longer duration between injections. The present sequence is that of a human FVII expression cassette, encompassing the short form of the full length oDNA encoding FVII, for expression of human FVII in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determination of polymorphisms in genes, especially those identifying predisposition to vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; coding sequence polymorphism; vascular pathology gene;
polymorphic site; phenotype correlation; forensic; paternity testing;
medicine; genetic analysis; vascular disease; ds.
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0.6%; Score 20.8; DB 1; Length 1357;
Best Local Similarity 57.8%; Pred. No. 2.4e+02;
Matches 37; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1357 BP; 249 A; 435 C; 414 G; 259 T; 0 U; 0 Other;
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                                                                                                                                                                                                 Example 2; Page 63-64; 89pp; English.
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                                                                                                                          to polypeptide group.
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P-PSDB; AAR13622.
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                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic site is different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis. AAV49550 to AAV49573 represent the proteins which correspond to some of
                                                                                                                                                                                                                                                                                                                                                                                                   453 CICCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAGCTGTGGATGTGAC 512
                                                        AAZ32159 to AAZ32194 represent reference alleles for specifically claimed
                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                Length 1366;
                                                                                                                                                                                                                                                                                      Sequence 1366 BP; 302 A; 388 C; 425 G; 251 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            Score 20.8; DB 1; Length 13
Pred. No. 2.4e+02;
0; Mismatches 27; Indels
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195. 1451
195. -650
195. -650
/*tag= d
/*tag= d
/*tag= d
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note= "heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ13357 standard; cDNA; 1754 BP
                  Claim 1; Fig 12; 134pp; English.
                                                                                                                                                                                                                                                                                                                          0.6%;
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/*tag= a
69. .194
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.8<sup>4</sup>
Marches 37; Conservative
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                                                                                                                                                                                                                                                   the reference alleles
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04-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 215
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Db.
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                                                                                                                    The cDNA sequence encodes human protein C (HPC). It can be obtd. from a lambda-gtll cDNA library prepd. from human liver mRNA by standard methods. The activated protein can comprise one of 3 different truncated light chains, 195 to 644, 647 or 650. The activated HPC, with a truncated light chain is more stable during storage. It can be administered for prophylactic and/or therapeutic treatments of disease states or injuries capabillities. See also W09109951 (AAQ12649). (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1573 CTCCAGAAGAGCCCAAAAGAGGGATGGAAGGACAGAACAGCAGGCCGGTGTGCTTGTTAC 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 CTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAGGTGTGGATGTGAC 512
Activated human protein C with truncated light chain - used in therapy and prophylaxis to enhance anticoagulant and fibrinolytic capabilities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20.8; DB 1; Length 1754;
Pred. No. 2.4e+02;
0; Mismatches 27; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 1754 BP; 378 A; 506 C; 540 G; 330 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/label= prepro peptide
195. .1454
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anticoagulant; fibrinolysis; ss.
                                                                       Example; Fig 1; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ12649 standard; cDNA; 1754
                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%;
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(first entry)
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Best Local Similarity 57.8 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein C precursor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC. (TEIJ ) TEIJIN LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foster DC, Holly RD,
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P-PSDB; AAR13074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 TGGT 516
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02-OCT-1991
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The sequence was determined from a clone isolated from a cDNA library proped. From mRNA from Hep G2 cells. It encodes a protein C precursor. Including light and heavy chains, which is cleaved to produce activated controlled in cleaved to produce activated controlled in the for details). The sequence can be manipulated by genetic engineering techniques to express a protein comprising (when cativated) a heavy chain and a truncated light chain comprising (when controlled) a heavy chain and a truncated light chain comprising residues comprises the precursor of formula Pre-Dro-L-X-H Pre-pro = pre-pro peptide of protein C with all/part replaced by the corresponding peptide of either protein S, factors VII, IX or X, or prothrombin; L = AAs 1-149, 150, 151 or 152 of light chain; X = 3-10 Lys/arg residues; and H = heavy chain. Cells transformed with expression vectors contey the modified DNA sequences produce the new proteins which can be used to regulate anticoagulant and fibrinolytic systems. See also W09112320 (AAQ13357).

(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                          453 CTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAGCTGTGGATGTGAC 512
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phopholipid, binding protein; lipocortin, domain; vitamin K, PBP; gla-domain; VKDP; ss.
                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                          Query Match
0.6%; Score 20.8; DB 1; Length 1754;
Best Local Similarity 57.8%; Pred. No. 2.4e+02;
Matches 37; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                            Sequence 1754 BP; 378 A; 505 C; 540 G; 331 T; 0 U; 0 Other;
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/*tag= a

/product= "protein_C"

70. .195

/*tag= b

/*tag= c
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AAQ12678 standard; cDNA; 1755 BP.
Disclosure, Fig 1; 60pp; English
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(first entry)
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P-PSDB; AAR13081.
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30-SEP-1991
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                                                                                                                                                                                                                                                                      512
Recombinant prodn. of hybrid phospholipid-binding proteins - comprising lipocortin phospholipid-binding domain and vitamin=K-dependent protein.
                                                                                                                                                                                                                                                                      453 CTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAGCTGTGGATGTGAC
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activated protein C; serine protease; thrombosis; thrombolytic; fibrinolytic; antithrombotic; blood clotting; therapy; ss.
                                                                                                                                                                                                                    Query Match 0.6%; Score 20.8; DB 1; Length 1755; Best Local Similarity 57.8%; Pred. No. 2.4e+02; Matches 37; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                           Sequence 1755 BP; 378 A; 506 C; 541 G; 330 T; 0 U; 0 Other;
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product= "protein C prepro-protein"
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/*teg= b
/function= "prepro-peptide"
196. .1452
/*tag= c
/*tag= c
/*tag= c
/*tag= c
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                                        Disclosure; Fig 2; 57pp; English.
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AAT32795 standard; cDNA; 1755 BP.
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86US-00924462.
87US-00130370.
89US-00517205.
90US-00582131.
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29-OCT-1986;
08-DEC-1987;
28-FEB-1989;
10-SEP-1990;
04-DEC-1992;
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05-NOV-1996
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Matches
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AAC02548/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1574 CTCCAGAAGAGCCCAAAAGAGGGATGGAAGGACAGAAAAGCAGCAGGCCGGTGTGTTGTTAC 1515
                                                                                                                                                                                                                                                                         A cDNA clone (AAT32795) codes for human full-length protein C (AAW02600), a zymogen of a serine protease that plays an important role in blood clotting and in the generation of fibrinolytic activity in vivo. It was obtd. from a cDNA library produced from Hep G2 cells by screening with a genomic fragment contg. an exon corresponding to amino acids -42 to -19 of the prepro-peptide. A genomic clone (AAT32796) was also obtd. The cDNA can be used for large-scale produ. of protein C, or versions of protein C modified to improve cleavage brewnen the heavy and light chains of the circulating intermediate. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                New DNA encoding modified forms of opt. activated protein C - and related transformed cells for prodn. of recombinant protein C for use e.g. as an anti-thrombotic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCAGAAAGAATGAAGAGAGCCAAAGCAAAAAAAAATACCCAGCTGTGGATGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 20.8; DB 1; Length 1755; 57.8%; Pred. No. 2.4e+02; ive 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1755 BP; 378 A; 506 C; 541 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; blood coagulation disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
71. .1456
                                            Foster DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkner KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/label= protein C
                                                                                                                                                                                                                                      Claim 3; Fig 2A-C; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA sequence encoding protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN81563 standard; cDNA; 1756 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87EP-00309528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conservative
(ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC.
                                            Murray MJ, Berkner KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oster DC, Murray MJ,
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                                                                                   WPI; 1996-251006/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-121259/18.
P-PSDB; AAP81205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                        P-PSDB; AAW02600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1986;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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1575 CTCCAGAAGAGCCCAAAAGAGGGATGGAAGGACAGAACAGCAGGCCGGTGTGCTTGTTAC 1516
                                                                                                                In the construction of the full length protein C gene this sequence is joined to a genomic clone (following removal of the introns). The desired genomic:cDNA is then generated by looping out of unwanted sequences using oligomicleotide-directed deletion mutagenesis. The protein produced upon transformation of mammalian host cells, contg. the recombinant DNA, has substantially the same biological activity as natural protein C and is hence useful in the treatment of blood coagulation disorders. See also AAN81564. (Updated on 25-MAR-2003 to correct PA field.)
Protein C DNA coding sequence and expression vector for prodn. - used for treating blood coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 CTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAAGAATACCCAGCTGTGGATGTGAC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The S' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from olygo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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                                                                                                                                                                                                                                                                                                                                                                                                Match 0.6%; Score 20.8; DB 1; Length 1756; Local Similarity 57.8%; Pred. No. 2.4e+02; Los 37; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                  Sequence 1756 BP; 379 A; 507 C; 540 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 2546; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein 5' EST, SEQ ID NO: 2546.
                                                                           Disclosure, Page ?; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC02548 standard; cDNA; 228 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1515 ATGT 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 TGGT 516
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obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                             773 CAGTACTIGGAIGCAGICTCAAAAACGACAGAATGAICTCTCTGITTTCCAAGGCAAAC
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      protein; Factor X; Factor IX; anticoagulant; protein-C; ss.
                                                                                                                 ö
                                                                                           Length 228;
                                                                                         Score 20.6; DB 1; Length 2
Pred. No. 1.8e+02;
8; Mismatches 28; Indels
                                                                      Sequence 228 BP; 51 A; 54 C; 37 G; 71 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                    Leader sequence of Factor X and Gla domain of Factor IX
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                                                                                                                                                                                                                                                                                                                                                                                                               Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "AAs 44-46 of protein C"
                                                                                                                                                                                                                                                                                                                                                                                                                                           "AAs 1-43 of Factor IX"
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                                                                                                                                                                                                                                                                                                                                                                                                             "leader sequenc
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                                                                                                                                                                                                                                              AAN93747 standard; DNA; 271 BP.
                                                                                          ch
1 Similarity 47.8%;
33; Conservative
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263. .271
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/*tag= a
/product=
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                                                                                                                                                                                                                                                                                                                                                                                         .133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                          833 CATTCAATA 841
                                                                                                                                                                                            128 CWKAAAATD 120
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                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Signal peptide
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                                                                                                                                                                                                                                                                                                 04-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1987;
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                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                   AAN93747;
                                                                                          Query Match
                                                    vectors
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                                                                                                                                                                                                                                                                                                                                        Fusion
                                                                                                                                                                                                                             RESULT 221
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The nucleotide sequence of synthetic DNA encodes the amino acid sequence including the Gla domain of Factor-XI. See also AAN93063 and AAN93746-49. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)

Hybrid protein of protein C_with replaced Gla domain - using human vitamin=K dependent proteins, e.g. factor X, to give improved anticoagulation activity.

Table 5, Page 14; 23pp; English.

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                                                                                                    3056 CITTAAAATTATTAATTTCTCTTTAGTGTTTTACCAGTTCTTTCAGGCTACTTCTTTGA 3115
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                                                                                                                                 CTTCCAAAATTCAGTTGTCTTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                            disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1654 CCTCTGTATCATGGAAAAAGCAAGAGTTCCAGAAAAACATCTATTTCTGCTTTATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 CATCTTGATCATGGACCTGGCAAACTTGGTCCTGAAAGTCGCCTGGCTGCGCACGAAGGA
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                                            Length 271;
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                                                                         Indels
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icke D, Zhu T;
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               0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 312 BP; 69 A; 92 C; 95 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Maize gene conferring disease resistance in plants.
                                         Score 20.6; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 20.6; DB 1;
54.7%; Pred. No. 1.9e+02;
tve 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Briggs S, Cooper B, Goff S?
Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1375; 299pp; English.
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E⊣
            Sequence 271 BP; 77 A; 57 C; 77 G; 60
                                                                                                                                                               3116 TITATITGGICCIATCITICIC 3138
                                                                                                                                                                                            ACACTTTTCTTCCATACATTCTC 180
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                                                                                                                                                                                                                                                                       BP
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26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
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                                         0.6%;
llarity 53.0%;
Conservative
                                                                                                                                                                                                                                                                       ADA49305 standard; DNA; 312
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                                                                                                                                                                                                                                                                                                                                    entry)
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                                         Query Match
Best Local Similarity
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Katagiri F, K
                                                                       44;
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1714 CTATGCAAAAGCCTT 1728

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New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                          Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                          Bovine EST associated with lactation/muscle/fat deposition #10052
                                                                                                                                                                                                                                                                               Warren WC;
                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 10052; 245pp; English.
                                                                                                                                                                                                                                                                               Tao N,
                                         ABX44887 standard; cDNA; 396 BP
123 GrcGACCAGGGCCTT 109
                                                                                                                                                                                           24-SEP-2001; 2001US-00960352.
                                                                                                                                                                                                            12-JAN-1999; 99US-0115707P.
                                                                         (first entry)
                                                                                                                                                                                                                                                                             Mathialagan N,
                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                     (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                              WPI; 2003-110599/10.
                                                                                                                                                           US2002137139-A1.
                                                                          21-FEB-2003
                                                                                                                                                                            26-SEP-2002.
                                                                                                                                           Bos Taurus.
                                                                                                                                                                                                                                                                              Byatt JC,
                                                         ABX44887;
                                ABX44887
                         RESULT
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated IMPD), derived from cattle, and the IMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if (1) a transformed cell having a nucleic acid comprising an IMPD nucleic acid linked to a promoter and a 3 non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mark and addition of polyadenylated ribonucleotides to a 3 end of the mark and addition of the 15112 nucleic acid molecule of an anchecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue. Complementary nucleic acid molecule obtained from the molecule, and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the molecule. The LMPD molecule, and is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping gene identification and analysis, cattle breather sequence mapping gene identification and analysis, cattle breather sequence and engagement the molecule of the present sequence is one of the present sequence and proved the province and analysis, and the propagation of any part of any province tag) nucleic acid acid and the present sequence and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and analysis and ovine LMFD EST (expressed sequence tag) nucleic acids. Note: The sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: segdata.uspto.gov/sequence.html?DocID=20020137139 present

Seguence 396 BP; 109 A; 83 C; 95 G; 109 T; 0 U; 0 Other;

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o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and prediction of an and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose useeptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3139 AAGTTTTGAATTGGCTACGTAACTCATTTATCTTTATTTTTTGTAAATTAGCTCTTTAAA 3198
                                                                         429 TACTGGAGATCAGTGGAGAAATAACTCCAGAAAGAATGAAGAGATGGAGCCAAAGCAAAA 488
                                                                                                               160 racidricirceagicargadaracaccaaaagcaagaaccracagagcaaaagcgaaa 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Single nucleotide polymorphism; SNP; human, genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
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0.6%; Score 20.6; DB 1; Length 717;
Best Local Similarity 54.7%; Pred. No. 2.4e+02;
Matches 41; Conservative 0; Mismatches 34; Indels (
   Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 717 BP; 231 A; 133 C; 151 G; 201 T; 0 U; 1 Other;
                                       34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Single nucleotide polymorphism containing sequence #392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altshuler D, Cargill M, Daley GQ, Ireland JS,
Lipshutz RJ, Patil N, Sklar P;
   Score 20.6; DB 1;
Pred. No. 2.1e+02;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                   AAC71346 standard; DNA; 717 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 5; 214pp; English.
0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2000; 2000WO-US008440.
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                                                                                                                                                                                        220 TGTGATCCGTGCTAT 234
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                       Conservative
                                                                                                                                                  489 AGAATACCCAGCTGT
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000.
 Query Match
Best Local S:
Matches 41
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Gaps

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Indels

Pred. No. 2.7e+02; 0; Mismatches 24;

59.3%;

Local Similarity

Best Loca Matches

ઢ g

35; Conservative

1507 TTACAAATAGCTGTGAAAAGAAGAAGTGAAAAGCAAAGGAAAAAAGGAAAAGGAAAGGTAAAA 1565 

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Efficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence; formation of circulation requires: removal of the signal sequence; formation of distinction of the signal sequence; formation of circulation dends; modification of one aspatic acid; modification of N = and O-linked oligosaccharides to the activation peptide; converse of an internal tripeptide to yield two-chain factor X and removal of the propeptide just prior to secretion. While some of these of the signal sequence, propeptide, internal tripeptide and full gamma-converse of biologically active factor X/Fxa. Isolated chimeric of the signal sequence, propeptide, internal tripeptide and full gamma-converse or biologically active factor X/Fxa. Isolated chimeric of production of biologically active factor X/Fxa. Isolated chimeric polymucleocides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin X-dependent protein gamma-carboxylation enhancers and are useful for optimising the gamma-carboxylation of a WKDP to produce a fully gamma-carboxylation of a WKDP to produce a fully gamma-carboxylation of fully gamma-carboxylated manure WKDP. The clusion proteins and recombinant cells expressing them are useful in the production of fully gamma-carboxylated mature WKDP. The clusion proteins of fully gamma-carboxylated mature wKDP. The chologically active. The invention encompasses all combinations of the signal, propeptide and mature protein sequence encodes the signal, propeptide and mature protein sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitamin K dependent protein, VXDP, gamma-carboxylation, chimeric protein, fusion protein; coagulation factor, Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human;
700 AAGTGATTAGTTAGTGAGGCCCTGTTAATTTTCAATTCCAATGAATTAACCTTGGAAA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stafford DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHILDRENS HOSPITAL PHILADELPHIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larson PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein C coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           AAA54035 standard; DNA; 1843 BP.
                                                                                                 3199 TTCATTATTCTTTGA 3213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-638152/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200054787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA54035;
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                                                                                                                                                                                                                                                                                                                            RESULT 225
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5. UTR; 5. untranslated region; age-regulatable expression construct; PBA-3 element; polyoma virus activator 3; antisense therapy; gene therapy; thrombosis; cardiovascular disease; diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;

osteoarthritis; dementia; ds.

WO200075279-A2.

14-DEC-2000

Homo sapiens.

Age-related gene regulation; gene expression; human protein C; hPC;

Human protein C gene, SEQ ID NO:49.

(first entry)

30-MAR-2001

AAF54050;

AAF54050 standard; DNA; 1843 BP.

226

AAF54050 RESULT

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The invention relates to nucleic acid sequences which regulate gene expression in an age-related manner and/or in a liver-specific manner. The invention identifies regions of the human factor IX (hFIX) gene, and a region of the human protein C (hPC) gene, which are age-related ca region of the human protein C (hPC) gene, which are age-related ceglatory sequences. The hFIX age-related regulatory sequences are region of the human protein C (hPC) gene, which are age-related in the 5, or the position 2164-2165 of AAF54018) and 3 'UR (at position 34383-00 or the lifespan of an individual; howers, they can independently exert effects on hFIX mRNA, in an age-related manner, with AES acting to stabilise hFIX mRNA, and AE3 acting to increase hFIX mRNA in an age-related manner, with AES acting to stabilise hFIX mRNA, and AE3 acting to increase hFIX mRNA, and or a serial activator of the contains two PEA-3 (polyoma virus activator 3) elements of the invention, along with their homologues, variants and fragments, may be used in the construction of recombinant expression vectors for the expression of desired sequence in an age-related fashion in a host call. Preferred target genes for expression in such age-regulated feature call. Preferred target genes for expression in such age-regulated feature call antitrypain, PEA-3 protein and reporter proteins such as luciferase.

Coagulants protein C and antithrombin III), human alpha-1-
coagulants protein C and antithrombin III), human alpha-1-
coagulants protein C and antithrombin III), human alpha-1-
coagulants protein C and antithrombin HEA speciatory correct or and the SP6 promoter. The expression vectors of the invention may be used in gene therapy to provide age-related and/or liver-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 12; 225pp; English.
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v regulatory elements that control age-related gene expression, useful gene therapy and for reducing Factor IX expression.

99US-00328925.

19-40D-1999;

Kurachi S;

Kurachi K,

WPI; 2001-061708/07.

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(UNMI ) UNIV MICHIGAN.

06-JUN-2000; 2000WO-US015728.

DB 1; Length 1843;

Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other;

0.6%; Score 20.6;

Query Match

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of target genes. Age-regulatable constructs may be used in the treatment disease, diabetes. Alzelmer's disease, Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia. Specifically, they may be used to express factor IX antisense mRNA in the treatment of thrombotic conditions associated with the natural age-related rise in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these diseases, in screening for potential therapeutic agents and for studying normal processes such as ageing and gene expression. Fragments and homologues of age-related regulatory sequences, are useful as probes to detect, isolate or identify other such sequences in samples. The present sequence represents the hPC

Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other;

Gaps ö Length 1843; 24; Indels Score 20.6; DB 1; Pred. No. 2.7e+02; 0; Mismatches 24; Match 0.6%; Local Similarity 59.3%; les 35; Conservative ( Query Match

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RESULT 227 ABN9717 

ABN97175 standard; DNA; 1843 BP ABN97175;

13-AUG-2002 - (first entry)

Gene #3673 used to diagnose liver cancer.

Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

Homo sapiens

WO200229103-A2.

11-APR-2002.

02-OCT-2001; 2001WO-US030589.

02-OCT-2000; 2000US-0237054P.

(GENE-) GENE LOGIC INC.

Vockley JG; Peres-Da-Silva S, Horne D, Alvares C,

WPI; 2002-426119/45.

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

Claim 1; SEQ ID NO 3673; 298pp; English.

The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism. Note: The sequence data

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We protein modification and mainterance molecule; PWDM;

We protein modification; protein maintenance; protein function;

We protein modification; protein stabilisation; protein degradation; kinase;

We protein conformation; protein stabilisation; protein degradation; kinase;

We protein conformation; proteins stabilisation; protein degradation; kinase;

We molecular chaperone; anti-HIV; antiallergic; antiinflammatory;

We manianemic; antiparkinsonian; nocropic; anticonvulsant;

Mentigout; thyromimetic; neuroprotective; osteopathic; antithyroid;

We antiparasitic; neuroprotective; osteopathic; antiathritic;

We antiparasitic; antihelminic; antibacterial; virucide; proteoracide;

We maintenantic; naemostatic; antibacterial; virucide; proteoracide;

We hapatitis; polycythaemia vera; psoriasis; primary thromobocytopaenia;

We patitis; polycythaemia vera; psoriasis; primary thromobocytopaenia;

We patitis; autoimmune disorder; anaemia; mental retardation;

We pullepsy; autoimmune disorder; inflammatory disorder; Albs; allergies;

We pellepsy; autoimmune disorder; inflammatory disorder; Albs; allergies;

We phentilepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We pollepsy; autoimmune disorder; inflammatory disorder;

We principle sclerosis;

We arthritis; oseeoporosis; pancreatiifs; Sjogren's syndrome;

We microbial infection; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                  for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                               Human protein modification and maintenance molecule (PMMM)-30 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name= "Single_nucleotide_polymorphism"
replace(109,G)
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/standard_name= "Single nucleotide polymorphism"
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0
                                                                                                                                                                                    0.6%; Score 20.6; DB 1; Length 1843; 59.3%; Pred. No. 2.7e+02; ive 0; Mismatches 24; Indels 0;
                                                                                                                          Sequence 1843 BP; 417 A; 530 C; 564 G; 332 T; 0 U; 0 Other;
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replace(108,A)
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replace(419,G)
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ADE79050 standard; DNA; 1982
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akar A, Baughn MR;
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ng W, Ison CH, Marquis JP;
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Lehr-Mason PM;
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transgranges and minimary damperatures. Compounds which incontact the invention may have anti-HIV, antiallergic, antiinflammatory, antianaemic antiparkinsonian, nootropic, antiinflammatory, antianaemic antiparkinsonian, nootropic, antidabetic, continuously cytostatic, hyromimetic, dermatological, antidabetic, antiparaticic, antibarintic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, antiparaticic, uropathic ophthalmological, antiparaticic, antibarcterial, virucide, protozoacide or fungicide activities. The DNA sequence which encode the protein modification and maintenance molecules (PMMMs), the buwan or protein modification and maintenance molecules (PMMMs), the buwan or protein modification and maintenance molecules (PMMs), the buwan or protein modification and maintenance molecules (PMMs), the buwan or preventing disorders associated with aberrant expression of PMMW, particularly cell proliferative disorders (for example anteriosclerosis, hepatitis, polycythaemia vera, psoriasis, commune/inflammatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disorders (for example Alzhahamatory disord
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Pred. No. 2.7e+02;
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27-MAR-2001; 2001WO-US009761.

This invention relates to novel isolated human proteins, which are human protein modification and maintenance molecules (PMMM). The cellular processes regulating modification and maintenance of protein molecules coordinate their function, conformation, stabilisation and degradation. Each of these processes is mediated by key enzymes or proteins such as kinases, phosphatases, proteases, protease inhibitors, isomerases,

Claim 5; SEQ ID NO 88; 405pp; English.

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDRU2A), ABC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus (CDRU2A), haemoglobin alpha locus 2 (HBA2), MLHI, MBH2, MBH6, apollipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGTI), anyloid precursor protein (APC), presentilin-1 (PSENI) and presentilin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, arious syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention
                                                                                                                                                                                                                                            Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 181; 294pp; English.
27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-019219P.
01-UIN-2000; 2000US-026838P.
30-OCT-2000; 2000US-0244989P.
                                                                                                                                                            Gamper HB,
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ö Gaps 838 54 daadiririrdaaadacidaadaadadadadiariricdacaraaraccerida 1 785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA . 0 0.6%; Score 20.4; DB 1; Length 121; 61.1%; Pred. No. 1.7e+02; tive 0; Mismatches 21; Indels C 33; Conservative Local Similarity Query Match Matches ò

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Human; gene therapy, adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2, CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGTI; syndrome; APP; PSEN1; antisense; UDP-Glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
                                                                                                                                                Factor IX mutation correcting oligonucleotide SEQ ID NO: 2412.
                                     ABA79566 standard; DNA; 121 BP
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                                                                                                             24-JAN-2002
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RESULT 230
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be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MH2, MSH2, MSH6, apolipoprotein E (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentian-1 (FSEN1) and presentian-2 (FSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting
                                                                                                                                                                                                                                                                                                                                                               The present invention provides single-stranded oligonucleotides which can
                                                                                                                                                                                                                                       Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 20.4; DB 1; Length 121; 61.1%; Pred. No. 1.7e+02; ive 0; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121 BP; 46 A; 15 C; 29 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         Claim 7; Page 181; 294pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  various syndromes. The present secoligonucleotides of the invention
                                                                                                                                                            Rice MC
                                  2000US-0192179P.
2000US-0208538P.
2000US-0244989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 61.1
nes 33; Conservative
                                                                                                                 (UYDE ) UNIV DELAWARE
                                                                                                                                                            Gamper HB,
                                                                                                                                                                                                 WPI; 2001-639230/73.
                 27-MAR-2000; 27-MAR-2000; 201-JUN-2000; 2
                                                                             30-OCT-2000;
                                                                                                                                                            Kmiec EB,
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121 68 GAAGTITITGAAACACTGAAAGAACAGTGAGTATITCCACATAATACCCTTCA

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ABA79583 standard; DNA; 121 BP (first entry) 24-JAN-2002 ABA79583; RESULT 231 ABA79583/

Factor IX mutation correcting oligonucleotide SEQ ID NO: 2429.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKV2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismacch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercholesterolaemia; UGTI; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentilin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss

Homo sapiens

WO200173002-A2

04-OCT-2001

27-MAR-2001; 2001WO-US009761.

MO200173002-A2

34-OCT-2001

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, rectinoblascoma, BRCA1, BRCA2, CFTR, cyclin-dependent Kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus (CDKN2A), haemoglobin alpha locus 2 (HBA2), manyloid precursor protein (APC), presentin-1 (BSEN1) and presentilin-2 (PSEN1). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemoghila, hypercholesterolaemia, thalasseamia, sickle cell anaemia, alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting
                                                                                                                                                                                                                                                   Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 121 BP; 31 A; 29 C; 16 G; 45 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 182; 294pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligonucleotides of the invention
                                                                                                                                                                              Rice MC;
                                     2000US-0192176P.
2000US-0192179P.
2000US-0208538P.
2000US-0244989P.
27-MAR-2001; 2001WO-US009761
                                                                                                                                                                              Gamper HB,
                                                                                                                                       (UYDE ) UNIV DELAWARE
                                                                                                                                                                                                                  WPI; 2001-639230/73.
                                       27-MAR-2000;
27-MAR-2000;
01-JUN-2000;
                                                                                                   30-OCT-2000;
                                                                                                                                                                              Kmiec EB,
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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the coligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cationblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDRNA), APC, Pactor VIII, Factor IX, haemoglobin alpha locus (CDRNA), APC, Pactor VIII, Factor IX, haemoglobin alpha locus (CDRNA), APC, pactor VIII, SayConton State (CDRNA), APC, presential cours (ADLN), UDL receptor (LDLN), UDP-glucuronosyltransferase (UGTI), anyloid precursor protein (ADC), presentian (PSENI) and presentian-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemoghilia, hypercholeserolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention

Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.

Rice MC,

27-MAR-2000; 2000US-0192176P. 27-MAR-2000; 2000US-0192179F. 01-UTN-2000; 2000US-0208538F). 30-OCT-2000; 2000US-0244989F.

(UYDE ) UNIV DELAWARE Kmiec EB, Gamper HB, WPI; 2001-639230/73

27-MAR-2001; 2001WO-US009761

Claim 7; Page 182; 294pp; English

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                                   Gaps
                                                                   838
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                                 0;
                                                                   785 GCAGTCTCAAAAACGACAGAATGATCTCTCTTTTGTTTCCAAGGCAAACCATTCA
                                                                                                  GAAGITITIGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCA
0.6%; Score 20.4; DB 1; Length 121; 61.1%; Pred. No. 1.7e+02;
                                   21; Indels
                                     0; Mismatches
                 Best Local Similarity 61.1%;
Matches 33; Conservative
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     Query Match
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Human, gene therapy, adenosine deaminase deficiency; p53; beta-globin, retinoblastoma, BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDRVA2, melanoma, APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VI; Factor IX; thrombosis; haemophilia, alpha thalassaemia, haemoglobin alpha locus 1; MLH1; APOE; mismatch repair, MSH2; MSH6; hyperlipidaemia, apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
                                                                                                                                    Factor IX mutation correcting oligonucleotide SEQ ID NO: 2441.
              ABA79595 standard; DNA; 121 BP
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                 antilipemic; ss
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                                                                                                24-JAN-2002
                                                         ABA79595;
ABA79595/
                     DXBX8XEEEEEEEEEE
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WO200173002-A2

04-OCT-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGTITITGAAACACTGAAGAGAGTGAGTATITCCACATAATACCCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121 BP; 29 A; 30 C; 16 G; 46 T; 0 U; 0 Other;
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les 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cetinoblascoma, BRCAI, BRCAZ, CFTR, CYCLIN-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VIII, Factor IX, heemoglobin alpha locus (HBAI), haemoglobin alpha locus 2 (HBAI), haemoglobin alpha locus 2 (HBAI), amyloid precursor protein (APC), presentin-1 (PSENI) and presentin-2 (PSENI). The gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, chaemophila, hypercholesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and conventing and colon and conventing and colon and conventing and colon and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 182; 294pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                     Kmiec EB, Gamper HB, Rice MC;
                                                                                                                                    27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-0192179P.
01-UTN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
                                                                27-MAR-2001; 2001WO-US009761.
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04-OCT-2001
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ô Gaps 785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA 838 61 GAGITITICAAAACACIGAAAGAACAGIGAGIATITICCACATAATACCCTICA 8 ö 0.6%; Score 20.4; DB 1; Length 121; 51.1%; Pred. No. 1.7e+02; 21; Indels Similarity 61.1%; Pred. No. Local Similaric, hes 33; Conservative Query Match à

Human; gene therapy, adenosine deaminase deficiency; p53, beta-globin, retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V, cyclin-dependent kinase inhibitor ZA, DDNZA; melanoma, APC; HBA1; HBA2, adenomatous polyposis of the colon; Factor VI; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1, APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; Factor IX mutation correcting oligonucleotide SEQ ID NO: 2424. ABA79578 standard; DNA; 121 BP. 24-JAN-2002 (first entry) antilipemic; ss Homo sapiens ABA79578; RESULT 234 ABA7957 

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27-MAR-2001; 2001WO-US009761
04-OCT-2001.
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27-MAR-2000; 2000US-0192179P. 01-UUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P. 2000US-0192176P. 27-MAR-2000;

(UYDE ) UNIV DELAWARE.

Gamper HB, Rice MC; Kmiec EB,

WPI; 2001-639230/73.

Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.

Claim 7; Page 182; 294pp; English.

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes; adenosine deaminase, p53, beta-globin.

The following genes; adenosine deaminase, p53, beta-globin alpha locus of the following a BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBM1), haemoglobin alpha locus 2 (HBM2), MBM6,

COGKN2A), APC, FORD, LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentlin-1 (PSEN1) and precursor protein (APC), presentlin-1 (BSEN1) and cannear, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, various syndromes. The present sequence is one of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention

Sequence 121 BP; 45 A; 16 C; 29 G; 31 T; 0 U; 0 Other;

/ Match 0.6%; Score 20.4; DB 1; Length 121; Local Similarity 61.1%; Pred. No. 1.7e+02; les 33; Conservative 0; Mismatches 21; Indels 0; Gaps Query Match Matches

785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA 838 63 GAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCA 116 g à

RESULT 235 ABA79590

ABA79590 standard; DNA; 121 BP

ABA79590;

24-JAN-2002 (first entry)

Factor IX mutation correcting oligonucleotide SEQ ID NO: 2436.

Human, gene therapy, adenosine deaminase deficiency; p53;, beta-globin, retinoblastoma, BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor ZA; CDRVA2, melanoma, APC; HBA1, HBA2, adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia, alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; WSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome, APP; PSEN1, antisense; UDP-glucurchosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss

Homo sapiens

WO200173002-A2.

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Factor IX mutation correcting oligonucleotide SEQ ID NO: 2425.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR, cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN24; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOR; mismatch repair; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercholesterolaemia; UGTI; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss. ABA79579/XX
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AC ABA7
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KW HUMA
KW CYCII
KW AGEN
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KW MAGEN
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Homo sapiens,

The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin.

The following genes: adenosine deaminase, p53, beta-globin.

The following genes: adenosine deaminase, p53, beta-globin.

The following genes: adenosine deaminase, p53, beta-globin.

The following genes: adenosine deaminase deficiency. The middle and alpha locus approprient E (APCB), LDL receptor (LDLR), MDF-glucuronesyltransferase (UGTI), amyloid precursor protein (APC), presentlin-1 (PSENI) and presentlin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, hemophilia, hypercholesteroleemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and correcting and an anaemia, and also seems the colon and all and an anaemia, and also seems the colon and all and an anaemia, and a cancer of the colon and all and an anaemia and an anaemia, and a seems and a seems and a seem to seem the colon and a seem and a seems and a seem to seem the sequence is one of the gene correcting and an anaemia. Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical Claim 7; Page 182; 294pp; English. oligonucleotides of the invention 27-MAR-2000; 2000US-0192176P. 27-MAR-2000; 2000US-0192179P. 01-JUN-2000; 2000US-0208538P. 30-OCT-2000; 2000US-0244989P. 27-MAR-2001; 2001WO-US009761 Gamper HB, (UYDE ) UNIV DELAWARE WPI; 2001-639230/73. WO200173002-A2. modification. 04-OCT-2001 Kmiec EB,

.. 0 Gaps ö 0.6%; Score 20.4; DB 1; Length 121; 61.1%; Pred. No. 1.7e+02; tive 0; Mismatches 21; Indels ( Sequence 121 BP; 46 A; 16 C; 30 G; 29 T; 0 U; 0 Other; Query Match
Best Local Similarity 61.1
Matches 33; Conservative

61 GAÁGITITIGAAAACACTGAAAGAACAGTGAGTATITICCACATAATACCCTICA 114 785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA

à 셤 579/c ABA79579 standard; DNA; 121 BP.

(first entry)

be used for the transfer alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, the fet collowing genes: adenosine deaminase, p53, beta-globin, the fet collowing genes: adenosine deaminase, p53, beta-globin alpha locus (CDENADA), APC, Factor VI, Factor VII, Factor IX, haemoglobin alpha locus (HBAI), haemoglobin alpha locus 2 (HBA2), with, MSH2, MSH2, MSH6, apoliopprotein E (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase presentin. 2 (PSBN2). These can be used in the gene therapy of diseases haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia, halassemia, sickle cell anaemia, althabiner's disease, melanoma, adenomatous polyposis of the colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and colon and The present invention provides single-stranded oligonucleotides which can Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification. Sequence 121 BP; 31 A; 29 C; 16 G; 45 T; 0 U; 0 Other; Claim 7; Page 182; 294pp; English. various syndromes. The present secoligonucleotides of the invention Rice MC; 27-MAR-2000; 2000US-0192176P. 27-MAR-2000; 2000US-0192179P. 01-UUN-2000; 2000US-0206538P. 30-OCT-2000; 2000US-0244989P. 27-MAR-2001; 2001WO-US009761 (UYDE ) UNIV DELAWARE Gamper HB, WPI; 2001-639230/73. WO200173002-A2 04-OCT-2001 Kmiec EB, 

Gaps . 0 Score 20.4; DB 1; Length 121; Pred. No. 1.7e+02; 21; Indels 0; Mismatches 0.6%; Local Similarity 61.1%; nes 33; Conservative Query Match Best Loca Matches

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838 785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA 

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ABA79582 standard; DNA; 121 24-JAN-2002 ABA79582; RESULT 237

BP

Factor IX mutation correcting oligonucleotide SEQ ID NO: 2428. (first entry)

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN24; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MIH1; APOS; manamentor repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LDLR; familial hypercholesterolaemia; UGTI; syndrome; APP; PSENI; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Albahamet's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss 

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cetinoblascoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolicipoprotein (APC), Leceptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentlin-1 (PSENI) and presentlin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia; thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and variants syndromes. The present sequence is one of the gene correcting
                                                                                                                                                                                                                                                                                                                                                                                             Oligonuclectide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                27 - MAR - 2000; 2000US - 0192176P.
27 - MAR - 2000; 2000US - 0192179P.
01 - UJN - 2000; 2000US - 020838P.
30 - OCT - 2000; 2000US - 0244999P.
                                                                                                                        27-MAR-2001; 2001WO-US009761.
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                                        WO200173002-A2.
Homo sapiens.
                                                                                  04-OCT-2001.
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Gaps ö 0.6%; Score 20.4; DB 1; Length 121; 51.1%; Pred. No. 1.7e+02; 0; Mismatches 21; Indels Sequence 121 BP; 45 A; 16 C; 29 G; 31 T; 0 U; 0 Other; 61.1%; 33; Conservative Local Similarity Query Match Matches

oligonuclectides of the invention

; 0 785 GCAGTCTCAAAAACGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA 838 63 GAAGITITIGAAAACACIGAAAGAACAGIGAGIAITITCCACAIAAIACCCIICA 116 à

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCAL; BRA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemoglobin alpha locus 1; MLHI; APCB; mismatch repair; MST2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDD-glucuronosyltransferase; amyloid precursor protein; presentlin-1; altinimer's disease; cytostatic; antisioned antisinaemic; haemostatic; antilipemic; ss. Pactor IX mutation correcting oligonucleotide SEQ ID NO: 2432. ABA79586 standard; DNA; 121 BP. 24-JAN-2002 (first entry) ABA79586; RESULT 238 

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic equence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, rectantibulascoma, BRCAH, BRCAL, CFTR, CYCLIN-dependent kinase inhibitor 2A (CDKNZA), APC, Ractor V, Factor VIII, Factor IX, haemoglobin alpha locus 2 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, applicable in E (APC), L receptor (LDLR), UDF-glucuronesyltransferase (UGT1), amyloid precursor protein (APC), presentin-1 (PSENI) and presentin-2 (PSENI). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, hemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, althermer's disease, melanoma, adenomatous polyposis of the colon and control of the present sequence is one of the gene correcting
                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 182; 294pp; English.
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                                                                                                                                                                                                                                                                                                                              Gamper HB, Rice MC;
                                                                                                                                                                                                 27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
                                                                                                                                          27-MAR-2001; 2001WO-US009761.
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                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639230/73.
                                                       WO200173002-A2
                 Homo sapiens.
                                                                                                  04-OCT-2001.
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Factor IX mutation correcting oligonucleotide SEQ ID NO: 2440. ABA79594 standard; DNA; 121 BP. 24-JAN-2002 (first entry) ABA79594; RESULT 239 . MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA MASSA M

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Human, gene therapy, adenosine deaminase deficiency, p53, beta-globin, retinoblastoma, BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V, cyclin-dependent kinase inhibitor 2A; CDRV2A; melanoma, APC; HBA1; HBA2, adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein B; LbLR; familial hypercholesterolaemia; uGT1; syndrome, APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;

antilipemic; ss

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be used for the targeted alteration of genomic sequences, where the oligonuclectide has at least one mismatch compared with the genomic sequence to be alterated. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, cetinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2h (CDRAN2), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus (CDRAN2), APC, Factor VIII, Factor IX, haemoglobin alpha locus (CDRAN1), and locus (CDRAN2), APC, Factor VIII, Factor IX, haemoglobin alpha locus (CUGTI), anyloid precursor protein (LDRA), WLH1, WSH2, WSH6, apolipoprotein B (APOE), LDL receptor (LDRA), UDP-glucuronosyltransferase (UGTI), anyloid precursor protein (APC), presentin-1 (PSEN1) and presentin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophila, hypercholesterolaemia, thalassaemia, sickle cell anaemia, various syndromes. The present sequence is one of the gene correcting cligonucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides single-stranded oligonucleotides which can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 121 BP; 46 A; 16 C; 30 G; 29 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                    Rice MC;
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                                                                                                                                                                                                     27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-0192179P.
1UTN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244589P.
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les 33; Conserv
                                                                             WO200173002-A2
                                      Homo sapiens
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                                                                                                                       04-OCT-2001
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The present invention provides single-stranded oligomucleotides which can be used for the targeted alteration of genomic sequences, where the oligomucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, bera-globin, cetinobastoma, BRCAL, BRCAS, CFTR, cyclin-dependent kinase inhibitor 2A (CDXIZA), APC, Factor VII, Factor IX, haemoglobin alpha locus (HBA1), haemoglobin alpha locus (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APC), Leceptor (LDLR), UDP-glucuronosyltransferase (UCT1), amyloid precursor protein (APC), presentiln-1 (PSEN1) and presentiln-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, such as cancer, adenosine deaminase deficiency, cystic fibrosis, altabamer's disease, melanoma, adenomacous polyposis of the colon and colonial and altabamer's disease, melanoma, adenomacous polyposis of the colon and coling and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial and colonial an
Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic; antilipemic; ss.
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27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
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                                                                              Homo sapiens
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WO200058519-A2.

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Kreps J,
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Katagiri F,
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                                                                       pathogen.
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                                                                                                                                                                                                                            The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases. Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G
                                                                                                                                                       Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1643 ATTGCCAACATCCTCTGTATCATGGAAAAAGCAAGAGAGTTCCAGAAA 1690
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                                                                                                                                                                                                                                                                                                                                                                              Length 268;
                                                                                                       Lander ES;
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                                                                                                                                                                                                                                                                                                                                                         BP; 51 A; 89 C; 65 G; 62 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize gene conferring disease resistance in plants.
                                                                                                     Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                             Score 20.4; DB 1;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                     , Daley GQ,
Sklar P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                            Claim 1; Fig 5; 214pp; English
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2001US-0352277P.
2002US-0366535P.
                                 30-MAR-2000; 2000WO-US008440.
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                                                                                                                                                                                                                                                                                                                                                                            0.6%;
ilarity 62.5%;
Conservative
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                                                                                                      Cargill M,
Patil N, 8
                                                                                   (AFFY-) AFFYMETRIX INC
                                                                                                                                    WPI; 2000-611722/58.
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
Les 30; Conserv
                                                                                                                                                                                         genetic analysis.
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26-SEP-2001;
22-MAR-2002;
                                                                                                       Altshuler D,
Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                          Sequence 268
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                                                     31-MAR-1999;
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             05-OCT-2000
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AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their
                                                                                                                                              New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or telerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; cancer; immunopathology; neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cedcecerredageacerchedecacearedeerredereceaage 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 270 BP; 45 A; 74 C; 106 G; 45 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pancreas specific cDNA sequence SEQ ID NO:165.
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   zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20.4; DB 1;
Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 1222; 299pp; English
       Ricke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watson GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 127; 327pp; English
   Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0163508P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000; 2000WO-US030396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH57325 standard; cDNA; 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-291057/30.
                                                                               WPI; 2003-184052/18
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                agents. Expression of (I) in a sample indicates the differentation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76831. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I) regulatory elements and to follow inheritance of desirable characteristics through hybrid annews. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image, to
    drug compounds and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs, inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                                                                                                                                                                                                                                        974
                                                                                                                                                                                                                                                                                                                                                CTCACAGITGIAGCCCCCAACGATCTIGICATCATCATCAAAGGGGGCAGCAA 44
                                                                                                                                                                                                                                                                                                                    921 CCTTTTAGAACTAACACCCAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA
                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                       0.6%; Score 20.4; DB 1; Length 285; 1.11%; Pred. No. 2.1e+02; ve 0; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corn tassel-derived polynucleotide (cdps) SEQ ID NO:585.
                                                                                                                                                                                                 Sequence 285 BP; 66 A; 78 C; 73 G; 68 T; 0 U; 0 Other;
  fragments, immunoglobulins, inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 585; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL71211 standard; cDNA; 290 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00294093
                                                                                                                                                                                                                                                            ilarity 61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0082567P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LALGUDIRV.
ITO LY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITOL/) ITO L Y. SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-163647/21
                                                                                                                                                                                                                                                            Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2001051335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2002
                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          programs
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL71211/
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clone regulatory elements for use in transformation vectors, to express polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening a test agent for hepatotoxicity by contacting with cells expressing HEPATOX nucleic acid sequences, measuring expression of the nucleic acids and comparing with a control.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatotoxic compound; hepatotoxicity; HEPATOX protein;
                                                                                                                                                                                                                                                                                    CCTITIAGAACTAACACCCAAAAAGAIGICCTICTCATIAIAGGGGACTGGAA 974
                                                                                                                                                                                                                                                                                                                      ccrcacagrreradecceccaacearcrrerearcarcarcaaagggggggaggaa 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene fragment HBPATOX17 differentially regulated by troglitazone.
                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                             Length 290;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                       Sequence 290 BP; 66 A; 82 C; 74 G; 68 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                         0.6%; Score 20.4; DB 1;
61.1%; Pred. No. 2.2e+02;
tive 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Page 21; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1999; 99US-0129763P.
28-SEP-1999; 99US-0156924P.
13-APR-2000; 2000US-00548589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2000; 2000WO-US010076.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAC62325 standard; DNA; 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1:
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687188/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gould-Rothberg BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200063435-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proglitazone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogen; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2003
19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2000
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                                                                                                                                  sednences
                                                                                                                                                                                                                                                                                    921
                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC62325;
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 245
                                                                                                                                                                                                                                                                                                                                                                                               AAC62325,
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Length 315;

DB 1;

Score 20.4;

0.6%;

Query Match

Sequence 315 BP; 69 A; 95 C; 62 G; 89 T; 0 U; 0 Other;

04-DEC-2003 (first entry)

AAD58761;

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The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted BST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested scrivities include nucritional activity, immune stimulating or suppressing activity, heamatopoiesis regulating activity, issue growth activity, activity, chemotociclohemokinetic activity, and heamatopy activity, chemotociclohemokinetic activity, inflammatory activity, cadherin/twour invasion suppressor activity, inclument invasion suppressor activity.
                                                                                                                                                                                                                                                                                                                                   Human, secreted protein, expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs K, Mccoy JM, Lavallie BR, Racie LA, Merberg D, Treacy M, Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 CCTITIAGAACTAACACCCAAAAAAGAIGICCTTCTCATTATAGGGGACTGGAA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 cercacaerrerascececeaacearerrereareareareaaseseseaa 63
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0
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                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 334 BP; 78 A; 95 C; 85 G; 76 T; 0 U; 0 Other;
                                                      1960 GAAGCACAAGCTGGAATCAAGATTGCCGGGAGAATAG 1997
                                                                                  272 GCATCACAAGCTGGGGTGAAGGCTGCGGCCAGAAAGAG 235
Fred. No. 2.2e+02;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 168; 618pp; English.
                                                                                                                                                                                      AAV89281 standard; cDNA; 334 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD58761 standard; DNA; 394 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US006955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00838821.
  71.18;
                                                                                                                                                                                                                                                          15-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
                    27; Conservative
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; ss.
                                                                                                                                                                                                                                                                                                EST clone CG175.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1998.
                                                                                                                                                                                                                          AAV89281;
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Best Local S
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ID AAD58'
                                                                                                                                                    RESULT 246
                                                                                                                                                                      AAV89281/c
                      Matches
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The invention relates to purified human transmembrane serine protease (TSP) polypeptide, comprising a protease domain of a type-II membrane-type serine protease or its biologically active portion. The invention is useful for cleaving a TSP substrate protein by contacting TSP with a substrate protein under serine protease activity permissive conditions. The invention is useful as an immunogen to generate antibodies that bind TSP or TSP1-TSP43 proteins, useful for treating disease e.g. cancer and autoimmune disease. The present sequence is human TSP1-TSP34 gene exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified transmembrane serine protease polypeptides (TSP1-TSP34) comprising a protease domain or its biologically active portion, useful for identifying modulators of proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BSSP2; serine protease; mouse; mBSSP2; human; hBSSP2; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; inflammatory disorder; infertility; prostatic hypertrophy; ss.
                                                                                                                   Human, transmembrane serine protease, TSP, therapy, immunogen, ca
autoimmune disease, immunomodulatory, immunosuppressive, enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:1.
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                                                                                Human transmembrane serine protease (TSP1-TSP34) gene exon 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 0.6%; Score 20.4; DB 1; Length 394; Local Similarity 71.1%; Pred. No. 2.38+02; Nes 27; Conservative 0; Mismatches 11; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 394 BP; 76 A; 143 C; 114 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2683 GIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAG 2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 drakaccaacrarcarcarcaraacraaraaraaccka 199
                                                                                                                                                                                                                                                                                                                                                                               Saudrais C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 232-233; 276pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA61659 standard; cDNA; 717 BP
                                                                                                                                                                                                                                                                          24-JAN-2003; 2003WO-EP000756.
                                                                                                                                                                                                                                                                                                           30-JAN-2002; 2002US-0352806P.
                                                                                                                                                                                                                                                                                                                                                                               Bougueleret L, Niknejad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                             (GENE-) GENEPROT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-627608/59.
                                                                                                                                                                                                         WO2003064641-A1
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                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                        07-AUG-2003.
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The invention relates to novel serine proteases designated BSSP2

(AAB11695-B11699), and to nucleic acids encoding them (AAA61659-A61663).

The invention also relates to vectors and transformants comprising BSSP2

nucleic acids; transgenic animals in which the expression level of BSSP2

can be varied; and an mBSSP2 knockout mouse. The invention additionally

encompasses anti-BSSP2 antibodies and methods of production of such

encompasses anti-BSSP2 antibodies and methods of production of such

encompasses anti-BSSP2 antibodies. And the use
of BSSP2 proteins or fragments as diagnostic markers for certain medical

conditions. Nucleotides encoding BSSP2 were initially isolated in a mouse

brain cDNA library using degenerate PCR primers (AAA61674)

based on conserved regions of serine proteases. The BSSP2 serine

proteases and nucleotides encoding them are useful in detecting

proteases and nucleotides encoding them are useful in detecting

conditions such as Alzheimer's disease, epilepsy, cancer, inflammation,

blood, urine, brain, prostate gland and testis) as diagnostic markers for

conditions such as Alzheimer's disease, epilepsy, cancer, inflammation,

infertility and prostatic hypertrophy. Sequences AAA61659-A61662

represent cDNAs encoding nurine BSSP2 (ABSSP2), and sequence

AAA61663 represents cDNA encoding human BSSP2 (HBSSP2)
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51.1%; Pred. No. 2.7e+02;
ve 0; Mismatches 21; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease BSSP2, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, cancer, inflammation and prostate hypertrophy, using blood, urine or other tissues.
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99WO-JP006475
                                                                                                                                                     98JP-00347785
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Local Similarity 61.1%;
es 33; Conservative
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Synthetic.
19-NOV-1999;
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The invention relates to a conjugate (I) comprising at least one non-
polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to
a procein C polypeptide comprising an amino acid sequence which differs
created protein C polypeptide (III) in at least one
introduced and/or at least one removed amino acid residue comprising an
attachment group for the non-polypeptide group (e.g. an N-glycosylation
created and/or at least one removed amino acid residue comprising an
attachment group for the non-polypeptide group (e.g. an N-glycosylation
comprising of the position (P) where (P) is an amino acid with at least
created and/or at least one temoved amino acid with at least
created and/or at least one temoved amino acid with at least
created and/or hardyfale/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln (III)
comprising (N) or (VI); (3) an expression vector (VI); (3) an expression vector (VI); (3) an expression vector (VI); (3) an expression vector (VI); (3) an expression vector (VI); (3) an expression vector (VI); (4) a not ending
(IV); (3) an expression vector (VI); (3) an endicate for the treatment (and
conjugates, variants and protein (C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
conjugates, variants and protein C proteins are useful as medicaments,
and in the manufacture of medicaments for the treatment (and
conjugates, variants pregnancy emboli, transplantation and alpha-1
crespiratory distress syndrome (ARBS). The variant protein C has an
antitrypsin. The conjugates have an increased and plasma and alpha-1
creased sectum half-life, increased resistant to inhibitors, reduced
antitrypsin. The conjugates have an increased bloavailability.
The conjugate offers a number of advantages over the currently available.
ARC products, including longer duration between injections,
conforted anticoagulant activity is beneficial to reduce the risk of
cleativated protein C) conjugates. This must be especially important when
the conjugate base an extended plasma the endiant secto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           located on chromosome 2q13-q14. The present sequence encodes precursor
/note= "No stop codon shown"
1. 126
(*tag= b
                                                                                                                                 /product= "Mature_protein_C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen KV, Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 74-76; 92pp; English.
                                                                                                                                                                                                                                                                                                                        18-OCT-2000; 2000US-0242268P.
21-JUN-2001; 2001DK-00000970.
21-JUN-2001; 2001US-0300154P.
                                                                                                                                                                                                                                                             15-OCT-2001; 2001WO-DK000679.
                                                                                                                                                                                                                                                                                                      18-OCT-2000; 2000DK-00001560
                                                                                                                                                                                                                                                                                                                                                                                                          (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
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127. .1383
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                                                                                                                                                                          WO200232461-A2
                                                                                                                                                                                                                  25-APR-2002.
                                               sig_peptide
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Length 1383;

0.6%; Score 20.4; DB 1; 55.7%; Pred. No. 2.9e+02;

Query Match Best Local Similarity

Sequence 1383 BP; 286 A; 418 C; 440 G; 239 T; 0 U; 0 Other;

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2651 GATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGG 2710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nascent human protein C produces inactive protein C. It is used as an anti-coagulant in myocardial infarction and deep vein thrombonis. The patent discloses a recombinant way of making activated protein C.

Nucleorides 1-125 encode the signal peptide and propeptide; 126-589
592 residues are believed to be removed to form 2-chain protein C; 598-631 are the activation peptides removed from the zymogen to form c; 598-631 are the activation peptides removed from the zymogen to form activated protein C; 634-1380 constitute the activated heavy chain after post-translational modification. (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct PD 5-MAR-2003 to correct P
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                                                                                       94 GCTCGCTGCTGGAGAACACTGAGTCAAGAGGAGCTGGTGTGCCGGAAATTCCCCAGGTGG 35
  Gaps
  ö
31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein C; anti-coagulant; myocardial infarction; deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jaskunas SR;
  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nascent human protein C DNA.
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598..631
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634..1380
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(first entry)
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126. .589
/*tag= c
587. .592
  Matches 39; Conservative
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01-NOV-1989
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Sequence 1386 BP; 287 A; 419 C; 440 G; 240 T; 0 U; 0 Other;

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                                                                                     2651 GATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGG 2710
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                                             Gaps
                                             .
0.6%; Score 20.4; DB 1; Length 1386; 55.7%; Pred. No. 2.9e+02; ive 0; Mismatches 31; Indels 0.
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Job time : 1400 secs
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Matches 39; Conservative
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TISSUE TYPE: Blood
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Best Local Similarity
Matches 34; Conserv
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ANTI-SENSE: NO
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US-07-882-202A-3
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6440864
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                                                                      August 9, 2004, 16:34:29; Search time 17 Seconds (without alignments) 3.877 Million cell updates/sec
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Sequence 1
Sequence 2
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-021-615A-3

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US-08-021-77-13

US-08-08-217-71-13

US-08-23-778-16

US-08-23-778-16

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US-08-25-636-8

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US-08-25-636-9

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Maximum Match 100%
Listing first 250 summaries
                                              - nucleic search, using sw model
                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
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Maximum DB
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                                                                                                                                                                                                                                                         Sequence 3, Application US/07882202A;
Sequence 3, Application US/07882202A;
Patent No. 5374617;
GENERAL INFORMATION:
TILLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
STATE: Floppy disk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC DOS/MS.
SOFTWARE: PatentIn Release #1.0, Version #1.25
CLASSIPTATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIPTATION NUMBER: NEADMATE.
                Sequence Sequence Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 2
    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 36..1433
; OTHER INFORMATION: /note= "Coding portion of human
; OTHER INFORMATION: factor VII cDNA"
US-07-882-202A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 18.4; DB 1;
llarity 56.7%; Pred. No. 2.7;
Conservative 0; Mismatches 26;
US-09-558-027-4

US-08-293-778-20

US-08-293-778-10

US-08-293-778-16

US-08-293-778-16

US-08-293-778-20

US-08-293-778-20
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NAME: Hansen, Bugenia 3.5.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 0MRF B34290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid_
STRANDEDNESS: double
TOPOLOGY: linear
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STREET: P.O. Book CITY: Houston STATE: Texas
                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-321-777-3
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                                                                                                    GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: Fissue Factor in Combination with an Activator of TITLE OF INVENTION: FVII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:

STREET:

STREET:

STREET:

STATE

COUNTRY:

US

COUNTRY:

US

ZIP: 75270-2197

COMPUTER: READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,615A

FILING DATE: 19-FEB-1993

CLASSIFICATION NUMBER: US 07/882,202

FILING DATE: 13-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Hansen, EUGenia S

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 31,966

REFERENCE/CATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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Patent No. 5504064
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Patent No. 5504067
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
-08-021-615A-3
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1 Sequence 13, Application US/09009217

2 Sequence 13, Application US/09009217

3 Sequence 13, Application US/09009217

4 Sequence 13, Application US/09009217

5 GENERAL INFORMATION:

APPLICANT: Thorpe, Philip E.

APPLICANT: King, Steven W.

APPLICANT: Go, Boning D.

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND

TITLE OF INVENTION: AND TUMOR TREATMENT

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
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0.5%; Score 18.4; DB 1; Length 1440;
Best Local Similarity 56.7%; Pred. No. 2.7;
Matches 34; Conservative 0; Mismatches 26; Indels 0
Tissue Factor in Combination with FVIIa
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LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE DOCKET NUMBER: 0MRF B34290C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TOPOLOGY: linear
                                                                                                                                               E: Richards, Medlock & Andrews
1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                               NUMBER OF SEQUENCES: 4
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                              STREET: 1201
CITY: Dallas
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1445 GGATCGAGACCATCCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGG 1504
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APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
TITLE OF INVENTION: FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.5%; Score 18.4; DB 1; Length 1 Best Local Similarity 56.7%; Pred. No. 2.7; Matches 34; Conservative 0; Mismatches 26; Indels
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COUNTRY: USAGE
COUNTRY: USAGE
COMPUTER READABLE FORM:
MEDIUW TYPE: Flogby disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM:
COMPATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19330512
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTONEY/AGENT INPORMATION:
NAME: TTUJILIO, DOLEGN Y.
REGISTRATION NUMBER: 35,713
REGISTRATION NUMBER: 35,713
REGISTRATION NUMBER: 35,713
REGISTRATION NUMBER: 35,713
REGISTRATION NUMBER: 35,713
REGISTRATION NUMBER: 35,713
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REGISTRATION NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBER: 30,000 PC NUMBE
APPLICATION NUMBER: US bu, v.z.,
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
MAME: HIDLE: DAVIG W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:537
TELECOMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
TELEPHONE: S12/418-3000
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Sequence 3, Application PC/TUS9304493
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1440 base pairs
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TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
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US-09-009-656-13

Sequence 13, Application US/09009656

Patent No. 6132730

GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 0.5%; Score 18.4; DB 1; Length 1440; al Similarity 56.7%; Pred. No. 2.7; 34; Conservative 0; Mismatches 26; Indels 0:
                                                                                       COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: Concurrently Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-MAR-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
PRIOR APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: UTSD:536
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
TUNCORMATION FOR SEQ ID NO: 13:
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21P: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: CONCURRENT HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
TOPOLOGY:
US-09-009-217-13
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LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TISSUE TYPE: Blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 GGAGCAC 278
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 GCAAAAATACCTATTCTAGAAAAAAAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGG 680
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 36..1433
COTHER INFORMATION: /product= "Tissue Factor"
COTHER INFORMATION: /note= "Coding portion of human factor VIII cDNA"
COTHER INFORMATION: /citation= [[1]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

0.5%; Score 18.4; DB 1; Length 1440;
Best Local Similarity 56.7%; Pred. No. 2.7;
Matches 34; Conservative 0; Mismatches 26; Indels. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-882-202A-3/C
US-07-882-202A-3/C
Sequence 3, Application US/07882202A
Patent No. 5374617
GENERAL INFORMATION:
APPLICANT: Comp., Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Dallas
STREET: 1201 Elm Street, Suite 4500
STREET: 1201 Elm Street, Suite 4500
STREET: 1201 Elm Street, Suite 4500
STATE: 1201 Elm Street, Suite 4500
STATE: 1201 Elm Street, Suite 4500
STATE: 1202
STATE: 1203
STATE: 1203
STATE: 1203
STATE: 1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
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REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERE
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
ORGANISM: Homo sapie
TISSUE TYPE: Blood
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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NESOLI 615A-3/C
; Sequence 3, Application US/08021615A
; Patent No. 5504064
; Patent No. 5504064
; Patent No. 5504064
; APPLICANT: Comp. Philip C.
; APPLICANT: Comp. Philip C.
; TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Freatment of Bleeding with an Activator of
TITLE OF INVENTION: FVII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STREET: Texas
                                                                                                                                                                                                                                                                                        871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
                                                                                                                                                                                                                                                                                                                                                     344 AGAAATCCAGAACAGCTTCGTCCTCTCGCGTCTTGAAGATCTCCCGGGCCTCCTCGAA 285
                                                                                                                                                                                                                           ö
                                                                                                                                                        Query Match 0.5%; Score 17.4; DB 1; Length 1440; Best Local Similarity 53.7%; Pred. No. 8.3; Matches 36; Conservative 0; Mismatches 31; Indels 0
; LOCATION: 36..1433
; OTHER INFORMATION: /note= "Coding portion of human;
; OTHER INFORMATION: factor VII cDNA"
US-07-882-202A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
1.1433
1.0CATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human;
OTHER INFORMATION: factor VII cDNA"
US-08-021-615A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: 1638

ZIP: 75270-2197

COUNTRY: US

COMPUTER READABLE FORM:
MEDIUM TYBE: FLOSDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
FILING DATE: 19-FEB.1993
CLASSIFICATION NUMBER: US 07/882,202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Bugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
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REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUINCE CHARACTERISTICS:
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871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
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0.5%; Score 17.4; DB 1; Length 1440;
Best Local Similarity 53.7%; Pred. No. 8.3;
Matches 36; Conservative 0; Mismatches 31; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAIL:
COUNTRY: USA
ZIF: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: LBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUSRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
PTI.ING DATE: CONCULTENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: CONCURENTLY HERWITH PRIOR APPLICATION WITHER: US 60/042,427 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205 FILING DATE: 27-JAN-1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920 FILING DATE: 12-JAN-1997 ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 11,071
REGISTRATION NUMBER: 12,24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09009217; Patent No. 6132729; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERICITICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                     931 CTAACAC 937
                                                                                                                                                                                                   284 GGAGCAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 CTAACAC 937
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US-09-009-217-13
                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-009-217-13/c
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                                                                                                                                                                  871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
                                                                                                                                                                                                                      344 AGAAAICCAGAACAGCTICGICCTCTCGGGTCCTTGAAGATCTCCCGGGCCTCCTCGAA 285
                                                                                                   Gaps
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                      Query Match 0.5%; Score 17.4; DB 1; Length 1440; Best Local Similarity 53.7%; Pred. No. 8.3; Matches 36; Conservative 0; Mismatches 31; Indels 0.
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OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
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ZIP: 75270-2197
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 514
PLORA APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia 8:
REGISTRATION NUMBER: 31,966
REGISTRATION INFORMATION:
TELEPHONE: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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FEATURE:
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Best Local Similarity
Matches 36; Conserva
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CITY: Dallas
STATE: Texas
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ORIGINAL SOURCE:
ORGANISM: HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: Goo, Boning
TITLE OF INVENTION: COMMINISTERATED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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344 AGAAATCCAGAACAGCTTCGTCCTCTCGCGTCCTTGAAGATCTCCCGGGCCTCCTCGAA 285
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ITLE OF INVENTION: FVII Activator for Blood Coagulation
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/882202

FILING DATE: 13-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021615

FILING DATE: 19-FEB-1993

ATTORNEY/AGENT INPORMATION:

NAME: TTUJ110, Doreen Y.

REGISTRATION NUMBER: 35,719

REFERENCE/CONCET NUMBER: 35,719

REFERENCE/COKET NUMBER: 35,719

REFERENCE/COKET NUMBER: 35,719

REFERENCE/COKET NUMBER: 35,719

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REFERENCE/COKET NUMBER: 36,719

REFERENCE/COKET NUMBER: 36,719

REFERENCE/C
                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
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LOCATION: '36.1433
OTHER INFORMATION: /
OTHER INFORMATION: /
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                                      NESCULATE APPLICATION US/09009656

Sequence 13, Application US/09009656

Sequence 13, Application US/09009656

Sequence 13, Application US/09009656

Sequence 13, Application US/09009656

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Sequence 13, Application US/09009656

Sequence 13, Application US/09009656

Sequence 13, Application US/09009656

Sequence 13, Sequence 14, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September 15, September
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-CS93-04493-3/c; Sequence 3, Application PC/TUS9304493; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         931 CTAACAC 937
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US-09-009-656-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P.O. Bo
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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344 AGAAATCCAGAACAGCTTCGTCCTCTCGCGTCTTGAAGATCTCCCGGGCCTCCTCGAA 285 /product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1]) 871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA Gaps .; 0 Query Match

0.5%; Score 17.4; DB 1; Length 1440;
Best Local Similarity 53.7%; Pred. No. 8.3;
Matches 36; Conservative 0; Mismatches 31; Indels 0 Factor VII Fragment 82-128 and its use US-08-849-248-6; Sequence 6, Application US/08849248; Patent No. 5948759; GENERAL INFORNATION: APPLICANT: Husbyn, Mette; APPLICANT: Fischer, Peter; APPLICANT: Fischer, Peter; TITLE OF INVENTION: Factor VII Fra

; 0 930

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APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
                                                                                                   132 cacciceircreceageagadaracectresideseceagadadecerridereces 73
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                    Gaps
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                    40; Indels
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                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nelsequen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF THE REPERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/293,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 1;
Pred. No. 23;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2597 CCCTGATGCTGGGAGGGATTGGGGGGCAGGA 2626
Best Local Similarity 48.1%; Fred. No. 71;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ccagecrecredeaceaacerecrecaesa 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
CONTY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PROR PELICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 16, Application US/08293778; Patent No. 5880560; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08955636A
Patent No. 6017882
                                                                                                                                                     2541 GCTGAACTCCAGTACT 2557
                                                                                                                                                                                               72 dredrcachecachach 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%;
ilarity 63.3%;
Conservative
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Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-293-778-16
                                                                                                                                                                                                                                                                    SULT 15
-08-955-636-8
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APPLICANT: Husbyl, Mette
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
TITLE OF INVENTION: Factor VII Fragment 82-128 and its use
TITLE OF INVENTION: in blood clotting disorders
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
STRETT: 622 Slaters Lane, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.6; DB 1; Length 141; 69.0%; Pred. No. 9.1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
INFORMATION FOR SEQ 1D NO: 6:
SEQUIENCE CHARACTERISTICS:
             FITLE OF INVENTION: in blood clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2757 GAGTIGGACACGACTGAGCAACTGAACTG 2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JAMESSEE: BACON and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08849248
Patent No. 5948759
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/desc = "recom
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 141 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.0°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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0.4%; Score 13; DB 1; Length 141;

Query Match

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69.6%; Pred. No. 54;
tive 0; Mismatches 7; Indels
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| Patent No. S476777
| GENERAL INFORMATION:
| APPLICANT: Holly, Richard D. |
| APPLICANT: Foster, Donald C. |
| TITLE OF INVENTION: METHODS FOR PRODUCING THROWBIN NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: 4 |
| CORRESPONDENCE ADDRESS: 4 |
| CORRESPONDENCE ADDRESS: 4 |
| STREET: Townsend and Townsend STREET: Townsend and Townsend STREET: Twentieth Floor |
| STREET: Twentieth Floor |
| CITY: Sam Francisco |
| STREET: CA |
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; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 Accaderecraecaececaacececaecrecre 1
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US-08-955-636-8/c
Sequence 8, Application US/08955636A
Fatent No. 6017802
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
ITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
ITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
                                                                                                                                                                                                                                                                                                                                                                                  0.3%; Score 12.2; I ilarity 56.1%; Pred. No. 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1192 TGGAGAGCTCTATACAGTCAGC 1214
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ORGANISM: Artificial Sequence
                                      LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC6337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.65
Matches 16; Conservative
            SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 23; Conserv
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USA
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                                                                                                                                                                                                                                                                                            US-08-756-506-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-998-972A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carner, Ian
APPLICANT: Cattingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Element in Per-Dos/Ms-Dos
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Savislak, Deborah A
REGISTRATION NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: FCT/DK88/00103
FILING DATE: 24-UN-1988
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGIS, Cheryl H.
REGIGTRATION NUMBER: 34,086
RETERENCE/DOCKET NUMBER: 3129.224-US
TELEPHONE: 12-867-0123
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TELEPHONE: 12-867-0123
TELEPHO
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STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
FILING DATE: 25-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206-442-6672
206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 68.0
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206-442-6678 INFORMATION FOR SEC ID NO:
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USA
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MOLECULE TYPE:
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STATE: WA
COUNTRY: US
ZIP: 98102
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SEQUENCE CHARACTERISTICS:
                                     35 base pairs
                                   LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         linear
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IMMEDIATE SOURCE:
CLONE: ZC1324
                                                                                                       TOPOLOGY: line;
HWMEDIATE SOURCE:
CLONE: ZC1324
US-08-463-953-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-462-261-7
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0.3%; Score 11.4; DB 1; Length 35;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08463953
Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CTITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-192
PRIOR APPLICATION DATE: 30.07816,281
PILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATEMENCE/COCKET VUMBER: 31,990
REGISTRATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TYPE: NUMBER: 206-467-9600
STRANDENDESS SINGLE
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APPLICATION NUMBER: US/08/463,953
FILING DATE:
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: PARTWELES, SCEVEN W
REGISTRATION NUMBER: 13952-12-2
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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TOPOLOGY: lines
IMMEDIATE SOURCE:
CLONE: ZC1324
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Query Match
0.3%; Score 11; DB 1; Length 36;
Best Local Similarity 63.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 10; Indels
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0.3%; Score 11.4; DB 1; Length 35;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 6; Indels
                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
ITILE OF INVENTION: METHODS FOR PRODUCING THROMBIN WUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-08-955-636-9/c
Sequence 9, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REPRESENCE: 09531/002001
CURRENT PELLING DATE: 1997-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/860,701 FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/816,281 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION:
2484 CCAGTCCATTCTGAAGGAGAT 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105
COMPUTER READABLE FORM:
COMPUTER: REPORT disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19921230
CLASSIFICATION:
PRIOR APPLICATION DATA:
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CLONE: ZC1324
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                                                                                                                             PCT-US92-11357-7
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                                                                                                                                                                                                                                                                      Query Match 0.3%; Score 11.4; DB 1; Length 36; Best Local Similarity 71.4%; Pred. No. 72; Matches 15; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                              ; FEATURE:
, OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-955-636-10
) Sequence 10, Application US/08955636A
) Patent No. 6017802
) GENERAL INFORMATION:
) APPLICANT: Nelsestuen, Gary
) TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
) TITLE OF INVENTION: POLYPEPFIDES
) FILLE REFERENCE: 09531/00201
) CURRENT APPLICATION NUMBER: US/08/955,636A
) CURRENT FILING DATE: 1997-10-23
) NUMBER OF SEQ ID NOS: 35
) SOFTWARE: FRACESQ for Windows Version 3.0
) SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT APPLICATION NUMBER: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOPTWARE: PastSEQ for Windows Version 3.0
SEQ ID NOS: 36
LENGTH: 36
NUMBER OF SEQ ID NOS: 35
SOFTWARE FRANKED for Windows Version 3.0
SEQ ID NO 9
LENGTH: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                   31 AGAGGAGCTGCGCCACGGCAA 11
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                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Gaps

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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%; Score 11; DB 1; Length 36; 63.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Indels
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Sequence 4, Application US/09558027

Sequence 4, Application US/09558027

Sequence 4, Application US/09558027

Patent No. 6329176

APPLICANT: Wiberg, Finn

APPLICANT: Wiberg, Finn

APPLICANT: Wiberg, Finn

TILE OF INVENTION: Wethod for the Production of FVII

FILE REFERENCE: 5565-204-US

CURRENT APPLICATION NUMBER: US/09/558,027

CURRENT FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 60/108,065

PRIOR APPLICATION NUMBER: 60/108,065

PRIOR APPLICATION WIMBER: 60/108,065

BRIOR FILING DATE: 1998-11-12

NUMBER OF SEC ID NOS: 4

SEC ID NO 4

LENGTH: 38

TYPE: DNA

ORGANISM: Saccharomyces cerevisiae

US-09-558-027-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-10
                                                                                                                                                                                                                                                                   US-016-25-636-10/c
| Sequence 10, Application US/08955636A
| Patent No. 6017Papel
| Patent No. 6017Papel
| Patent INFORMATION |
| APPLICANT Nelsestuen, Gary |
| TITLE OF INVENTION | POLYPEPTIDES |
| TITLE OF INVENTION | POLYPEPTIDES |
| TITLE OF INVENTION | POLYPEPTIDES |
| TITLE OF INVENTION | POLYPEPTIDES |
| TITLE OF INVENTION | POLYPEPTIDES |
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| TITLE OF INVENTION | POLYPEPTION |
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| TITLE OF INVENTION | POLYPETION |
| TITLE OF INVENTION | POLYPETION 
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40 TCCAAGGTAAGGAGCAGTAGCTGCGCT 66
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GENERAL INFORMATION:
APPLICANT: Garner, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
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US-08-756-506-13
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                   APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Proster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-998-972A-7/C
; Sequence 7, Application US/07998372A;
; Patent No. 5476777
; GENERAL INFORMATION:
; APPLICANT: FOILY, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES:
ADDESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/756,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105

ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      ADDRESSER: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 AAGGAGCAGTAGCTGCGCTT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGGAAGGAGTTGGCGCGCTT 21
Cottingham, Ian R.
Temperley, Simon M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
| IMMADIATE SOURCE:
| CLONE: ZC6337
US-08-756-506-13
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22 AGGAGTTGGCTCGCCGGA 5
  INFORMATION FOR ERQ ID NO: 7 SEQUENCE CHARACTERISTICS: LENGTH: 35 base pairs TYPE: uncleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                      OCTODOR: linear
IMMEDIATE SOURCE:
CLONE: ZC1324
8-463-951-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-08-462-261-7/c
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                                                                                                                                                                                            US-08-463-953-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3%; Score 10; DB 1; Length 35; 72.2%; Pred. No. 3.6e+02; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08463953

Patent No. 5502034

GENERAL INFORMATION: Method D. APPLICANT: Foster, Donald C. TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN INTERFORMENCES: 48

CORRESPONDENCE ADDRESS: ADDRESSE: TOWNSEND and Townsend and Townsend and Townsend STREET: Twentieth Floor CITY: San Francisco

CITY: San Francisco

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94105
COMPUTER FREADBLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
APPLICATION NUMBER: US/07/998,972A FILING DATE: 19921230 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 07/860,701 FILING DATE: 31-MAR-1992 PRIOR APPLICATION NUMBER: US 07/816,281 FILING DATE: 31-DEC-1991 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/ACENT INFORMATION:
NAME: PARMEL-POCKET UNMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                           13952-12-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13952-12-2
                                                                                                                                                                                                           NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFRENCE/DOCKET NUMBER: 13952
TELECOMMUNICATION INPORMATION:
TELEFAX: 206-467-9600
TELEFAX: 415-543-5043
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYRDE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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Best Local Similarity 72.24
Matches 13; Conservative
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INTORMATION PRE SEG IN 00: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPES unclaid acid

STRANDERMESS: single

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STRANDERMESS: single

STRANDERMESS: single

STRANDERMESS: single

OGENTY ANAGACICACTACTACA P. 18, Score 10; DB 1; Length 35;

Best Local Stillarity 72.39, Pred. No. 3.64-62;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps

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Db 22 AGGARTIGCTACTACTACA 5

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TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.3%; Score 9.8; DB 1; Length 27; Il Similarity 66.7%; Pred. No. 3.5e+02; 14; Conservative 0; Mismatches 7; Indels
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Sequence 4, Application US/095S8027

Sequence 4, Application US/095S8027

Sequence 4, Application US/095S8027

Sequence 4, Application US/095S8027

Settle No. 6329176

APPLICANT: Wielsen, Helle

APPLICANT: Wielsen, Lars

TITLE OF INVENTION: Method for the Production of FVII

FILE REFERENCE: 556-204-US

CURRENT APPLICATION NUMBER: 05/09/558,027

CURRENT FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 60/108,065

PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                     STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/00/104,009
FILING DATE: 25-UN-1987
FILING DATE: 25-UN-1987
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/896,248
FILING DATE: 24-UN-1988
PRIOR APPLICATION NUMBER: US 07/896,248
FILING DATE: 12-UN-1992
APPLICATION NUMBER: US 07/896,248
FILING DATE: 12-UN-1992
APPLICATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 GAGAGATCTGACAGAATGTGG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: CDNA US-08-293-778-17
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Matches 14; Conserv
                                                                                                                                    New York
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           5; Indels
                                                                                                                                                                                                    PCT-US92-11357-7/c

Sequence 7, Application PC/TUS9211357

Sequence 7, Application PC/TUS9211357

GENERAL INFORMATION:

APPLICANT: Holly, Richard D.

APPLICANT: FOSTEr, Donald C.

TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend

STREET: One Market Plaza, Stewart Street Tower,

STREET: Twentieth Floor

CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: 74109
COMPUTE: 74109
COMPUTE: FLORY disk
MEDIUM TYPE: Flory disk
COMPUTER: 1EM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC/US92/11357
FILING DATE: 19921230
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 131-AMR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 131-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PERMEDIE. STEVEN W
REGISCRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELEFRAX: A15-543-5603
TELEFRAX: A15-543-5603
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2574 AAGAGCTGACTCACTGGA 2591
                                                       2574 AAGAGCTGACTCACTGGA 2591
                                                                                        22 AGGAGTTGGCTCGCCGGA 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
     Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; INMEDIATE SOURCE:
; CLONE: ZC1324
PCT-US92-11357-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Sar
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
US-08-293-778-17
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Best Local Similarity
Matches 13; Conserr
                                                                                                                                                                                            RESULT 36
US-08-293-778-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
CITY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
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COUNTY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
COUNTY: New York
COMPUTE: 10174-6201
COMPUTE: 128 FORD AMS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,776
                                                                                                                                                                                         Gaps
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                                                                                                                                    Ouery Match 0.3%; Score 9.6; DB 1; Length 38; Best Local Similarity 62.5%; Pred. No. 4.5e+02; Matches 15; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nicolaisen, Else M.
APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
ATPLE OF INVENTION: MODIFIED FACTOR VII/VIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
FILING APPLICATION: 435
PROOF APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE: 25-UN-1987
PRIOR APPLICATION NUMBER: DK 3235/87
PRIOR APPLICATION NUMBER: DK 7/434,149
FILING DATE: 13-NOV-198
FILING DATE: 13-NOV-198
FILING DATE: 14-UN-198
FILING DATE: 24-UN-198
FILING DATE: 24-UN-1982
FILING DATE: 12-UN-1992
ATTORNEY ABPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
ATTORNEY AGENT INFORMATION:
NAME: AGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 34,086
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFANOR: 212-867-0298
                                                                                                                                                                                                                                706 TACTGCGGCAGGAATCCCTCAGA 729
                                                                                                                                                                                                                                                                         38 rccrecartroccraca 15
                                           ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-558-027-4
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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US-08-293-778-22
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                US-08-293-778-22
SEQ ID NO 4
LENGTH: 38
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Sequence 1,0, Application US/0829378

Patent No. 558056

GREEZAL INFORMATION. Screin C.

APPLICANT: NICOLAISEN, Else M.

APPLICANT: NICOLAISEN, Else M.

APPLICANT: NICOLAISEN, Else M.

APPLICANT: NICOLAISEN, Else M.

APPLICANT: NICOLAISEN C.

ADDRESSEE: NO. 55805600 No. 5880560418K of No. 5580560th America, Inc.

CITY: New York

CONFUTER: District C.

CONFUTER: District C.

CONFUTER: Else M. Compatible Form:

MEDIUM TYPE: Floppy disk

COMPUTER: Else M. Compatible

COMPUTER: Else M. Compatible

COMPUTER: INSt No. C.

CONFUTER: INSt No. C.

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                                              Gaps
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                                              Indels
ilarity 68.4%; Pred. No. 4.8e+02;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08293778
                                                                                                    2749 GTCACAAGAGTTGGACAC 2767
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Best Local Similarity 68.44
Matches 13; Conservative
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nucleic acid
EDNESS: single
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APPLICANT: Bjorn, Soren E.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIA
TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08293778
| Patent No. 5580560
| Patent No. 5580560
| APPLICANT: Nicolaisen, Else M. APPLICANT: Bjorn, Soren E. APPLICANT: Wiberg, Finn C. APPLICANT: Woodbury, Richard TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa NUMBER OF SEQUENCES: 26
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: No. 5580560016k of No. 5580560th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAFLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1935
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE: 25-UN-1987
FILING DATE: 25-UN-1987
PRIOR APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATE: 24-UN-1989
PRIOR APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGISTALION NUMBER: 34,086
REGISTALION NUMBER: 34,086
REGISTALION NUMBER: 34,086
REGISTALION NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
NAME: AGISTALION NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  STATE: New York
COUNTRY: United States of America
ZIP: 10.74-6.201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 913 CTACAAGACCTTTTAGAACT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMICAL 212-80, C. TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTER.ESTICS: LENGTH: 27 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 crececercerreadearer 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-293-778-22/c
                                                                                                                                                                                                                                                                                                                                     SEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.: 405 Lexington Avenue, 62nd Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.3%; Score 9; DB 1; Length 27; 70.6%; Pred. No. 6.2e+02; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: United States of America
ZIP: 10.74-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAMER: US/08/293,778
                                          Sequence 17, Application US/08293778

Sequence 17, Application US/08293778

Patent No. 5580560

APPLICANT: Nicolaisen, Else M.
APPLICANT: Wiberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APLICATION WIMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION DATA: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 31,086
REFERENCE/DOCKET NUMBER: 31,086
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONS: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING MAIN 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-293-778-16/c
; Sequence 16, Application US/08293778
; Patent No. 2580560
; GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1655 CTCTGTATCATGGAAAA 1671
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SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 CTCCGCGTCCTGGAAGA 11
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Best Local Similarity 70.67
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: CDNA
US-08-293-778-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Nev
STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 38
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RESULT 40

US-08-203-778-20/C

Sequence 20, Application US/08293778

Patent No. 5580560

GENERAL INFORMATION:

APPLICANT: Bjorn, Soren E.

APPLICANT: Wiberg, Finn C.

APPLICANT: Woodbury, Richard

TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS: 26

CORRESPONDENCE ADDRESS: 36

CORRESPONDENCE ADDRESS: 36

CONTRY: New York

COUNTRY: New York

COUNTRY: United States of America

ZIP: 10774-6201

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
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                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATION TAPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
: 405 Lexington Avenue, 62nd Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Agris, Cheryl H.
REGIGTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0298
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-NOV-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                             United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1786 CCACCTGACCTGACT 1800
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear , MOLECULE TYPE: CDNA US-08-293-778-22
                                                            New York
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
PILING DATE:
PILING DATE:
PILING DATE:
PRIOR APPLICATION NUMBER: US/08/104,509
FILING DATE: 25-JUN-1987
FILING DATE: 25-JUN-1987
FILING DATE: 25-JUN-1987
FILING DATE: 25-JUN-1989
FILING DATE: 24-JUN-1989
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1992
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1992
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
APPLICATION NUMBER: 31-34.086
FILING DATE: 12-JUN-1988
FILING DATE: 21-300-1992
APPLICATION NUMBER: 31-36-60-005
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Perfect score:
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Database :

Result No.

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1443 AGGGATCGAGACCATCCCCATGGAAAAGAATGCAAAAAGCAAAATGGCTGTCTGGGGA 1502
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57.8%; Pred. No. 0.76;
tive 0; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                            Sequence 3,
Sequence 2,
Sequence 3,
                                                                                                                                      Sequence 3,
Sequence 4,
                                                                                      Sequence 2,
Sequence 3,
                                                                                                                                                                            Sequence 6,
Sequence 7,
                                     Sequence 3,
                                                                     Sequence 6,
                                                                                                                         Sequence 2,
                                                                                                                                                                                                            Sequence 2,
                    Sequence
                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                        US-09-782-587B-2

/ Sequence 2, Application US/09782587B

/ Bedience 2, Application US/09782587B

/ Publication No. US20030096338A1

/ GENERAL INFORMATION:

/ APPLICANT: PEDERSEN, ANDERS H.

/ APPLICANT: BORNAES, CLAUS

/ TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES

/ TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES

/ TURENT APPLICATION NUMBER: US/09/782,587B

/ CURRENT APPLICATION NUMBER: BA 2000 00218

/ PRIOR FILING DATE: 2000-02-11

/ PRIOR FILING DATE: 2000-02-12

/ PRIOR FILING DATE: 2000-02-22

/ PRIOR FILING DATE: 2000-02-22

/ PRIOR APPLICATION NUMBER: 60/241,916

/ PRIOR FILING DATE: 2000-02-13

/ PRIOR FILING DATE: 2000-02-13

/ NUMBER OF SEQ ID NOS: 13

/ SOFTWARE: PACENTIN VEY: 2.1

/ SEG ID NOS: 1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4. Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: REVENSES: GLAUS
; TITLE OF INVENTION: FACTOR VI OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
US-10-281-727-2
US-10-281-727-3
US-10-109-498-5
US-10-109-498-6
US-09-951-121A-2
US-10-951-121A-3
US-10-295-682-2
US-10-295-682-2
US-10-295-682-3
US-10-295-682-3
US-10-281-727-6
US-10-281-727-7
                                                                                                                                                                                                        US-09-951-121A-2
US-09-951-121A-3
US-10-295-682-2
US-10-295-682-3
                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 57.8%
Matches 37, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (115)..(1332)
US-09-782-5678-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1503 GGCC 1506
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                                                      TYPE: DNA
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1443 AGGGATCGAGACCATCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGA 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: Expression ; OTHER INFORMATION: cassette for expression of FVII in mammalian cells US-09-782-587B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-782-587B-2/C

is Sequence 2, Application US/09782587B

publication No. US20030096338A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEDERSEN, ANDERS H.
APPLICANT: BORNAES, CLAUS

TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT FILING DATE: 2002-03-26
FRICK APPLICATION NUMBER: 05/09/762,587B

CURRENT FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

SEVEN IN NUMBER OF SEQ ID NOS: 19

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AGGTAAGGAGCAGTAGCTGCGCTTTGCTGGAGCAGCCGT 82
CURRENT APPLICATION NUMBER: US/09/782,587B
                         CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUNBER: PA 2000 00218
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUNBER: 60/184,036
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALENTIN VEY: 2.1
LENGTH: 1357
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LUCATION: (115)..(1332)
US-09-782-587B-2
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1503 GGCC 1506
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LOCATION: (11
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RESULT 4 US-09-782-587B-4/c ; Sequence 4, Application US/09782587B 512 AAGAAATGCCAGCAAACCCCAAGGCCGAATTGTGGGG 548

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Publication No. US20030096338A1

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TITLE OF INVENTION: AIPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: AIPHA GALACTOSIDASE A
TITLE OF INVENTION: GALACTOSIDASE A
FILE REFERENCE: 0.04632-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-6-19
PRIOR FILING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-15
PRIOR PELING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR SPOLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
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PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
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PRIOR PILING DATE: 2002-08-16
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE REFERENCE: 040853-01-5053
FILE REFERENCE: 040853-01-5053
FILE REPRESIDENT APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: US 60/387,292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520 ggaaaatacctattctagaaaaaadaaatigccagcaaacccaaggccaattgtggg
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Best Local Similarity 56.7%; Pred. No. 12;
Matches 34; Conservative 0; Mismatches 26;
                                                                                                                                                                                                                                                  APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10411026 Publication No. US20040063911A1 GENERAL INFORMATION:
                                                                                                                              Sequence 7, Application US/10411037
Publication No. US20040043446A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-411-037-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Expression of OTHER INFORMATION: cassette for expression of FVII in mammalian cells US-09-782-587B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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// Sequence 35, Application US/10382248

// Sequence 35, Application No-US20040058347A1

// Sequence 35, Application No-US20040058347A1

// SERNEAL INPORMATION:

// APPLICATI'S ALGODROW, et al.

// TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

// TILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

// TILLE OF INVENTION: NOVER: US 003-05, 026

// CURRENT FILING DATE: 2003-03-05

// PRIOR APPLICATION NUMBER: 60/366,928

// PRIOR PILING DATE: 2002-03-05

// PRIOR PILING DATE: 2002-03-19

// PRIOR FILING DATE: 2002-03-19

// PRIOR FILING DATE: 2002-03-19

// PRIOR FILING DATE: 2002-03-19

// PRIOR FILING DATE: 2002-03-06

// PRIOR FILING DATE: 2002-03-06

// PRIOR FILING DATE: 2002-03-19

// PRIOR FILING DATE: 2002-03-06

// NUMBER OF SEQ ID NOS: 82

// SOFTWARE: CuraSeqList version 0.1
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0.5%; Score 18.6; DB 1; Length 1361;
Best Local Similarity 49.5%; Pred. No. 10;
Matches 48; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.6%; Score 19.8; DB 1; Length 1 Best Local Similarity 69.2%; Pred. No. 2.6; Matches 27; Conservative 0; Mismatches 12; Indels
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEDERSON, KIM V.
APPLICANT: ANDERSON, KIM V.
APPLICANT: BORNAES, CLAG
APPLICANT: BORNAES, CLAG
APPLICANT: BORNAES, CLAG
FILE REFERENCE: 31-001100US
CURRENT PELICANTION: FACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: PA 2000 00218
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/184,036
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 19
SOSTWARE: PALENTIN VET: 2.1
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; LOCATION: (45)..(1301)
US-10-382-248-35
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LENGTH: 13
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FILING DATE: 2002-06-07

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TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US2004007936A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GRANULOCYTE COLONY
TITLE OF INVENTION: GRANULOCYTE COLONY
TITLE OF INVENTION: GRANULOCYTE COLONY
FILE REFERENCE: 040853-01-504-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
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0.5%; Score 18.4; DB 1; Length 1332;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 34; Conservative 0; Mismatches 26; Indels 0
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Best Local Similarity 56.7%; Pred. No. 12;
Matches 34; Conservative 0; Mismatches
PRIOR FILING DATE: 2002-000

PRIOR FILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR PILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-28

NUMBER OF SEQ ID NOS: 75

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA;
ORGANISM: Homo sapiens
US-10-411-026-7
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; ORGANISM: Homo sapiens
US-10-410-962-7
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1332
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Garyn
ITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCOMJUGATION OF INTERFERON
ITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCOMJUGATION OF INTERFERON
ITLE OF INVENTION: INTERFERON
ITLE OF INVENTION: INTERFERON
ITLE OF INVENTION NUMBER: US/10/410,930
CURRENT APPLICATION NUMBER: US/0328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
                                                                                                                                                   APPLICANT: NOSE INCLINIOUSES, INC.
APPLICANT: DeFrees, Shawn
APPLICANT: ZOPF, David
APPLICANT: Adver, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: APPLICANT: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
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PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
Sequence 7, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
                                                                                                                      APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10410930 Publication No. US20040115168A1 GENERAL INFORMATION:
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APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1445 GGATCGAGACCATCCCCATGGAAAAGAAATGCAAAAAAGCAAAATGGCTGTCTGGGGAGG 1504
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APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCCONJUGATION OF PEPTIDES
FILE REFRENCE: C40853-01-505-00
CURRENT APPLICATION NUMBER: US 60/326,523
PRIOR APPLICATION NUMBER: US 60/326,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-17
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                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 040653-01-5051
CURRENT APPLICATION NUMBER: US/10/411,012
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PILING DATE: 2001-10-19
PRIOR PLILNG DATE: 2001-10-19
PRIOR PLILNG DATE: 2002-06-07
PRIOR PLILNG DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
                                                                                                 APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
                                 ; Sequence 7, Application US/10411012; Publication No. US20040132640A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-012-7
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0.5%; Score 18.4; DB 1; Length 1332;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 34; Conservative 0; Mismatches 26; Indels 0; Gaps
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PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-410-997-7
                                                                                                                                                                                                                    SEQ ID NO 7
LENGTH: 1332
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RESULT 12

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APPLICANT: Thorpe, Philip E
APPLICANT: Thorpe, Philip E
APPLICANT: Thorpe, Steven W
APPLICANT: Thorpe, Steven W
APPLICANT: Go, Boning
ITTLE OF INVENTION: TISSUE FACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
ITTLE OF INVENTION: TREATMENT
FILE REPERENCE: 4001.01999
CURRENT APPLICATION NUMBER: US/10/375,741
FILE REPERENCE: 2003-02-27
FILE REPERENCE: 2000-05-18
FILE REPERENCE: 2000-05-18
FILE REPERENCE: 60/042,427
FRICA PAPLICATION NUMBER: 60/042,427
FRICA REPLICATION NUMBER: 60/036,205
FRICA REPLICATION NUMBER: 60/036,205
FRICA REPLICATION NUMBER: 60/036,205
FRICA RELING DATE: 1997-01-27
FRICA RELING DATE: 1997-01-27
FRICA RELING DATE: 1997-01-27
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Fublication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E
APPLICANT: Micolaisen, Else M
APPLICANT: JOZGENSEN, Anker S
TITLE OF INVENTION: T'E Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR PLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-07-13
SOFTWARE: PatentIn version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENTH: 2040
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Pred. No. 13;
0; Mismatches 26;
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56.7%; Pred. No. 16;
tive 0; Mismatches
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Best Local Similarity 56.7%;
Matches 34; Conservative
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Matches 34; Conservative
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ORGANISM: Artificial
FEATURE:
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| Fublication No. US20040142856A1
| GENERAL INFORMATION | US20040142856A1
| GENERAL INFORMATION | US20040142856A1
| GENERAL INFORMATION | US20040142856A1
| APPLICANT: Necset rechnologies, Inc. |
| APPLICANT: Devices, Shawn |
| APPLICANT: Devices, Shawn |
| APPLICANT: Devices, Shawn |
| APPLICANT: Devices, David |
| APPLICANT: Bayer, Robert |
| APPLICANT: Bayer, Robert |
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| FRICR PLING DATE: 2003-04-092 |
| PRICR FILING DATE: 2002-06-25 |
| PRICR PLING DATE: 2002-06-25 |
| PRICR FILING DATE: 2002-06-17 |
| PRICR FILING DATE: 2002-06-16 |
| PRICR FILING DATE: 2002-08-16 |
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56.7%; Pred. No. 12;
tive 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/404,249 PRIOR PRIJNG DATE: 2002-08-16 PRIOR APPLICATION NUMBER: US 60/407,527 PRIOR FILING DATE: 2002-08-28 NUMBER OF SEQ ID NOS: 62 SOFTWARE: Patentin version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-375-741-13
Sequence 13, Application US/10375741
Publication No. US20030232753A1
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-287-994-7
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; ORGANISM: Homo sapiens
US-10-410-913-7
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US-10-410-913-7
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RESULT 17 US-10-617-619-9

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                                                                                                                                                                         149 CGAAGGCCAGCGTCCTCTCAGAGAACGTCCGTTCGGGCAGGGGAGGGGCACCACATGGT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ---GCGCTTTTGCTGGAGCAGCCGTAAAGAGATACCCCACGCCCAAGGTAAGAGAAACCCA 118
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                                                      119 AGTAAGATGGTAGGTGTTGTGAGAGGGCATCAGAGGGCAGACATACTGAAACCATACACG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TCAGGAAGGGCGGCAGTGAGGAGAGGTACCTACCTCCTCCAAGGTAAGGAGCAGTAGCT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/10382248

Publication No. US20040058347A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REPERENCY: 21402-568C

CURRENT APPLICATION NUMBER: US/10/382,248

CURRENT APPLICATION NUMBER: US/20/366,928

PRIOR APPLICATION NUMBER: 60/366,928

PRIOR APPLICATION NUMBER: 60/366,928

PRIOR APPLICATION NUMBER: 60/361,974

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR APPLICATION NUMBER: 60/365,477

PRIOR PILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-03-19

PRIOR FILING DATE: 2002-03-19

PRIOR FILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-03-06

NUMBER OF SEQ ID NOS: 82

NUMBER OF SEQ ID NOS: 82

SOFTWARE: CURASGELIST VERSION 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (45)..(1301)
                                                                                                                                                                                                                                      179 CAG 181
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US-10-382-248-35/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 35
LENGTH: 1361
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: BXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                            APPLICANT: Bjorn, Soren E
APPLICANT: Bjorn, Soren E
APPLICANT: Bjorn, Soren E
APPLICANT: Micolaisen, Else M
APPLICANT: Jorgensen, Anker S
TITLE OF INVENTION: FP Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT PAPLICATION NUMBER: US/10/617,619
CURRENT FILING DATE: 2003-07-11
PRIOR FILING DATE: 2003-07-12
PRIOR PLICATION NUMBER: US 60/404,568
PRIOR APPLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH. 2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.5%; Score 18.4; DB 1; Length 2106; Best Local Similarity 56.7%; Pred. No. 16; Matches 34; Conservative 0; Mismatches 26; Indels 0.
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BALL | 1
OTHER INFORMATION: EXPRESSED IN LIVE, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: WISSPROT HIT: P08709; EVALUE 7.00e-63
OTHER INFORMATION: BY HIT: J02933.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: ALS31727.1, EVALUE 5.00e-76
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Sequence 9, Application US/10617619
Publication No. US20040110929A1
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Artificial
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US-10-029-386-9623
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Best Local
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243 AGABATCCAGARCAGCTTCGTCTCCGCGTCCTTGARGATCTCCCGGGCCTCCTCGAR 184
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APPLICANT: Devices, Shawn
APPLICANT: Devices, Shawn
APPLICANT: Applicant: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bovid
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: CRIVANT: CATYN
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND TITLE OF INVENTION: GLYCOCCONJUGATION OF G-CSF
FILE REFERENCE: 040853-01-5054
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Publication No. US20040077836A1
GENERAL INFORMATION:
SOFTWARE: Patentin version 3.2; SEQ ID NO 7
LENGTH: 1332
TYPE: DNA
                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-411-026-7
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ORGANISM: Homo sapiens
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                   APPLICANT: Ore Carn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: ALLPHA GALACTOSIDASE A
FILE REFERENCE: 040833-01-5082
CURRENT FILING DATE: 2003-04-09
FRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                871 AGTAATGCTGAAGAAGCTGAAGTTGAACGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
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FILE REPRENCE: 040853-01-5053

CURRENT APPLICATION NUMBER: US/10/411,026

CURRENT FILING DATE: 2003-04-09

PRIOR PEDICATION NUMBER: US 60/328,523

PRIOR PELING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-0-19

PRIOR PELING DATE: 2002-06-07

PRIOR PELING DATE: 2002-06-07

PRIOR PELING DATE: 2002-06-07

PRIOR PELING DATE: 2002-06-07

PRIOR PELING DATE: 2002-06-17

PRIOR PELING DATE: 2002-06-17

PRIOR PELING DATE: 2002-07-17

PRIOR PELING DATE: 2002-07-17

PRIOR PELING DATE: 2002-07-17

PRIOR PELING DATE: 2002-08-16

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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEC ID NOS: 75
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871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
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0.5%; Score 17.4; DB 1; Length 1332;

Best Local Similarity 53.7%; Pred. No. 28;

Matches 36; Conservative 0; Mismatches 31; Indels 0; Gaps
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PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR PELICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2002-10-19
PRIOR PLING DATE: 2002-66-07
PRIOR PLING DATE: 2002-66-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
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PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR FILING DATE: 2002-06-07
PRIOR PEDICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-39
PRIOR APPLICATION NUMBER: US 60/496,594
PRIOR PELING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PRIOR DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
NUMBER: OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
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CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-997-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
, ORGANISM: Homo sapiens
US-10-410-930-7
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, Caryn
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DeFrees, Shann
APPLICANT: DeFrees, Shann
APPLICANT: DeFrees, Shann
APPLICANT: Copf, David
APPLICANT: Askes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA: 105/10/410,930
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR PRILOR APPLICATION NUMBER: US 60/387,292
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0.5%; Score 17.4; DB 1; Length 1332;
Best Local Similarity 53.7%; Pred. No. 28;
Matches 36; Conservative 0; Mismatches 31; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
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   US-10-411-049-7/c
; Sequence 7, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION; FSH
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US-10-410-913-7/C

Sequence 7, Application US/10410913

Publication No US2004014285641

GENERAL INFORMATION

Publication No US2004014285641

GENERAL INFORMATION

PREDICANT: Neces Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: DeFrees, Shawn

APPLICANT: DeFrees, David

APPLICANT: DeFrees, David

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Caryn

ITTLE OF INVENTION: GITCOCCNUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

ITTLE OF INVENTION: METHODS

FILE REFERENCE: 04083-01-5081

CURRENT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR PLING DATE: 2002-06-15

PRIOR PLING DATE: 2002-06-15

PRIOR PLING DATE: 2002-06-15

PRIOR PLING DATE: 2002-06-25

PRIOR PLING DATE: 2002-06-25

PRIOR PLING DATE: 2002-06-28

PRIOR PLING DATE: 2002-08-28

**NUMBER OF SEQ ID NOS: 75

**SOFTWARE: Patentin version 3.2

**SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: REMODELING AND GLYCOCONUTGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-00
CURRENT PAPLICATION NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR PAPLICATION NUMBER: US 60/328,523
PRIOR PAPLICATION NUMBER: US 60/324,692
PRIOR PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-0-19
PRIOR PLING DATE: 2002-0-0-7
PRIOR PLING DATE: 2002-0-0-7
PRIOR PLING DATE: 2002-0-0-7
PRIOR PLING DATE: 2002-0-17
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ORGANISM: Homo sapiens
US-10-287-994-7
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APPLICANT: Chen, Xi

THE PERIOD HOLD SAND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

CURRENT APPLICATION NUMBER: US/10/411,012

CURRENT APPLICATION NUMBER: US/10/411,012
                     871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
                                                                     243 AGARANTCCAGARCAGOTTCGTCCTCTCGCGTCCTTGARGATCTCCCGGGCCTCCTCGAR 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR DATE: 2002-06-25
PRIOR PRIOR DATE: 2002-06-25
PRIOR PRIOR DATE: 2002-06-16
PRIOR PRIOR DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-16
PRIOR PLING DATE: 2002-08-18
PRIOR PLING DATE: 2002-08-18
PRIOR PLING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
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Publication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Necse Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
APPLICANT: Hakes, David
APPLICANT: Caryn
APPLICANT: Caryn
APPLICANT: Caryn
APPLICANT: Caryn
APPLICANT: Chen, Xi
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Publication No. US20040137557A1
GENERAL INFORMATION:
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US-10-411-012-7
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871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
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| Sequence 9, Application US/20640110929A1
| Publication No. US20040110929A1
| GENERAL INFORMATION:
| APPLICANT: Bjorn, Soren E
| APPLICANT: Micolaisen, Else M
| APPLICANT: Usergensen, Anker S
| TILLE OF INVENTION: TF Binding Compound
| FILE REFERENCE: 6455.200-02
| FILE REFERENCE: 6455.200-03
| CURRENT FILING DATE: 2003-07-11
| PRIOR PILING DATE: 2002-07-12
| PRIOR PILING DATE: 2002-07-12
| PRIOR PILING DATE: 2002-07-12
| PRIOR PILING DATE: 2002-08-19
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: PATENTH VERSION 3.2
| SEQ ID NO 9
| LANGTH 12106
| LANGTH 12106
| LANGTH 12106
| LANGTH 12106
| LANGTH 12106
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                   PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099 PRIOR FILING DATE: 2002-07-12 PRIOR APPLICATION NUMBER: US 60/404,568 PRIOR FILING DATE: 2002-08-19 NUMBER OF SEQ 1D NOS: 13 SOFTWARE: Patentin version 3.2
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0.5%; Score 17.4; DB 1; Length 2
Best Local Similarity 53.7%; Pred. No. 23;
Matches 36; Conservative 0; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic US-10-617-619-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-23323
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LENGTH: 2040
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Sequence 13, Application US/10375741

Publication No. US2003023753A1

GENERAL INFORMATION:

APPLICANT Thorpe, Philip E

APPLICANT Thorpe, Philip E

APPLICANT HORDE, Philip E

TITLE OF INVENTION: TESATWENT

TITLE OF INVENTION: TESATWENT

TITLE OF INVENTION: TESATWENT

TITLE OF INVENTION: TS200-02-27

PRIOR PPLICATION NUMBER: 09/573,835

PRIOR PLILING DATE: 2000-05-18

PRIOR PLILING DATE: 1998-01-20

PRIOR PLILING DATE: 1998-01-20

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

PRIOR PLILING DATE: 1997-01-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                         DB 1; Length 1332;
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0.5%; Score 17.4; DB 1; 1
Best Local Similarity 53.7%; Pred. No. 28;
Matches 36; Conservative 0; Mismatches 31;
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0; Mismatches
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Publication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bjorn. Soren E
APPLICANT: Nicolaisen, Blse M
APPLICANT: Norgensen, Anker S
TITLE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/10/617,619
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US-10-375-741-13
       LENGTH: 1332
TYPE: DNA
ORGANISM: Homo sapiens
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Matches 36; Conserva
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                                                                                            ) US-10-410-913-7
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246 CTCCCTGGAGGAGGAGGAGGAGGAGGAGTGCTCCTTCGAGGAGGCC 294
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Best Local Similarity 44.1%;
Matches 71; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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US-10-029-386-9623/c
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LENGTH: 555
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APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 23323

LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
N: EXPRESSED IN BRAIN, SIGNAL = 1
N: EXPRESSED IN UNG, SIGNAL = 0.46
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 0.95
N: EXPRESSED IN HEART, SIGNAL = 0.95
N: M: THIT: 914783796, EVALUE 1.00e-122
N: STIT HUMAN HIT: AL531727.1, EVALUE 3.00e-26
N: SWIŠSPROT HIT: P08709, EVALUE 3.00e-26
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O.5%; Score 17.1; DB 1; Length 222;
Best Local Similarity 47.1%; Pred. No. 8;
Matches 82; Conservative 0; Mismatches 89; Indels
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Fublication No. US2003007362341
GENERAL INPORMATION:
APPLICANT: PHYSOG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: RROW VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTHARE: FastSEQ for Windows Version 3.0
LENGTH: 483
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; LCCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-999-8429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 29; Conserva
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERBUCE: AROMICA.x.2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEC ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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N: EXPRESSED IN BRAIN, SIGNAL = 1
N: EXPRESSED IN LUNG, SIGNAL = 0.46
N: EXPRESSED IN DONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 1.3
N: EXPRESSED IN HEART, SIGNAL = 1.3
N: SITSERFOT HIT: P08709, EVALUE 7.00e-63
N: NI HIT: J02933.1, EVALUE 0.00e+00
N: EST_HUMAN HIT: AL531727.1, EVALUE 5.00e-76
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| Sequence 4829, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: RROW VARIOUS CDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| PRIOR APPLICATION NUMBER: US/09/235,076
| PRIOR FILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 8429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 1; Length 555;
Pred. No. 24;
0; Mismatches 90; Indels
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ORGANISM: Homo sapiens
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US-10-2/2-50-10.

US-10-2/2-50-10.

US-10-2/2-50-10.

US-10-2/2-50-10.

US-10-2/2-50-10.

ITILE OF INVENITON: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PRITIES OF INVENITON: GENERIC MARKERS

ITILE OF INVENITON: GENERIC MARKERS

ITILE OF INVENITON: GENERIC MARKERS

FILER REPERBNCE: 24736-2033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT APPLICATION NUMBER: G0/217,658

PRIOR FILING DATE: 2000-07-10

PRIOR PLING DATE: 1099-10-13

PRIOR PELING DATE: 1099-10-13

PRIOR PELING DATE: 2000-07-10

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PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

NUMBER OF SEQ ID NOS: 118

COFTWARE: FastSEQ for Windows Version 4.0
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US=10-273-228-107

Sequence 107, Application US/1027328

Sequence 107, Application US/1027328

Sequence 107, Application US/1027328

Sequence 107, Application US/102731

Sequence 107, Application US/102731

GENERAL INFORMATION:

METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PRITE REFERENCE: 24736-20330

FILE REFERENCE: 24736-20330

CURRENT APPLICATION NUMBER: 09/687,483

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/217,251
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59.5%; Pred. No. 49;
tive 0; Mismatches 17; Indels
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NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 107
LENGTH: 100
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Best Local Similarity 59.5
Matches 25; Conservative
                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-107
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ORGANISM: Homo sapien
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US-10-722-665-107

Sequence 107, Application US/10272665

Publication No. US2030180748A1

GENERAL INFORMATION:

TITLE OF INVERMATION:

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| Publication No. US2030180749A1
| GENERAL INFORMATION:
| TUTLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: GENETIC MARKERS
| TITLE OF INVENTION: GENETIC MARKERS | FILE REPERENCE: 24736-2033B | CURRENT APPLICATION NUMBER: US/10/273,321 |
| CURRENT APPLICATION NUMBER: 09/687,483 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR FILING DATE: 1999-10-13 |
| PRIOR FILING DATE: 1999-10-13 |
| PRIOR FILING DATE: 2000-07-10 |
| PRIOR APPLICATION NUMBER: 60/127,551 |
| PRIOR PELLING DATE: 2000-07-10 |
| PRIOR PELLING DATE: 2000-07-10 |
| PRIOR PELLING DATE: 2000-07-10 |
| PRIOR PELLING DATE: 2000-09-19 |
| PRIOR FILING DATE: 2000-09-19 |
| PRIOR FILING DATE: 2000-09-19
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Best Local Similarity 59.5%; Pred. No. 49;
Matches 25; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                Query Match 0.5%; Score 16.6; DB 1; Length 4 Best Local Similarity 64.1%; Pred. No. 32; Matches 25; Conservative 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                  44 AGGTAAGGAGCAGTAGCTGCGCTTTGCTGGAGCAGCCGT
; NAME/KEY: misc_feature
; LCCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8429
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US-10-272-665-107
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LENGTH: 100.
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RESULT 42

US-10-272-756-106

Sequence 106, Application US/10272756

Sedimence 106, Application World US/10272756

SEDIMENT WORKATION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: MUMBER: US/10/272,756

CURRENT APPLICATION NUMBER: 09/637,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PAPLICATION NUMBER: 60/217,558

PRIOR PELING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,251

PRIOR SPELING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

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US-10-273-228-106

US-10-273-228-106

Sequence 106, Application US/10273228

Publication No. US20030207297A1

GENERAL INFORMATION:

APPLICANT: Brann et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL WARKERS

FILE REPREMENCE 24713-2033D

CURRENT APPLICATION UNMBER: US/10/273,228

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483
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O.4%; Score 14.4; DB 1;
Best Local Similarity 60.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 16;
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60.0%; Pred. No. 78;
tive 0; Mismatches
                    PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 100
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; ORGANISM: Homo sapien
US-10-273-321-106
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CORGANISM: Homo sapien
US-10-272-756-106
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Matches 24; Conserva
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Sequence 106, Application US/10272665

PUBLICALNO NO. US2030180748A1

SEQUENCE 106, Application US/10272665

PUBLICALNO NO. US2030180748A1

APPLICALNO NO. US2030180748A1

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERIC MARKERS

FILE REFERENCE: 24736-2033E

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT FILING DATE: 2000-07-10

PRIOR PELICATION NUMBER: 60/217,658

PRIOR PELICATION NUMBER: 60/159,176

PRIOR PELICATION NUMBER: 60/159,176

PRIOR PELICATION NUMBER: 60/159,176

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 106

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Publication No. US20030180749A1
APPLICATION NO. US20030180749A1
APPLICATION NO. US20030180749A1
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING FILE REFERENCE: 24736-2033B
CURRENT PELLOR UNMER: US/10/273,321
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR PLILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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0.4%; Score 14.8; DB 1; Length 100;
Best Local Similarity 59.5%; Pred. No. 49;
Matches 25; Conservative 0; Mismatches 17; Indels
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PASTSEQ for Windows Version 4.0
LENGTH: 100
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CORGANISM: Homo sapien
US-10-273-228-107
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 24; Conserv
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0.4%; Score 14.2; DB 1; Length 38;
Best Local Similarity 84.2%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 3; Indels
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1990-10-13
PRIOR PILING DATE: 1990-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PSELSEQ for Windows Version 4.0
ENGTH: 100
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                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-228-106
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LENGTH: 38
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RESULT 45

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Gaps
us-vs-ys-by-zs/-zs/-z

sequence 2, Application US/09969357

publication No. US2020137673A1

publication No. US2020137673A1

publication No. US2020137673A1

publication No. US2020137673A1

APPLICANT: Novo Nordisk Pharmaceuticals, Inc.

APPLICANT: Riamen, Niels K

APPLICANT: Riamen, Niels K

TITLE OF INVENTION: Factor VII Glycoforms

FILE REFERENCE: 6207.510-US

CURRENT APPLICATION NUMBER: Danish Application No. PA 2000 01456

PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00262

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 2

SEGFWARE PLEATER PARENTIN VARFSION 3.2
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| Publication No. US20030096366A1
| GENERAL INFORMATION: Ida Molgaard
| APPLICATION TRUGBER. Ida Molgaard
| TITLE OF INVENTION: Method for Production of Recombinant
| TITLE OF INVENTION: Proteins in Eukaryote Cells
| TITLE OF INVENTION: Proteins in Sukaryote Cells
| CURRENT PELICATION WINBER: US/10/254,394
| CURRENT PILING DATE: 2002-09-25
| PRIOR PILING DATE: 2001-10-02
| PRIOR FILING DATE: 2001-10-02
| PRIOR FILING DATE: 2001-10-02
| PRIOR FILING DATE: 2001-10-02
| PRIOR PILING DATE: 2001-10-04
| PRIOR PILING DATE: 2002-09-26
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0.4%; Score 14.2; DE
Best Local Similarity 84.2%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic US-09-969-357-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial
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US-10-254-394-2
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Sequence 22, Application US/10272756

Sequence 22, Application US/10272756

Sequence 22, Application US/10272756

Bublication No. US20030190644A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO

TITLE OF INVENTION: GENERIC MARKERS

TITLE OF INVENTION: GENERIC MARKERS

TILE REFERENCE: 2473-62033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT APPLICATION NUMBER: US/10/15

PRIOR PILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-09-19

SEQUENCE: AUTHOR DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

LENGTH: 60

LENGTH: 60

LENGTH: 60
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Publication No. US20030207297A1

GENERAL INFORMATION:

FULL OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PG
TITLE OF INVENTION: GENERAL CARRERS
FILE REFERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228

CURRENT APPLICATION NUMBER: US/87,483

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR APPLICATION NUMBER: 60/17,658

PRIOR APPLICATION NUMBER: 60/17,658

PRIOR APPLICATION NUMBER: 60/19,176

PRIOR APPLICATION NUMBER: 60/19,176

PRIOR APPLICATION NUMBER: 60/19,176

PRIOR PILING DATE: 1999-10-13
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                                                                                                                                                   OTHER INFORMATION: Probe US-10-273-321-22
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                                             TYPE: DNA
ORGANISM: Homo Sapien
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US-10-273-228-22
        LENGTH: 60
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERAL GRAND BATABASES AND DATABASES FOR IDENTIFYING PRITE OF INVENTION: GENERAL GRAND BATABASES AND DATABASES FOR IDENTIFYING PATE: 2002-10-15
CURRENY FILING DATE: 2002-10-15
FRIOR APPLICATION NUMBER: 09/687,483
FRIOR FILING DATE: 2000-07-10
FRIOR FILING DATE: 1000-07-10
FRIOR FILING DATE: 1999-110-13
FRIOR FILING DATE: 1999-110-13
FRIOR FILING DATE: 2000-07-10
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Sequence 22, Application US/10273321

Publication No. US20030180749A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL US/10/273,321

CURRENT FILING DATE: 2002-10-15

FILE REPERENCE: 24736-2033B

CURRENT FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

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Query Match 0.4%; Score 14.2; DB 1; Length 38; Best Local Similarity 84.2%; Pred. No. 33; Matches 16; Conservative 0; Mismatches 3; Indels
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0.4%; Score 13.2; DB 1; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10272665 Publication No. US20030180748A1 GENERAL INFORMATION:
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PROPERTIES OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PROPERTY OF INVENTION: GENERAL ("S.10/272,756"); CURRENT APPLICATION WYMBER: ("S.10/272,756"); CURRENT PILING DATE: 2000-10-15 prior APPLICATION WYMBER: (0/15), prior APPLICATION WYMBER: (0/15), prior APPLICATION WYMBER: (0/15), prior APPLICATION WYMBER: (0/15), 176 prior APPLICATION WYMBER: (0/15), 176 prior APPLICATION WYMBER: (0/15), 176 prior APPLICATION WYMBER: (0/12), 176 prior APPLICATION WYMBER: (0/12), 180 prior APPLICATION WYMBER: (0/15), 180 prior APPLICATION WYMBER: (0/15), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLICATION WYMBER: (0/16), 180 prior APPLIC
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PA
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033D
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0.4%; Score 13.2; DB 1; Length 100;
Best Local Similarity 69.2%; Pred. No. 2.66+02;
Matches 18; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 13.2; DB 1; Length 100; Best Local Similarity 69.2%; Pred. No. 2.6e+02; Matches 18; Conservative 0; Mismatches 8; Indels (
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SOFTWARE: FastSEQ for Windows Version 4.0
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                 PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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PRIOR FILING DATE: 2000-07-10
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US-10-272-756-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-106
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Sequence 106, Application US/10272665

publication No. US20030180748A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL MARKERS

TITLE OF INVENTION: GENERATION MARKERS

FILE REPERBENCE: 24736-2033E

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR PILING DATE: 2006-07-10

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR PILING DATE: 2006-07-10-13

PRIOR PILING DATE: 2006-07-10

PRIOR FILING DATE: 2006-07-10

PRIOR FILING DATE: 2006-07-10

PRIOR FILING DATE: 2006-07-10

PRIOR FILING DATE: 2006-07-10

PRIOR FILING DATE: 2006-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: RESESE FOR WINDOWS Version 4.0
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Publication No. U520030180749A1
CENDIACATION:
CENDIACATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POT TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033B
CURRENT APPLICATION NUMBER: 105/0273,321
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR APPLICATION NUMBER: 09/687,483
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PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FARENSEQ for Windows Version 4.0
LENGTH: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Probe US-10-273-228-22
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CORGANISM: Homo sapien
US-10-272-665-106
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
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GENERAL INCRMINION:

GENERAL INCRMINION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO

TITLE OF INVENTION: MARKERS

TITLE OF INVENTION: MARKERS

CURRENT APPLICATION NUMBER: 05/21/658

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

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TITLE OF INVENTION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERIC MARKERS

FILE REPERBACK: 24736-2033C

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT APPLICATION NUMBER: US/10/215,756

CURRENT APPLICATION NUMBER: 05/217,658

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1900-07-10

PRIOR PRIOR PRIOR NUMBER: 05/217,251

PRIOR PRIOR PRIOR PRIOR NUMBER: 05/217,251

PRIOR PRIOR PRIING DATE: 2000-07-10

PRIOR PRIOR FILING DATE: 2000-07-10

PRIOR PRIOR PRIOR NUMBER: 05/217,251

PRIOR PRIOR PRIOR NUMBER: 05/217,251

PRIOR PRIOR PRIOR NUMBER: 09/63,968

PRIOR PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 22

LENGTH: 60
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033E

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT AILING DATE: 2000-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-110-13

PRIOR FILING DATE: 1999-110-13

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PRIOR FILING DATE: 2000-07-10

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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/17,658
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
SEQIENT SEQIENT NOS: 118
NUMBER OF SEQIENT NOS: 118
SOFTWARE: FRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF THE TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH OF TABLE TRANCH 
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; Sequence 22, Application US/10273321
; Publication No. US20030180749A1
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CORGANISM: Homo sapien
US-10-273-228-106
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ORGANISM: Homo Sapien
FEATURE:
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PATTLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PATTLE OF INVENTION: GENERAL MARKERS
FILE REFERENCE: 24736-2033B
CURRENT APPLICATION NUMBER: 10/10/273,321
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-10-15
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTILE OF INVENTION: GENERAL ASSOCIATION OF THE REPERBING: 24736-2033C
CURRENT APPLICATION NUMBER: US/10/272,756
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
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                                                                                                        2680 GACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAGGCCTGTCCTGCGGCG 2739
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48.6%; Pred. No. 3.5e+02;
tive 0; Mismatches 37; Indels (
Best Local Similarity 48.6%; Pred. No. 3.5e+02;
Matches 35; Conservative 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 10 107
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 107, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                      2740 ATTCATGGGGTC 2751
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ORGANISM: Homo sapien
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Matches 35, Conserva
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Sequence 22, Application US/10273228

Publication No. US200320729741

SEQUENCE 21, Application US/10273228

Publication No. US200320729741

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FastSEQ for Windows Version 4.0

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Publication No. US20030180748A1
GENERAL INFORMATION:
JUSZO030180748A1
GENERAL INFORMATION:
JUSZO030180748A1
GENERAL INFORMATION:
JUSZO030180748A1
GENERAL INFORMATION:
JUSZO030180748A1

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
JURENT PELICATION NUMBER: US/10/272,665
CURRENT PELICATION NUMBER: US/10/272,665
CURRENT FILING DATE: 2000-07-10
PRIOR PELICATION NUMBER: 60/159,176
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
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       38 CTIGCAGGAGTCCTTGCTGCCATCCGAGTAGCCGGCA 2
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ORGANISM: Homo Sapien
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; ORGANISM: Homo sapien
US-10-272-665-107
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US-10-272-665-107/c
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10664775-2.rnpb

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Publication No. US20040058413A1

Sequence 20, Application US/10398422A

Publication No. US20040058413A1

GENERAL INFORMATION:

APPLICANT: Nicolaisen, Else Marie

APPLICANT: Nicolaisen, Lars Soegaard

TITLE OF INVENION: Method for the Production of Vitamin K-Dependent Proteins

FILE REFERENCE: 6270.204-US

CURRENT APPLICATION NUMBER: US/10/398,422A

CURRENT FILING DATE: 2003-09-02

PRIOR FILING DATE: 2003-09-02

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2010-03-14

PRIOR FILING DATE: 2010-03-14

PRIOR FILING DATE: 2010-03-14

PRIOR FILING DATE: 2010-03-14

PRIOR FILING DATE: 2010-03-16

PRIOR FILING DATE: 2010-03-16

PRIOR FILING DATE: 2010-03-16

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PRIOR FILING DATE: 2010-03-16

PRIOR FILING DATE: 2010-03-16

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PRIOR PRIOR DATE: 2010-03-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           737 GAGTAGCCATCATGGTCAACAAAGAG 763
                  CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Artificial
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Best Local Similarity
Matches 18; Conserva
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US-09-969-357-2/c
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US-10-273-228-107/c

US-10-273-228-107/c

Sequence 107, Application US/10273228

Publication No. US20030207297A1

GENERAL INFORMATION:

APPLICANT Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

CURRENT APPLICATION NUMBER: US/10/73,228

CURRENT FILING DATE: 2000-01-15

PRIOR PAPLICATION NUMBER: 60/217,658

PRIOR PLING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-10

PRIOR FILING DATE: 2000-09-10

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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-007
                                                                                                                                                                                                                                                                                                                                                            Length 100;
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48.6%; Pred. No. 3.5e+02;
tive 0; Mismatches 37; Indels
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48.6%; Pred. No. 3.5e+02;
tive 0; Mismatches 37;
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SSCYTARRE: FastSEQ for Windows Version 4.0
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.65
Matches 35; Conservative
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Best Local Similarity 48.6
Matches 35; Conservative
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18 CTTGCAGGAGTC 7
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                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-107
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; ORGANISM: Homo sapien
US-10-273-228-107
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US-10-017-122-4/c
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A PELCANT: Riggel, Mana K A PELCANT: Riggel, Mana K A PELCANT: Riggel, Mana K A PELCANT: Riggel, Mana K A PELCANT: Riggel, Mana K A TITLE OF LINEATION: Racco VII dlycocome Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the
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Publication No. US20030100506A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Modified Vitamin K-Dependent;
TITLE OF INVENTION: Modified Vitamin K-Dependent;
TITLE OF INVENTION: MODIFIED VITAMIN REPORT.
CURRENT APPLICATION NUMBER: US/10/298,330
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27-10-23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                           Sequence B, Application US/09803810; Sequence B, Application US/09803810; Publication No. US20010018414A1; GENERAL INFORMATION: G. US20010018414A1; APPLICANT: Nelsetuen, Gary L.; TITLE OF INVENTION: NODIFEED VITAMIN K-DEFENDENT; TITLE OF INVENTION: POLYPEETIDES; FILE REFERENCE: 09531/002001; CURRENT APPLICATION WUMBER: US/09/803,810; CURRENT FILING DATE: 2001-03-12; NUMBER OF SEQ ID NOS: 18; SEQ ID NOS: 18; SEQ ID NOS: 18; SEQ ID NO 8; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID NO 9; SEG ID 
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US-10-272-665-23/c
; Sequence 23, Application US/10272665
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ORGANISM: Artificial Sequence
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US-09-803-810-8
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Sequence 23, Application US/10272756

Publication No. US20330190644A1

GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POTILE OF INVENTION: GENERIC MARKERS
FILE REFERENCE: 24736-2033C
CURRENT APPLICATION UNMBER: US/10/272,756
CURRENT APPLICATION NUMBER: US/10/272,756
CURRENT PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

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PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-08-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 23

LENGTH RELEASED FOR WINDOWS VERSION 4.0
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Publication No. US20030207297A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL TITLE OF INVENTION:

TITLE OF INVENTION:

FITE OF INVENTION:

FITE OF INVENTION:

CURRENT APPLICATION UNBER: US/10/273,228

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: US/21/658

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

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US-10-272-756-23
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US-10-273-228-23
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US-10-273-228-23/c
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                         FULLCALUM.

APPLICANT: Braun et al.

TITLE OF INVENITION:

TITLE OF INVENITION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENITION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENITION: MEMBER: US/10/272,665

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PELLOR APPLICATION NUMBER: 60/159,176

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE: FESTSED FOR Windows Version 4.0

SEQ ID NO 23

LENGTH: 60
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Sequence 23, Application US/10273321

Sequence 23, Application US/10273321

Sequence 23, Application US/20030180749A1

SETILE OF UNENTION:

TITLE OF INVENTION:

FILE REFERENCE: 24736-2033

FILE REFERENCE: 24736-2033

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR FILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

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Publication No. US20030180748A1
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US-10-272-665-23
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; ORGANISM: Homo sapien
US-10-273-321-23
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US-10-255-032-8
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Sequence 8, Application US/10255032;
Publication No. US20030100075A1;
GENERAL INFORMATION:
APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S
TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
FRIOR PILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
LENGTH: 36
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                                                                                                                                                                                            | Sequence 9. Application US/09951121A
| Sequence 9. Application US/09951121A
| Publication No. US20030104978A1
| GENERAL INFORMATION:
| APPLICANT: Person, Egon
| APPLICANT: Olsen, Ole Hvilsted
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| FILE REFERENCE: 6224.200-US
| CURRENT APPLICATION NUMBER: US/09/951,121A
| CURRENT FILING DATE: 2001-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-29
| NUMBER OF SEQ ID NOS: 17
| SOFFWARE: FastSEQ for Windows Version 4.0
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US-10-255-032-9
; Sequence 9, Application US/10255032
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999 ACCTGGAGTAACAGG 1013
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                                                      23 Accredadeaceace 9
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US-09-951-121A-9
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LENGTH: 36
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APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OTHER OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ETHE REPERENCE: AECMICA.X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT TILING DAFE: 2001-12-20
SUMPARENT FILLING DAFE: 2001-12-20
SUMPARENT FILLING DAFE: 2001-12-20
SUMPARENT FILLING DAFE: 2001-12-20
SUMPARENT FILLING DAFE: 2001-12-20
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN DAGENY, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENY, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: MT HIT: 9114783796, EVALUE 1.00e-122
OTHER INFORMATION: EST HUMAN HIT: P08709, EVALUE 3.00e-26
US-10-029-386-23323
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APPLICANT: Olsen, Ole Hvilsted
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PA 2000
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER: OS SUPPLICATION NUMBER: 00/236,455
NUMBER: PERCISE 2000-09-29
NUMBER: PERCISE 2000-09-29
SOFTWARE: FREESEQ for Windows Version 4.0
SOFTWARE: PREESEQ for Windows Version 3.0
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39 CGAIGCCCGICAGGIACCACGIGCCCCGGIAGIGGGIG 2
                                                                                                                                            Sequence 23323, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                      RESULT 73
US-10-029-386-23323/c
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LENGTH: 222
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; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-9
                       GENERAL INFORMATION:
APPLICANT: NO. US20030100075A10 NO. US20030100075A1disk A/S
TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
FILE REFERENCE: 6357-WO
CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR FILING DATE: 201-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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0.3%; Score 11.8; DB 1; Length 36;
Best Local Similarity 86.7%; Pred. No. 4.8e+02;
Matches 13; Conservative 0; Mismatches 2; Indels
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Publication No US20030100740A1

GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Perseson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coequiation Factor VII Variants
FILE BEFRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682

CURRENT APPLICATION NUMBER: PA 2000 01361

PRIOR APPLICATION NUMBER: 60/236,455

PRIOR APPLICATION NUMBER: 60/236,455

PRIOR PILING DATE: 2000-09-13

PRIOR PILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FASELSEQ for Windows Version 4.0
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Publication No. US20030100740A1
GENERAL INFORMATION:
APPLICANT: Persson, Bgon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
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Publication No. US20030100075A1
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-10-295-682-8/c
                                                                                                                                                                                                                                                         SOFTWARE: Pace
SEQ ID NO 9
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LENGTH: 36
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## PROOF APPLICATION NUMBERS DA 2000 01361
## PRIOR APPLICATION NUMBERS 6026.455
## RIOR APPLICATION NUMBERS 6026.455
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## RIOR APPLICATION NUMBERS 6026.416.76 PB 1; Length 36;
## RIOR APPLICATION NUMBERS 6026.416.76 PB 1; Length 36;
## RIOR APPLICATION NUMBERS 6026.416.76 PB 2;
## RIOR APPLICATION NUMBERS 1030.00 PB 2;
## RIOR APPLICATION NUMBERS 1030.00 PB 2;
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## RIOR APPLICATION NUMBERS 1030.00 PB 2;
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## RIOR APPLICATION NUMBERS 1030.00 PB 2;
## RIOR
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10664775-2.rnpb

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RESULT 84
US-10-295-682-14
US-10-295-682-14, Application US/10295682
; Publication No. US20030100740A1
; GENERAL INFORMATION:
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                                                 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
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US-10-295-682-15/c
     US-09-951-121A-15
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Sequence 14, Application US/09951121A

Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Persson, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 624.200-03

CURRENT APPLICATION NUMBER: US/09/951,121A

CURRENT PILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 33
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Sequence 15, Application US/09951121A
Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Persson, Egon
ITILE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224-200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT APPLICATION NUMBER: US/09/951,121A
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILLING DATE: 2000-09-13
PRIOR PILLING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/236,455

PRIOR FILLING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 17

SOOFWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                Query Match 0.3%; Score 11.8; DB 1; Length 42; Best Local Similarity 69.6%; Pred. No. 5.4e+02; Matches 16; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%; Score 11.6; DB 1; Length 33; 77.8%; Pred. No. 5.5e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                1192 TGGAGAAGCTCTATACAGTCAGC 1214
                                                                                                                                                                                                                                                                                                                 38 TGGAGGAGCTCCGTCCCAGCAGC 16
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                            TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
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                                                                                             ; OTHER INFORMATION: Primer US-10-298-330-8
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LENGTH: 33
LENGTH: 42
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0.3%; Score 11.6; DB 1; Length 33; 77.8%; Pred. No. 5.5e+02; tive 0; Mismatches 4; Indels
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT APPLICATION NUMBER: DA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OLSEN, Ole Hvilsted
TITLE OLSEN, Ole Hvilsted
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTHARE: PERSERG for Windows Version 4.0
SEQ ID NO 14
LENGTH: 33
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US-10-295-682-15
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
PRIOR FILING DATE: 2005-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SIED NOS: 17
SOFTWARE: FASESO for Windows Version 4.0
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants;
FILE REFERENCE: 6224.200-US
CURRENT PEPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
FRIOR APPLICATION NUMBER: PA 2000 01361
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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; Sequence 14, Application US/09951121A
; Publication No. US20030104978A1
; GENERAL INFORMATION:
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2658 GGATGGCATCACTGACTC 2675
                                         25 GGATGGCGGCAAGGACTC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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CTHER INFORMATION: Synthetic
US-09-951-121A-14
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Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Person. Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT FILING DATE: 2002-11-15
CURRENT FILING DATE: 2002-11-15
PRIOR PPLICATION NUMBER: OS/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15
RESULT 88
US-10-25-682-14/C
| US-10-25-682-14/C
| Sequence 14, Application US/10295682|
| Publication No. US2033100740A1|
| GENERAL INFORMATION:
| APPLICANT: Person. Egon | APPLICANT: Olsen, Ole Hvilsted |
| TITLE OF INVENTION: Human Coagulation Factor VII Variants |
| TITLE OF INVENTION: Human Coagulation Factor VII Variants |
| FILE REPERENCE: 6224.200-US |
| CURRENT APPLICATION NUMBER: US/10/295,682 |
| CURRENT FILING DATE: 2000-09-13 |
| PRIOR FILING DATE: 2000-09-13 |
| PRIOR FILING DATE: 2000-09-13 |
| PRIOR FILING DATE: 2000-09-13 |
| PRIOR FILING DATE: 2000-09-13 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTHARE: PastSEQ for Windows Version 4.0 |
| SED ID NO 14 |
| LENGTH: 33
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0.3%; Score 11.4; DB 1; Length 33;
Best Local Similarity 62.1%; Pred. No. 6.7+02;
Matches 18; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 0.3%; Score 11.4; DB 1; Length 33; Local Similarity 62.1%; Pred. No. 6.7e+02; ls Conservative 0; Mismatches 11; Indels
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic US-10-295-682-14
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US-10-349-858-8/C
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; Sequence 8, Application US/10349858 ; Publication No. US20030220247A1

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10664775-2.rnpb

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0.3%; Score 11.2; DB 1; Length 32;
66.7%; Pred. No. 7.8e+02;
tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.3%; Score 11; DB 1; Length 35; Best Local Similarity 63.0%; Pred. No. 9.4e+02; Matches 17; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Persson, Egon
TITLE OF INVEXTION: Coaquiation Factor VII Derivatives
TILE SERENCE: 6286.200-US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
FRIOR APPLICATION NUMBER: 60/281,261
PRIOR PRIJING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
NUMBER: FASTER OF SEQ ID NOS: 20
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Persen, Egon
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286.200-US
CURRENT APPLICATION WHORER: US/10/109,498
PRIOR APPLICATION NUMBER: 60/281,261
               TITLE OF INVENTION: Human Coagulation Factor VII TITLE OF INVENTION: Human Coagulation Factor VII TITLE OF INVENTION: Polypeptides FILE REFERENCE: 6410.200-0.8 FILE REFERENCE: 6410.200-0.8 FILE REPRICATION NUMBER: PA 2001 01627 PRIOR APPLICATION NUMBER: PA 2001 01627 PRIOR PILING DATE: 2001-11-0.9 PRIOR FILING DATE: 2001-11-15 NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastERQ for Windows Version 4.0 SOFTWARE: FastERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2625 GAGGAGAGGGACGACAGAGGATGAG 2651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 93
US-10-109-498-5/c
; Sequence 5, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
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Olsen, Ole Hvilsted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.74
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-109-498-6
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       YPE: DNA
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                                                                     APPLICANT: CAMERE, RODNEY M.
APPLICANT: LARGON, PETER J.
APPLICANT: LARGON, PETER J.
APPLICANT: LARGON, PETER J.
APPLICANT: STAFFORD, DARREL W.
TITLE OF INVENITON: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT C
TITLE OF INVENITON: PACTORS
CURRENT APPLICATION NUMBER: US/10/349,858
CURRENT APPLICATION NUMBER: 09/226,947
PRIOR APPLICATION NUMBER: 00/226,947
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 22
SUFTHARE: PALENTIN VETER OF 3.1
SEQ ID NO 8
LENGTH: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32;
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US-10-281-727-6
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: BA 2001 01627
PRIOR PILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR PILING DATE: 2001-11-15
SROTWARE OF SEQ ID NOS: 7
SOFTWARE FASTSEQ for Windows Version 4.0
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                        APPLICANT: The Children's Hospital of Philadelphia APPLICANT: HIGH, KATHERINE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

0.3%; Score 11.2; DB 1;
Best Local Similarity 66.7%; Pred. No. 7.88+02;
Matches 16; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2598 CCTGATGCTGGGAGGGATTGGGGG 2621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown
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US-10-281-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-349-858-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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Sequence 23, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INPORMATION:
    APPLICATY: Braun et al.
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
    TITLE OF INVENTION: GENETIC MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Braun et al. THE DES FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POUR PLEADE OF INVENTION: METHODS FOR GENERAL TITLE OF INVENTION: METHODS FOR GENERAL FILLS REFERENCE: 24736-2033D FILLS REFERENCE: 24736-2033D CURRENT APPLICATION NUMBER: US/10/273,228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 CCAAGTAAGATGGTAGGTGTTGTGAGAGGGCATCAGAGGGCAG 158
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PRICR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRANKER: FRA
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CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT FILIMG DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR PILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PILING DATE: 2000-07-10

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; Publication No. US20030207297A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapien
US-10-272-756-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapien
US-10-273-321-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-272-756-23
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US-10-273-228-23
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Sequence 23, Application US/10272665

Publication No. US2030180748A1

GENERAL INPORMATION:

TILLE OF UNENTION:

FILLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TILLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TILLE OF INVENTION: MURBER: US/10/272,665

FILLE REFERENCE: 24736-2038

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

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Publication No. US20030180749A1
Publication No. US20030180749A1
Publication No. US20030180749A1
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTION OF INVENTION: GENERAL MARKERS
FILE OF INVENTION: 24736-2033B
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
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PRIOR FILING DATE: 2001-04-03
PRIOR: APPLICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NOS: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Nucleotide Primer US-10-109-498-6
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Publication No. US20030100075A1
Publication No. US20030100075A1
ABRIRAL INFORMATION:
APPLICANT: NO. US20030100075A1O NO. US20030100075A1disk A/S
TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
FILE REPERENCE: 6357-WO
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR FILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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Pred. No. 1.38+03;
0; Mismatches 11; Indels
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Pred. No. 1.3e+03;
0; Mismatches 11;
CURKENT FILING DATE: 2001-09-13
PRIOR PRIOR PAPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 36
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic US-09-951-121A-9
                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic US-09-951-121A-8
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US-10-255-032-8
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Sequence 8, Application US/10349858

Publication No. US2003022024A1

GENERAL INFORMATION:
APPLICANT: The Children's Hospital of Philadelphia
APPLICANT: THE CHILDRY M.
APPLICANT: CAMIRE, RODRY M.
APPLICANT: CAMIRE, RODRY M.
APPLICANT: STAFPORD, DARREL W.
TITLE OF INVENTION: ENFANCED GAWMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT CHRENT FILL OF INVENTION: ENFANCED GAWMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT CHRENT FILLING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR FILLING DATE: 2000-03-16
PRIOR FILLING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTY OF SEQ ID NOS: 22

SEQ ID NO 8

LUMBER OF SEQ ID NOS: 22

SEQ ID NO 8

LUMBER PATENTY OF SEQ ID NOS: 22

SEQ ID NO 8

LUMBER PATENTY OF SEQ ID NOS: 22

SEQ ID NO 8

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SEQ ID NOS: 22
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PSPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.3%; Score 11; DB 1;
Best Local Similarity 53.5%; Pred. No. 8.1e+02;
Matches 23; Conservative 0; Mismatches 20
                               PRIOR APPLICATION NUMBER: 09/687,463
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
SPRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
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                  2002-10-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-349-858-8
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Best Local Similarity
Matches 16; Conservat
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA CRGANISM: Homo sapien US-10-273-228-23
                  CURRENT FILING DATE:
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Sequence 2, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION:
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  Query Match
Best Local Similarity 60.7<sup>1</sup>
Matches 17; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                            US-10-295-682-9/c
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; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
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Sequence 9, Application US/10255032

Publication No. US20030100075A1

Publication No. US20030100075A1

PERERAL INFORMATION:

TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

FILE REFERENCE: 6357-WO

CURRENT PAPLICATION NUMBER: 2002-09-24

PRIOR APPLICATION NUMBER: DK FA 2001 01413

PRIOR APPLICATION NUMBER: DK FA 2001 01413

PRIOR FILING DATE: 2001-09-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1
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| Sequence 8, Application US/10295682
| Sequence 8, Application US/10295682
| Publication No. US20030100740A1
| GENERAL INFORMATION:
| APPLICANT: Person, Egon
| APPLICANT: Polsen, Ole Hvilsted
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| FILE REPRENCE: 624.200-US
| FILE REPRENCE: 624.200-US
| FILE REPRENCE: 2002-11-15
| PRIOR APPLICATION NUMBER: PA 2000 01361
| PRIOR APPLICATION NUMBER: EA 2000 01361
| PRIOR PILING DATE: 2000-09-13
| PRIOR PILING DATE: 2000-09-29
| NUMBER OF SEO ID NOS: 17
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 8
| LENGTH: 36
                                                                                                                                                                                                         Query Match 0.3%; Score 10.4; DB 1; Length 36; Best Local Similarity 60.7%; Pred. No. 1.3e+03; Matches 17; Conservative 0; Mismatches 11; Indels
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                                                   TYPB: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-255-032-9
  SEQ ID NO 8
LENGTH: 36
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; OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII
(S-10-281-727-2
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| Sequence 9, Application US/1025682
| Publication No. US20030100740A1
| GENERAL INFORMATION:
| APPLICANT: Person, Egon
| APPLICANT: Olsen, Bon
| TITLE OF INVENTION: Human Coagulation Factor VII Variants
| FILE REPRENT APPLICATION NUMBER: US/10/295,682
| CURRENT APPLICATION NUMBER: BA 2000 01361
| PRIOR APPLICATION NUMBER: PA 2000 01361
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-13
| PRIOR FILING DATE: 2000-09-29
| NUMBER OF SEQ ID NOS: 17 PARIOR PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAREST PAR
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          Length 36;
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0.3%; Score 10.4; DB 1; Length 36;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 16; Indels
                                                                                                                  11; Indels
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT FILING DATE: 2002-11-28
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 36
Score 10.4; DB 1;
Pred. No. 1.3e+03;
0; Mismatches 11;
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                                                                                                                                                                                                                         2341 GTCAAGGCTATGGTTTTTCCAGTGGTCA 2368
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US-10-281-727-3
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LENGTH: 36
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US-10-281-727-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII US-10-281-727-2
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                                                                                                                                                                                              Sequence 2, Application US/10281727
; Sequence 2, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL SEPERSON:
FILTE OF INVENTION:
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2001-11-02
; PRIOR PRILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; RENCETAL SECTION NOS: 7
; SEQ ID NO 2
; RENCETAL SECTION NOS: 7
; SEQ ID NO 2
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; Publication No. US20030130191A1
; Fublication No. US20030130191A1
; GENERAL INFORMATION:
    APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; FRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOUTWARE: FastSEQ for Windows Version 4.0
60 CIGCGCTITGCTGGAGCAGCCGTAAAGAGATACCCC 95
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ORGANISM: Unknown
                                                                                                                                                                                       US-10-281-727-2/c
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US-10-109-490-5

j Sequence 5, Application US/10109498

publication No. US20330044908A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

TITLE OF INVENTION: Coagulation Factor VI Derivatives

FILE REFERENCE: 6286.200-US

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR APPLICATION NUMBER: 9A 2001 00477

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 35
Sequence 3, Application US/10281727
Sequence 3, Application US/10281727
Sequence 3, Application US/10281727
Sequence 3, Application US/10281727
Septence 1 No. US20030130191A1
SEPTICANT: Perseon, Egon
APPLICANT: Perseon, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REPRESENCE: 4410.200-18
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR APPLICATION NUMBER: 2001-11-02
NUMBER: OF SEQ ID NOS: 7
SUPTWARE: FASTSEQ for Windows Version 4.0
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; OTHER INFORMATION: Nucleotide Primer
US-10-109-498-5
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US-10-109-498-6/c
; Sequence 6, Application US/10109498
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ORGANISM: Unknown
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| Sequence 2, Application US/0995121A
| Publication No US20030104978A1
| GENERAL INFORMATION:
| APPLICANT: Person, Egon
| TITLE OF INVERTION: Human Coagulation Factor VII Variants
| TITLE REFERENCE: 6224.200-US
| CURRENT APPLICATION NUMBER: US/09/951,121A
| CURRENT APPLICATION NUMBER: PA 2000 01361
| PRIOR APPLICATION NUMBER: E 000-09-13
| PRIOR APPLICATION NUMBER: 60/236,455
| PRIOR FILING DATE: 2000-09-29
| NUMBER OF SEQ ID NOS: 17
| SOOTHARE: FASTERQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.3%; Score 10; DB 1; Length 35; Best Local Similarity 61.5%; Pred. No. 1.46+03; Matches 16; Conservative 0; Mismatches 10; Indels
                                               TITLE OF INVESTION: Cogulation Factor VII Derivatives
FILE REFERENCE: 6286.200-US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 3, Application No. US20030104978A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Variants
; FILE REFERENCE: 6224.200-US
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Publication No. US20030044908A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), OTHER INFORMATION: Synthetic US-09-951-121A-2
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                            GENERAL INFORMATION:
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LENGTH: 34
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Publication No. US20030100740A1

GENERAL INFORMATION:

APPLICANT: Person. Egon

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/295,682

CURRENT PELING DATE: 2002-11-15

PRIOR FILING DATE: 2002-11-15

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 17

SOFFWARE: FastSEQ for Windows Version 4.0

LENGTH: 34
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| Sequence 3, Application US/10295682
| Publication No. US20030100740A1
| GENERAL INFORMATION:
| APPLICANT: Persenon, Egon
| APPLICANT: Olsen, Ole Hvilsted
| TITLE OF INVEXTION: Human Coagulation Factor VII Variants
| FILE REFERENCE: 6224.200-US
| CURRENT APPLICATION NUMBER: US/10/295,682
| CURRENT PILING DATE: 2002-11-15
| PRIOR PLILNG DATE: 2000-09-13
| PRIOR PLILNG DATE: 2000-09-13
| PRIOR PLILNG DATE: 2000-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.3%; Score 9.8; DB 1; Length 34; Best Local Similarity 84.6%; Pred. No. 1.5e+03; Matches 11; Conservative 0; Mismatches 2; Indels
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0.3%; Score 9.8; DB 1; Length 34;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
FRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
ELENGTH: 34
                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2200 TTTTGGGGGGCTC 2212
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                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 115
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT PELLOGATION NUMBER: US/09/951,121A
CURRENT FILING DATE: 2001-09-13
FRIOR APPLICATION NUMBER: PA 2000 01361
FRIOR FILING DATE: 2000-09-13
FRIOR FILING DATE: 2000-09-03
NUMBER OF SEQ ID NOS: 17
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO: 17
LENGTH: 34
                                                  0.2%; Score 8.8; DB 1; Length 32; 83.3%; Pred. No. 1.66+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: DNA primer for preparation of S314E-FVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

0.2%; Score 8.8; DB 1; Length 32;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Persson, Egon
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-06
FILE REPERSONCE: 6410.200-08
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT PILING DATE: 2002-10-28
FRIOR APPLICATION NUMBER: PA 2001 01627
FRIOR APPLICATION NUMBER: 60/335,383
FRIOR PILING DATE: 2001-11-02
FRIOR PILING DATE: 2001-11-15
NUMBER OF SEG ID NOS: 7
SOSTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09951121A, Publication No. US20030104978A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    RESULT 118
US-10-281-727-7
US-10-281-727-7
; Sequence 7, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
APPLICANT: Olsen, Ols Hvilsted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                    Query Match
Best Local Similarity 83.33
Matches 10; Conservative
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Best Local Similarity
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       US-10-281-727-6
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LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCCATCHY, Jeanette
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-007.
CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
LENGTH: 31
                                                                                                                                                                                                                                                                 Query Match 0.3%; Score 9.8; DB 1; Length 34; Best Local Similarity 84.6%; Pred. No. 1.5e+03; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.3%; Score 9.2; DB 1; Length 31; 78.6%; Pred. No. 1.6e+03; tive 0; Mismatches 3; Indels
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OTHER INFORMATION: DNA primer for preparation of S314E-FVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Person, Egon
; APPLICANT: Person, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REPRENCE: 6410-200-408
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-03
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SSCYTARE: FastSEQ for Windows Version 4.0
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10017122
Publication No. US20030087244A1
GENERAL INFORMATION:
                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                ; OTHER INFORMATION: Synthetic US-10-295-682-3
                                                                                                                                                                                                                                                                                                                                                                   2200 TTTTGGGGGGCTC 2212
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Best Local Similarity 78.68
Matches: 11; Conservative
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CORGANISM: Homo sapiens
US-10-017-122-4
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US-10-017-122-4
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LENGTH: 32
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Search completed: August 9, 2004, 16:36:07
Job time : 50 secs
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                                                                                                                                                                                                        Sequence 3, Application US/09951121A

publication No. US20030104978A1

GENERAL INNORMATION:
APPLICANT: Persson, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224. 200-US
CURRENT FILING DATE: 200-09-13
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 34
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TILE OF INVENTION: Human Coagulation Factor VII Variants
TILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: EA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PLILING DATE: 2000-09-13
PRIOR PLILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%; Score 8.6; DB 1; Length 34; Best Local Similarity 73.3%; Pred. No. 1.5e+03; Matches 11; Conservative 0; Mismatches 4; Indels
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0.2%; Score 8.6; DB 1; Length 34;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 4; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-295-682-2/c
; Sequence 2. Application US/10285682
; Publication No. US20030100740A1
; ENERAL INFORMATION:
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                                                246 CCCGTGGGCCAACCC 260
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                                                                                               33 cerridededeace 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-951-121A-3
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Matches 11; Conservative
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Sequence 3, Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

TITLE OF INVENTION: Human Cagulation Factor VII Variants

TILE REFERENCE: 6224.200-US

CURRENT APPLICATION NUMBER: US/10/295,682

CURRENT APPLICATION NUMBER: D02-11-15

PRIOR FILING DATE: 2002-11-15

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
0.2%; Score 8.6; DB 1; Length 34;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 CCCGTGGGCCAACCC 260
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OTHER INFORMATION: Synthetic
US-10-295-682-3
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RESULT 122
US-10-295-682-3
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GenCore version 5.1.6
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Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:
August 9, 2004, 16:36:28; Search time 5 Seconds
(without alignments)
3.936 Million cell updates/sec
Perfect score: 3572
Sequence:
1 gtcaggaaggcggcagtga......gcaacaacagcagaaagctt 3572
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters:

4 segs, 2755 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 250 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ACCESSION: AI099321 ACCESSION: AI116939 ACCESSION: AI099321 ACCESSION: AL531727 ACCESSION: AU099140 ACCESSION: AI116939 ACCESSION: AU099140 ACCESSION: AL531727 Description SUMMARIES AI099321 AI116939 AI116939 AU099140 AI099321 AL531727 AU099140 AL531727 ü Query Match Length DB 000000 23.2 21 21 18.4 18.4 17.4 17.2 Score . 8 Result 400000

## ALIGNMENTS

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		mRNA linear EST 23-MAY-2003	clone							Euteleostomi	; Homo.					2795220.				
		linear	sapiens cDNA							Vertebrata;	i; Hominidae		es, D.	ation		eplaced gi:13		ge		
			Ношо	ce.						niata;	arrhin		Polay	rmaliz		sion r		quenca		
		1201 bp	LIVER	seguen	ı					a; Cra	s; Cat		J. and	and no		ice ver		de Se	rance	
		120	FETAL	mRNA		529				hordat	Primate		Jessee,	aries		seguen		tional	lex - F	
		27	AL531727 Homo sapiens FETAL LIVER Homo sapiens cDNA clone	CS0DM003YI01 5-PRIME, mRNA sequence.	27	AL531727.2 GI:31069559		Homo sapiens (human)	Homo sapiens	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1201)	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	ength cDNA libz	Unpublished (2001)	On Feb 13, 2001 this sequence version replaced gi:12795220.	Contact: Genoscope	Genoscope - Centre National de Sequencage	BP 191 91006 EVRY cedex - France	
		AL531727	AL5317	CSODMO	AL531727	AL5317	ESI.	ношо в	Ношо в	Eukary	Mammal	.1 (pa	Li, W.B	Full-1	Unpubl	On Feb	Contac	Genosc	BP 191	
RESULT 1	AL531727/c	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT				

/organism="Mus musculus"

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1201 CCTTRARRWYCTTTTCCWTCRAWWACCGMAAAAATTTWTCCTDWWTTTGGGATTYCCC 1142
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,R., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                     /clone="CSODMOSYIO1"

/tissue_type="FETAL LIVER"

/dev stage="FETAL LIVER"

/dev stage="fetal"

/clone_lib="Home sapiens FETAL LIVER"

/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo (dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Nus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7252.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODW003AE01QP1&cluster=7252.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODM003AE01QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
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40.0%; Pred. No. 0.17;
tive 17; Mismatches 37;
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                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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High quality sequence stop: 289.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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Best Local Similarity 48.77
Matches 57; Conservative
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                                                                                                                                           / dev stage="adult"
/lab_nost="bulble"
/lab_nost="bulble"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTOTOTO); Site_2: DraIII (CACCATOTO); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (s' site CACTGTGT), 3' site CACATGTG]. XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGATAAAGCTGCG and 3' end
primer CGACTGCAGGCACA."
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Marra, M., Hilier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Unpublished (1996)
Contact: Marrah M/Mouse EST Project
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/mol_type="mRNA"
/strain="C57BL"
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High quality sequence stop: 483.
Location/Qualifiers
db xref="taxon:10090"
clone="IMAGE:1482509"
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AI116939.1 GI:3517263
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/dev_stage="adult"
/lab_host="bullob"
/cone_lib="Sugano mouse liver mlia"
/clone_lib="Sugano mouse liver; pMB185-F13; Site_l: DraIII
/chote="Organ: liver; Vector: pMB185-F13; Site_l: Brand cDNA
was primed with an oligo(dT) primer forCAGTGTGTG; Site_sib="adultob"
/ATGGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTAGTGG], digested
and cloned into distinct DraIII sites of the pWE185-F13
vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kD. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1450 GAGACCATCCCCATGGAAAAAAATGCAAAAAAGCAAAATGGCTGTCTGGGGAGGCC 1506
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Unpublished (1996)
Contact: Marram M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Final: mousesetSewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 rescecescreres de asas de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de reservados de 
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Location/Qualifiers
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/clone="IMAGE:1482509"
/clone="IMAGE:1481822"
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/strain="C57BL"
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AI099321.1 GI:3448846
                                                                                   sex="female"
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699

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vector. Library was not normalized."
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                                      0.5%;
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AII16939.1 GI:3517263
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                                                                                   Conservative
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36; Conservative
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Homo sapiens
                                                          Similarity
                                        Local S. 34;
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                                                               /CIOTE="Organ: liver; Vector: pWE185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pWE185-FL3
vector (5' site CACTGTGT, 3' site CACCATGTG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7252.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-c50DW003AE01QP1&cluster=7252.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODW003AE01QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL531727 AL00 Sapiens FETAL LIVER Homo Sapiens CDNA clone CSODM003XI01 5-PRIME, MRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           799 GACAGAATGATCTCTGTTTGCAAGGCAAACCATTCAATATCACAGTAATCCAAGTC 858
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/note="Organ: liver; Vector: pCWNSPORT 6; 1st strand cDNA
was primed with a NotI-ollgo(dT) primer: Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12795220.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 CCGACCTCAAAGTCTAGGAGGCAGAAGCAGACGTAAGAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859 TATGCCCCAACCAGTAATGCTGAAGAAGCTGAAGTTGAAC 898
                                                      clone_lib="Sugano mouse liver mlia"
                                                                                                                                                                                                                                                                                                                                                                          Score 18.4; DB
Pred. No. 4;
0; Mismatches
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mol_type="mRNA"
/db_xref="taxon:960s"
/dlone="CSODMO03YIO1"
/tissue_type="FETAL LIVER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dev_stage="fetal"
             'dev_stage="adult"
'lab_host="DH10B"
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AL531727.2 GI:31069559
                                                                                                                                                                                                                                                                                                                                                                          0.5%;
illarity 49.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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AL531727
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AU099140 AU099140 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone HEP20593 similar to Human factor VII serine protease precursor mRNA AU099140
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Unpublished (2001)
Context: Yutaka Suzuki
Department of Vivology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzukieina.u-tokyo.ac.jp
Suzuki,Y., Yoshiromo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                 1445 GGATCGAGACCATCCCCATGGAAAAGAAATGCCAAAAAAGCAAAATGGCTGTCTGGGGAGG 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI116939
452908.YI Sugano mouse liver mlia Mus musculus cDNA clone
10029908.YI Sugano mouse liver mlia Mus musculus cDNA clone
100268.1481822 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN); mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 AGTAATGCTGAAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAA 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
                                                                                                                                                                            610 GGAAAATACCTATTCTAGAAAAAAAAGCCCAGCAAACCCCCAAGGCCGAATTGTGGGG
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0
   Length 1201;
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/db_xref="texaon:9606"
/dbo="HEP20983"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 300;
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                                                          26;
   DB 1;
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53.7%; Pred. No. 12,
... 0; Mismatches
                                                          0; Mismatches
Score 18.4;
Pred. No. 2;
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Search completed: August
Job time : 6 secs .
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/lab host="adult"
/lab host="bllow"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver mlia"
/clone lib="Sugano mouse liver; bkEl85-FL3; Site_1: DraIII
/note="Organ: liver; Vector: pkEl85-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTATTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], diggested
and cloned into distinct DraIII sites of the pMEl85-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG), XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers
sequencing: 5' end primer CTTCTGATAAAGCTGCG and 3' end
primer CGACCTGCAGGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU099140
AU099140 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP20983 similar to Human factor VII serine protease precursor mRNA
Clone lambda-HVII2463, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 645)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R., and
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Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 Los 300)

(bases 1 Los 300)

Makamura,Y., Morishita,S.,
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S.,
Okubo,K., Suyama,A. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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0
                                                                                                                                                                                                                                                                     Unpublished (1996)
Contact: Marra MyNouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1233 TTACTGTGGCTCAGATCATGAACTCCTTATTGCCAAATTCAGACTT 1278
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                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
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High quality sequence stop: 483.
Location/Qualifiers
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/strain="C57BL"
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AUTHORS
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                                                                                                    AUTHORS
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In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by Oligo-capping method
Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Indels
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                                                                                                                                                                                                                                                                                                                                                               1. .300
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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/clone="HEP20983"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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9, 2004, 16:36:34

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

August 9, 2004, 15:28:50; Search time 13 Seconds (without alignments) 3.853 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

Title: us-10-664-775-1 Perfect score: 2715 Sequence: 1 ctgcaggaagaggcgacagg......ttgtaattctaggtgctgat 2715

IDENTITY_NUC Gapop 10.0 , Gapext 0.5 Scoring table:

20 seqs, 9225 residues Searched: Total number of hits satisfying chosen parameters:

40

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 250 summaries

rnidb:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 3, Appli	equence 3,	equence 3,	equence 13,	equence 13,	m	m	m	'n,	m i	Ę	'n	-	ý	ý,	4,	52	ຕັ	7	ω,	9			,	7	20	13	σ	10	16	e 22	equence 20	Sequence 7, Appli
SOMMERIES	ΩI	-07-882-202	-08-021-615A	-08-321-777	US-09-009-217-13	-09-009-656-1	L-US93-04493-	37-882	21-615A-	-08-321-777-3	-009-217-1	-969-600-	893-04493-	-558-027-	-08-849-248-	-08-849-	-09-558-027-4	-08-293-778-2	-08-756-5	-08-293-778-1	08-955-636-8	-08-293-7	-07-998-972A-	-08-463-9	18-462-261-7	.US92-11	18-293-778-2	18-756-506-1	08-922-636-9	8-955-636-1	18-293-778-1	8-293-778-	-08-293-778-2	Ł
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## ALIGNMENTS

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12.202A-3/C nce 3, Application E No. 5374617 E No. 5374617 E No. 5374617 EL ON CONTERNATION: FLICANT: Comp, PP TILE OF INVENTION: TILE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF INVENTION: THE OF	Similarity	TCAAT    -  TTGCT
12.202A-3/c nce 3, Applis, E No. 5374617 RAL INFORMATI PHICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PLICANT: Con PL	ເ ທທ	876 T 659 T
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Tissue Factor in Combination with FVIIa
                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSES: Richards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
CITY: Texas
COUNTRY: US
ZIP: 75270-2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMRF B34290C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-009-217-13/c
; Sequence 13, Application US/09009217
; Patent No. 6132729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFRENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SADI
TISSUE TYPE: Blood
  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
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                                   Sequence 3, Application US/08021615A

Sequence 3, Application US/08021615A

BAFELTON SSOGNER

APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.

TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: FVII

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Richards, Medlock & Andrews

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                              STATE: 150...
COUNTRY: US
ZIP: 75270-2197
ZIP: 75270-2197
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
-TUING DATE: 19-FEB-1993
-TUING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hansen, Bugenia S.
REGISTRATION NUMBER: 31,966
REPERENCET NUMBER: OMF B34290CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882,202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 36..1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Homo sap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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ANTI-SENSE: N
                JS-08-021-615A-3/c
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US-08-321-777-3/c
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Sequence 3, Application US/08321777 Patent No. 5504067 GENERAL INFORMATION: APPLICANT: MOTTISSEY, James H.

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GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: Cao, Buning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHENOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     876 TICAAITGICTITIAICIGICGAGACTIGCITIGIITTGAAAIAIGIATICAAITTIGG 934
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0.8%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 3.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0
COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
CLASSIFICATION S14
PRIOR APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS

COCATION: 36.1433
COTHER INFORMATION: /note= "Coding portion of cother information: factor vii cDNA"
US-08-321-777-3
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876 INCAATHGICTITIAICIGICGAGACTIGCITIGITITGAAATALGIAITCAATTTIGG 934
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0.8%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 3.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0.
PRILING DATE: 27-MAR-1997
PRILING DATE: 27-MAR-1997
PRIOR APPLICATION NUMBER: 405 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION NUMBER: 405 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W. 41,071
REFERENCE/DOCKET NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 10750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/4/18-3000
TELEPAX: 512/4/19-377
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
TENDER THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN T
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STRANDEDNESS: sing
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0.8%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 3.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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PCT-US93-04493-3/C

Sequence 3, Application PC/TUS9304493

GENERAL INFORMATION:

APPLICANT: MORTISSEY, James H.

APPLICANT: Comp, Philip C.

TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or TITLE OF INVENTION: TVII Activator for Blood Coagulation NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500

CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Dallas
STATE: Texas
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 07/882202
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: TTUJILO, DOTEON Y.
REGISTRATION NUMBER: 05.6607
TEBECOMMUNICATION NUMBER: 05.6607
TEBECOMMUNICATION NUMBER: 05.6607
```

Sequence 13, Application US/09009656

Beneral Information:

APPLICANT: Thorpe, Philip E.

APPLICANT: Thorpe, Philip E.

APPLICANT: Gao, Boning

TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR

TITLE OF INVENTION: TREATMENT

TITLE OF INVENTION: TREATMENT

NUMBER OF SEQUENCES: 27

CADRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

E: Arnold, White & Durkee P.O. Box 4433

ADDAL.
STREET: F.C.
TTY: Houston

STATE: TEARS
COUNTRY: USA
STATE: TA1210
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: CONCURRENTLY Herewith
TOFFICATION:
TOFFICATION:
TOFFICATION:
TOFFICATION DATA:

659 TITGCIGGCALITICTITITICIAGAATAGGTAITTITICCACATGGATAITCAACTGIGG 601

RESULT 5 US-09-009-656-13/c

10664775-1.rni

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COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL'SOURCE:
ORGANISM: HOMO SEN'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Blood
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Texas
                                                                                                                                                                                                                                                                                                                   US-08-021-615A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-021-615A-3
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                                                                                                                                                                                                                                                   /product= "Tissue Factor"
/note= "Coding portion of human factor VIII cDNA"
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                           876 ITCAATIGICITITAICIGICGAGACTIGCITIGITITGAAATATGIATICAATITIGG
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                                                                                                                                                                                                                                                                                                                                                       Query Match

0.8%; Score 20.6; DB 1; Length 1440;
Best Local Similarity 59.3%; Pred. No. 3.3;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip.
TITLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCE: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Texas
COUNTRY: US
ZIP: 75270-197
ZIP: 75270-197
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,202A
FILING DATE: 13-MAY-1992
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMRF B34290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/07882202A Patent No. 5374617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION UNTHER: 31,966
REFRENCE/DOCKET NUTHER: OMF
TELECOMMUNICATION INFORMATION:
TELEPAN: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                  ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 36.1433
; CTHER INFORMATION: /
; CTHER INFORMATION: /
; OTHER INFORMATION: /
                                                           MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sap
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                  ORGANISM:
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Sequence 3, Application US/08021615A
Sequence 3, Application US/08021615A
GENERAL INFORMATION:
APPLICANT: MORTISSEY, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of TITLE OF INVENTION: FVII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Richards, Medlock & Andrews
STREET: 1201 Blm Street, Suite 4500
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   ó.
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                                                                                                                                                                         Query Match 0.8%; Score 20.4; DB 1; Length 1440; Best Local Similarity 65.2%; Pred. No. 4.3; Matches 30; Conservative 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

0.8%; Score 20.4; DB 1; Length 1440;
Best Local Similarity 65.2%; Pred. No. 4.3;
Matches 30; Conservative 0; Mismatches 16; Indels 0
                                                                                                                                                                                                                                                                                      374 ACAGGCATGGCCATGGCTCCAGAGATTGCCTCTTCCAGGTGCAGGC 419
                                                                                                                                                                                                                                                                                                                                          4 ACAGGCAGGCAGCACTGCAGAGATTTCATCATGGTCTCCCAGGC 49
, LOCATION: 36..1433
; OTHER INFORMATION: /note= "Coding portion of human
; OTHER INFORMATION: factor VII cDNA"
US-07-882-202A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/682,202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEPHONE: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: MOLEIC acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 36..1433
LOCATION: 36..1433
LOTHER INFORMATION: factor VII cDNA"
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Gaps

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GENERAL INFORMATION:
                                                                                                                                                                                   RESULT 9
US-08-321-777-3
Sequence 3, Application US/08321777
Patent No. 5504067
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp. Philip C.
TITLE OF INVENTION: Tissue Factor in Combination with FVIIa
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
0.8%; Score 20.4; DB 1; Length 1440;
Best Local Similarity 65.2%; Pred. No. 4.3;
Matches 30; Conservative 0; Mismatches 16; Indels 0
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            374 ACAGGCATGGCCATGGCTCCAGAATTGCCTCTTCCAGGTGCAGGC 419
                                                                4 ACAGGCAGGCAGCACTGCAGAGATTTCATCATGGTCTCCCAGGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Texas
COUNTRY: US
ZIP: 7520-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BENEVICATION
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE: 07/882202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Bugenia S.
REGISTRATION NUMBER: 31,966
REBERNCE/COKET NUMBER: 31,966
REGISTRATION NUMBER: 31,966
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REGISTRATICATION
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NAME/KEY: CDS

LOCATION: 36.1433

OTHER INFORMATION: /note= "Coding portion of human orther information: factor VII cDNA"
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US-09-009-217-13
; Sequence 13, Application US/09009217
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
APPLICANT: King, Steven W.
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERABUTIC METHODS AND COMPOSITIONS FOR COAGULATION
TITLE OF INVENTION: AND TUMOR TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON
STREET: USA
CITY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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US-09-009-656-13
Squence 13, Application US/09009656
SGUERCAL INFORMATION:
Patent No. 6132730
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Gao, Boning
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
NUMBER OF SEQUENCES: 27
SORRESPONDENCE ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ACAGGCAGGGGACTCCAGGATTTCATCATGGTCTCCCAGGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 ACAGGCATGGCCATGGCTCCAGAGATTGCCTCTTCCAGGTGCAGGC
                                                                                                                                                                                                                                                                      ATTOKNET, MESCHALLOW,
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/414-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 144 0 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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4 ACAGGCAGGGCAGCACTGCAGAGATTTCATCATGGTCTCCCAGGC 49

PCT-US93-04493-3
; Sequence 3, Application PC/TUS9304493
; GENERAL INFORMATION:
 APPLICANT: Comp, Philip C.
 ITTLE OF INVENTION: Truncated Tissue Factor and FVIIa or TITLE OF INVENTION: FVII Activator for Blood Coagulation NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS: SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930512
CLASIFICATION:
PRICH APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: ADDRESSE: Lichards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500 CITY: Dallas STATE: Texas COMPUTER READABLE EORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: US ZIP: 75270-2197

LOCATION: 36..1433
OTHER INFORMATION: /product= "Tissue Factor"
OTHER INFORMATION: /note= "Coding portion of human factor VIII cDNA"
OTHER INFORMATION: /citation= ([1]) PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTONEX/AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35, 719
REFERRATION INFORMATION:
TELEPHONE: 214-939-4500 TELEFAX: 214-939-4600 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: 13-MAY-1992 LENGTH: 1440 base pairs TYPE: NUCLEIC ACID ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Homo sapiens TISSUE TYPE: Blood TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO NAME/KEY: CDS LOCATION: 36.

Gaps ., 0 Query Match
Ousting 65.2%; Score 20.4; DB 1; Length 1440;
Best Local Similarity 65.2%; Pred. No. 4.3;
Matches 30; Conservative 0; Mismatches 16; Indels 0 374 ACAGGCATGGCCATGGCTCCAGAGATTGCCTCTTCCAGGTGCAGGC 419 PCT-US93-04493-3 ઠે

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Gaps

Indels

16;

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4 ACAGGCAGGGCACACTGCAGAGATTTCATCATGGTCTCCCAGGC 49 Sequence 4, Application US/09558027

Patent No. 6329176

GRUERAL INFORMATION:
GRUERAL INFORMATION:
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Nielsen, Lare
TITLE REFERENCE: 5565.204-US
CURRENT APPLICATION NUMBER: 05/09/558,027
CURRENT FILING DATE: 1998-11-12

PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 38 RESULT 13 US-09-558-027-4

; ORGANISM: Saccharomyces cerevisiae US-09-558-027-4 TYPE: DNA

0.5%; Score 14.2; DB 1; Length 38; 70.4%; Pred. No. 1.1; Indels 0; Mismatches 434 GGTGATCACTCCTCTAGTGAAAGGTGG 460 3 deantreactracteracedaategee 29 Query Match Best Local Similarity 70.4% Matches 19; Conservative

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Gaps

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RESULT 14 US-08-849-248-6

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GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Wicolaisen, Else M.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55005600 No. 5580560th America, Inc.
STREE: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
AMERICAN FRADABLE FORM:
MEDIUM TYPES: Floppy disk
COMFUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
COMFUTER: IBM PC Compatible
COMFUTER: IBM PC Compatible
COMFUTER: IBM PC Compatible
COMFUTER: BEADABLE FORM:
MEDIUM TYPES
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
                                                                                                                                                                 Query Match
0.5%; Score 12.8; DB 1; Length 141;
Best Local Similarity 70.8%; Pred. No. 1.38+02;
Matches 17; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 12; DB 1; Length 38; 75.0%; Pred. No. 34; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Woldike, Helle, APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Wiberg, Finn
APPLICANT: Nielsen, Lars
TITLE OF INVENTION: Method for the Production of FVII
FILE REFERENCE: 5565.204-US
CURRENT APPLICATION NUMBER: US/09/558,027
CURRENT FILING DATE: 2000-04-25
PRIOR FILING DATE: 1998-11-12
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 38
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant DNA"
                                                                                                                                                                                                                                                                                             583 TCTGCTGGCAATACTTCTGGGGCT 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 25 rcaecreercarchrerecercr 2
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Patent No. 5580560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-558-027-4
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
US-09-558-027-4/c
; Sequence 4, Application US/09558027
; Patent No. 6329176
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-08-293-778-22
                                                                                                   ; DESCRIFIL
US-08-849-248-6
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                                                                                GENERAL INFORMATION:
APPLICANT: Husbyn, Mette
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
TITLE OF INVENTION: in blood clotting disorders
TITLE OF INVENTION: in blood clotting disorders
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STATE: Virginia
COMPUTRY: USA
ZIP: 22314
COMPUTRY: ISW PC compatible
COMPUTRY: ISW PC compatible
COMPUTRY: ISW PC compatible
COMPUTRY: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: AND DATA:
APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
LENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
TYPE: MUCLEIC CHARACTERISTICS:
TENGTH: 141 base pairs
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0.5%; Score 12.8; DB 1; Length 141;
Best Local Similarity 70.8%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 12231 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN RElease #1.0, Version #1.30 (BPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,248
FILING DATE: 27 Aug 1997
INFORMATION FOR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-849-248-6/c
iS-08-849-248-6/c
; Sequence 6, Application US/08849248
; Patent No. 5948759
; GENERAL INFORMATION:
APPLICANT: Husbyn, Mette
APPLICANT: Fischer, Peter
APPLICANT: Fischer, Peter
APPLICANT: Orning, Lars
TITLE OF INVENTION: in blood clotting disorders
; TUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Bacon and Thomas
STREET: 625 Slaters Lane, 4th Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GCACTGGGATGTTCAGATGTTCAG 105
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         6, Application US/08849248
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
               Sequence 6, Applicatic
Patent No. 5948759
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-849-248-6
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Sequence 17, Application US/08293778
Patent No. 5580560
GENERAL INFORMATION:
APPLICANT: Nicolaisen, Else M.
APPLICANT: Nicolaisen, Else M.
APPLICANT: Miberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADRESS:
ADDRESSEE: ADRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York.
                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 11.8; DB 1; Length 45; Best Local Similarity 56.4%; Pred. No. 76; Matches 22; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 408 CCAGGTGCAGGCCATGGCTCTGGTGATCACTCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
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FILING DATE: 25-JUN-1987
PRIOR APPLICATION DATA: 25-JUN-1987
PRIOR APPLICATION DATA: US 07/434,149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: POT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA: POT/DK88/00103
FILING DATE: 12-JUN-1982
ATTONEY/AGENT INFORMATION:
NAME: AGRISPA, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: DK 3235/87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of Americ
ZIP: 10174-6201
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 45 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SORRCE:
          TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-293-778-17/c
                                                                                                                                                                                                                                                                             US-08-756-506-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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APPLICANT: Garner, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Spredher, Cindy A.
APPLICANT: Prunkard, Donala E.
IITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREFT: Zymocar-
STREFT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

ZIP: 99102

COMPUTER READABLE FORM:
MEDLUM TYPE: FLOPPY disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/756,506
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SAWASIAK, Deborah A
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.8; DB
Pred. No. 15;
0; Mismatches
                                                                 PELLING DATE: 25-JUN-1987
FILING DATE: 25-JUN-1987
RICHARION DATE: 25-JUN-1987
APPLICATION DATE: 48-149
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION NUMBER: US 07/898,248
FILING DATE: 24-JUN-1988
RICHING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1988
FILING DATE: 12-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                     NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 26 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 GAGCAGGCAGGAAG 308
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US-08-756-506-13/c
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APPLICATION DUMBER: DK 3235/87
FILING DATE:
PRING DATE: 25-JUN-1987
PRIOR APPLICATION DATA: 07/434,149
FILING DATE: 13-NOV-1989
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA: PCT/DK88/00103
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 24-JUN-1988
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELEFRANCE/DOCKET NUMBER: 3129.224-US
TELEFRANCE/DOCKET NUMBER: 3129.224-US
TELEFRANCE/DOCKET NUMBER: 312867-0123
TELEFRAX: 212-867-0123
TELEFRAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 16:
FENGTH: 27 base pairs
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STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTRY: United States of America
ADDIUM TYPE: Floppy disk
COMPUTR: IBM PC compatible
COMPUTR: IBM PC compatible
COMPUTR: READABLE FORM: PC-DOS/MS-DOS
COMPUTR: PROMPUTR: PC-DOS/MS-DOS
COMPUTR: PROMPUTR: PC-DOS/MS-DOS
COMPUTR: PC-DOS/MS-DOS
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                                                                                                                                                     Query Match 0.4%; Score 11.2; DB 1; Length 27; Best Local Similarity 81.2%; Pred. No. 42; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 11.2; DB 1; Length 42; Best Local Similarity 59.4%; Pred. No. 1.40+02; Matches 19; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
COGANISM: Artificial Sequence
FEATURE:
COMPARE INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 8
ELENGTH: 42
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US-08-293-778-16
Squence 16, Application US/08293778
Squence 16, Application US/08293778
Spatent No. 5580560
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E.
APPLICANT: Wicolarey, Finn C.
APPLICANT: Woodbury, Richard
ITILE OF INVENTION: MODIFIED FACTOR VII/VIIa
CONTRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 CACTCCTCCAGGAGCAGGCAGGGAAGAGCCTC 314
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US-08-955-636-8
; Sequence 8, Application US/08955636A
; Patent No. 6017882
                                                                                                                                                                                                                                                               2224 GCTTCCTGGATGTTT 2239
                                                                                                                                                                                                                                                                                                                  23 GCGTCCTGGAAGATTT B
TYPE: nucleic acid
STRANDEDNESS: sing
                                             TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-293-778-17
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US/08/104,509

APPLICATION NUMBER:

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100.0%; Pred. No. 57;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              VS-07-996-972A-7/c

Sequence 7, Application US/07998972A

Sequence 7, Application US/07998972A

Patent NO. S476777

GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Tome Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco

STATE: CA
STATE: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE: PALOS
COMPUTE: PALOS
COMPUTE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-WAR-1992
PRIOR APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-WAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                 2523 TCTTCAAGGAC 2533
                                                                                                                                                                                                               11; Conservative
                                                                                                                                                                                                                                                                                                                11 rcrrcaaddac 21
TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                           Query Match
Best Local Similarity
                                                    , TOPOLOGY: lir
, MOLECULE TYPE:
US-08-293-778-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 94105
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                                                                                                                                                                                                              Sequence 7, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
FAPLICANT: FOSTER, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Townsend STREET: Townsend and Townsend STREET: Twentieth Floor
STREET: Twentieth Floor
STREET: Wentieth Floor
STREET: Usan Francisco
STATE: CAUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIDLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/462,261 FILING DATE: 05-UW-1995 CLASSIFICATION: 424
           Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION 1973

APPLICATION NUMBER: US 07/998,972
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US92-11357-7/c; Sequence 7, Application PC/TUS9211357; GENERAL INFORMATION:
      ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; P
Matches 11; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET UNBER: 13;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                        285 CTCCTCCAGGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 CTCCTCCAGGA 295
                                                                                                                 33 crccrccadda 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 CTCCTCCAGGA 23
      Best Local Similarity
Matches 11; Conserve
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USA
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                                                                                                                                                                                                                                                                                                              0.4%; Score 11; DB 1; Length 35; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08463953
| Patent No. 5502034
| GENERAL INFORMATION:
| APPLICANT: HOLLY, Richard D. APPLICANT: HOLLY, Richard D. APPLICANT: Foster, Donald C. TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
| CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor STATE: CA. STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
RECISTRATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
RECISTRATION NUMBER: 31,990
TELEPHONE: 206-467-9600
REFERENCE/DOCKET NUMBER: 1399:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERIS: LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   285 CTCCTCCAGGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                             33 crecrecedes 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                TOPOLOGY: linear;
IMMEDIATE SOURCE:
CLONE: ZC1324
US-07-998-972A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: ZC1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-463-953-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-463-953-7
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Holly, Richard D

Query Match

Mon Aug

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RESULT 27
US-08-756-13

Sequence 13, Application US/08756506

Sequence 13, Application US/08756506

Setuence 13, Application US/08756506

BENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Temperley, Simon M.
APPLICANT: Sprecher, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna B.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10.6; DB 1; Length 27;
Pred. No. 1e+02;
0; Mismatches 9; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
FILING DATE:
CLASSIFICATION NUMBER: US/08/104,509
FILING DATE:
APPLICATION NUMBER: US/08/104,509
FILING DATE: 25-UN 1987
PRICH APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-00/-1989
PRICH APPLICATION NUMBER: US 07/434,149
FILING DATE: 13-00/-1989
PRICH APPLICATION NUMBER: US 07/698,248
FILING DATE: 24-UN-1988
PRICH APPLICATION NUMBER: US 07/698,248
FILING DATE: 24-UN-1988
PRICH APPLICATION NUMBER: US 07/698,248
FILING DATE: 24-UN-198
PRICH APPLICATION NUMBER: 3129.224-US
FILING DATE: 12-2010-199
PRICH APPLICATION NUMBER: 3129.224-US
FILING DATE: 212-867-0238
TELEPHONE: 212-867-0238
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTER STICS:
LENGTH: 27 base pairs
word: Name: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTR: USA
ZIF: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GGAAGAGGCGACAGGGGACAGCGGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 GGCCGTGGCGCCCAGGTCCAGCAGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-293-778-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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Sequence 20, Application US/08293778

Patent No. 5580560

GENERAL INFORMATION:
MAPPLICANT: Nicolaisen, Else M.
APPLICANT: Miberg, Finn C.
APPLICANT: Wiberg, Finn C.
APPLICANT: Woodbury, Richard
TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
CITY: New York
STAFE: 405 Lexington Avenue, 62nd Floor
CITY: New York
STAFE: Now York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
0.4%; Score 11; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
      APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921230
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
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TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
TELEPRANCE/DOCKET NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 CTCCTCCAGGA 295
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Gaps

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0.4%; Score 9.8; DB 1; Length 27;
                                                                                                                                                 Query Match 0.4%; Score 10; DB 1; Length 36; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 10; Conservative 0; Mismatches 0; Indels
; TYPE: DNA
, ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-10
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08293778;
Patent No. 5880560;
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E.
APPLICANT: Woodbury, Richard
ITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55805600 No. 5580560disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: DK 3235/87
FILING DATE: 25-JUN-1987
PRIOR APPLICATION NUMBER: DK 3235/87
FILING DATE: 31-MOV-1989
FRIOR APPLICATION NUMBER: US 07/434,149
FRIOR APPLICATION DATE: APPLICATION NUMBER: PCT/DK88/00103
FRIOR APPLICATION NUMBER: DCT/DK88/00103
FRIOR APPLICATION NUMBER: US 07/898,248
FRIOR APPLICATION NUMBER: US 07/898,248
FRIING DATE: 12-JUN-1992
ATTORNOR/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129.224-US
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                   323 GCTCCTCTAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                  13 GCTCCTCTAG 4
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                                                                                                                                                                                                                                                                                                                                                                                                  US-08-293-778-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-293-778-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 10.4; DB 1; Length 45; Best Local Similarity 60.7%; Pred. No. 3.5e+02; Matches 17; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

0.4%; Score 10; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-08-955-636-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-955-636-9
Sequence 9, Application US/08955636A
Patent No. 6017891
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT PILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08955636A
| Retent No. 6017882
| GENERAL INFORMATION:
| APPLICANT: Nelsestuen, Cary | TITLE OF INVENTION: POLYPEPTIDES | TITLE OF INVENTION: POLYPEPTIDES | FILE REFERENCE: 09531/002001 | CURRENT APPLICATION NUMBER: US/08/955,636A | CURRENT APPLICATION NUMBER: US/08/955,636A | SOFTWARE: FastSEQ for Windows Version 3.0 | SOFTWARE: FastSEQ for Windows Version 3.0 | LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1078 GTTGGAGAGAATGGGGTATTGAAGTAGC 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 dridececerrececerrecacace 37
               CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 GCTCCTCTAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line;
HAMEDIATE SOURCE;
CLONE: ZC6337
US-08-756-506-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 29
US-08-955-636-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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ADDRESSEE: No. 55805600 No. 5580560th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor
STREET: 405 Lexington Avenue, 62nd Floor
STREET: New York
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,778
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10664775-1.rnı
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WESULT 31

US-08-293-778-22/C

US-08-293-778-22/C

US-08-293-778-22/C

US-08-293-778-22/C

US-08-293-778-22/C

US-08-293-778-22/C

US-08-293-778-22/C

APPLICANT WICH AND SCHEEN E.

APPLICANT WOODSTED FACTOR VII/VIIA

NUMBERS OF SEQUENCES: 26

CORRESPONDER ADDRESS: 26

CORRESPONDER ADDRESS: 26

CORRESPONDER ADDRESS: 26

CORRESPONDER ADDRESS: 26

CORRESPONDER ADDRESS: 26

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CORRESPONDER ADDRESS: 26

CORPERS I NAM YOUR WOOD FRIED FACTOR VII/VIIA

NUMBERS OF SEQUENCES: 26

CORPERS I NAM YOUR WOOD FRIED FACTOR VII/VIIA

MONDING SYSTEM: 16 PG COMPATIBLE PORC.

CORPUTER NAM YOUR COMPATIBLE PORC.

CORPUTER NAM YOUR WOOD AND ADDRESS: 26

CORPUTER IN PC COMPATIBLE PORC.

CORPUTER PRADALE PORC.

CORPUTER IN PC COMPATIBLE PORC.

CORPUTER IN PC COMPATIBLE PORC.

PELING DAYS: 12 PG VOOR 144, 149

FILING DAYS: 12 PG VOOR 144, 149

FILING DAYS: 25-UNA 1898

FILING DAYE: 23-UNA 1898

FILING DAYE: 23-UNA 1898

FILING DAYE: 23-UNA 1898

FILING DAYE: 23-UNA 1898

FILING DAYE: 13 PG VOOR 180 ADDRESS: 312 PG VOOR 180 ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADD
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Best Local Similarity 66.7%; Pred. No. 3.1e+02; Matches 14; Conservative 0; Mismatches 7; Indels
                                                                                                     989 GICIGIAAAIAICICIAGGIC 1009
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Best Local Similarity 75.0
Matches 12; Conservative
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US-08-293-778-22
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US-08-293-778-20

| Sequence 20, Application US/08293778
| Sequence 20, Application US/08293778
| Patent No. 5580560
| Patent No. 5580560
| APPLICANT: NICORANITONI SOUTH STATE OF THE CAPPLICANT: Woodbury, Kichard TITLE OF INVENTION: WOLDFIED FACTOR VII/VIIE NUMBERS OF SEGUENCES: 26
| APPLICANT: Woodbury, Kichard TITLE OF INVENTION: WOLDFIED FACTOR VII/VIIE NUMBERS OF SEGUENCES: 26
| APPLICANT: Woodbury, Kichard TITLE OF INVENTION: WOLDFIED FACTOR VII/VIIE NUMBERS OF SEGUENCES: 26
| APPLICANT: Woodbury, Kichard TITLE OF INVENTION: WOLDFIED FACTOR VII/VIIE NUMBERS OF SEGUENCES: 26
| APPLICANT: Woodbury, WOLK STATE OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF THE CAPPLICANT OF T
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APPLICANT: Holly, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 62.55
Matches 15; Conservative
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US-07-998-972A-7
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PatentIn Release #1.0, Version #1.25
                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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STATE: CA
COUNTRY: US
ZIP: 94105
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US-08-462-261-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 9.6; DB 1; Length 35; 75.0%; Pred. No. 4.8e+02; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor STREET: CA
COUNTRY: USA
                                                                                                                                                                                                                            CUDNIER: USA

CIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FLING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
REGISTRATION NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5502034
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                         STREET: Twentieth F. CITY: San Francisco
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                                                                                                                                                                                 CA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: line;
; IMMEDIATE SOURCE;
; CLONE: ZC1324
US-07-998-972A-7
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USA
                                                                                                                                                                                                                  COUNTRY:
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Gaps
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Fatent No. 5527692
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TILLE OF INVENTION: METHODS FOR PRODUCING THROWBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Flogyy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,261
FILING DATE: 05-JUN-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATE: US 07/998,972
APPLICATION NUMBER: US 07/998,972
APPLICATION NUMBER: US 07/896,701
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/866,701
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAIMHER STEVEN W
CLASSIFICATION 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMACE, Seeven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 DASE PAIRS
TYPE: INCleic acid
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0.4%; Score 9.6; DB 1; Length 35;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application PC/TUS9211357
GENURAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentieth Floor
STREET: Twentieth Floor
STRIE: CA.
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ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921230
CLLASSIFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31.AMR.1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31.AMR.1992
PRICK APPLICATION NUMBER: 31.952-12-2
FILING DATE: 31.505-000
FILING DATE: 31.505-000
FILING DATE: 31.505-000
FILING DATE: 31.505-000
FILING DATE: 31.505-000
FILING DATE: 31.505-000
FILING ADDITION NUMBER: 13952-12-2
FILING DATE: 35.505-000
FILING DATE: A15-54-5043
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 35.505-000
FILINGTH: 35.505-000
FILINGTH: 35.505-000
FILINGTH: SCOURCE ACID
STRANDEDNESS: SINGLE
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: Linear
THEORY
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1395.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-960
RELEFEX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOSY: linear
IMMEDIATE SOURCE:
CLONE: ZC1324
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MERSULT APPLICATION UNIVERSITY BY SEQUENCE 17, Application US/08293778

Sequence 17, Application US/08293778

Sequence 17, Application US/08293778

Sequence 17, Application US/08293778

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APPLICATI WASHED FACTOR VII/VIIa
NUMBER OF SCHUNGES. Exist C.
APPLICATI WOODLIVE AND SERVER SEASONS
CORRESPONDENCE ADDRESS:
APPLICATION WOODLIVE TO SERVER SEASONS
CORRESPONDENCE ADDRESS:
APPLICATION UNIVERS. IN 5 55005601 America
CORPUTER SEABORIS COMPLIAN
COMPUTER: INP PC Compatible
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Length 35;

DB 1;

Score 9.6;

0.4%;

Query Match

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0; Gaps

4; Indels

Best Local Similarity 75.0%; Pred. No. 4.8e+02; Matches 12; Conservative 0; Mismatches 4

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0.3%; Score 9.2; DB 1; Length 36;
Best Local Similarity 78.6%; Pred. No. 5.1e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
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; OTHER INFORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-10
RESULT 38
US-08-955-636-9/C
Squence 9, Application US/08955636A
Fatent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SSCTWARFE: Past SEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 36
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US-08-955-636-10
Sequence 10, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: NODIFIED VITAMIN K-DEPENDENT;
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002011
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 36
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US-08-955-636-8/C
i Sequence 8, Application US/08955636A
i Patent No. 6017882
i GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
ITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
ITLE PEPERENCE: 09531/00201
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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; SOFTWARE: FastSEQ for Windows Version 3.0.;
; SEQ ID NO 8
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: TRORMATION: Protein C mutagenic oligonucleotide
US-08-955-636-8

Query Match
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 12; Indels 0; Gaps

Qy 286 TCCTCCAGGAGCAGGAAGAGCCT 313

Db 41 TCCTGGAGGAGCTCCTCCAGGAGCCT 14

Search completed: August 9, 2004, 15:29:04
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Sequences Sequences Sequences		Sequence 10 Sequence 10 Sequence 10 Sequence 10	Sequence 10 Sequence 10 Sequence 10 Sequence 10	Sequence 8, Sequence 9, Sequence 8,	Sequence 9, Sequence 8,	Sequence 9, Sequence 2,	Sequence 3, Sequence 6, Sequence 7,	Sequence 8, Sequence 6, Sequence 7,		Sequence 22 Sequence 22 Sequence 22	^1 -1 -		Sequence 10			4 IO 10	നന	Sequence 20	1014	Sequence 14 Sequence 15	-	യത	80	დი	Sequence 23 Sequence 23	NO	NO	Sequence
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2106 1 US-10-617-619-9 Sequence 9, 0.8 483 1 US-09-918-995-8429 Sequence 84,	0.8 1440 1 US-10-375-741-13 Sequence 13 0.7 1361 1 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 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GenCore version 5.1.6 (c) 1993 - 2004 Compugen	search, using sw mode	04, 15:30:00 ; Search time 34 Seconds (without alignments) 4.015 Million cell updates/s	-1 ggcgacaggtrgtaattctaggtgctgat 271	TY_NUC 10.0 , Gapext 0.	seqs, 25143	satisfying chosen parameters:		Minimum Match 0% Maximum Match 100% Listing first 250	se : rnpbdb:*	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being print darrial with a part of the total score distribution.	s defived by analysis of the colar score distributes	Lenath DB ID Descripti	0.9 1361 1 US-10-382-248-35 Sequence 35.	0.8 1332 1 US-10-411-037-7 Sequence 7, 0.8 1332 1 US-10-411-026-7 Sequence 7, 0.9 1332 1 US-10-411-026-7 Sequence 7, 0.9 1332 1 US-10-411-026-7	0.8 1332 1 US-10-411-049-7 Sequence 7, 0.8 1332 1 US-10-410-930-7 Sequence 7,	0.8 1332 1 US-10-410-997-7 Sequence 7, 0.8 1332 1 US-10-411-012-7 Sequence 7,	0.8 1332 1 US-10-287-994-7 Sequence 7, 0.8 1332 1 US-10-410-913-7 Sequence 7,	0.8 1440 1 US-10-375-741-13 Sequence 13. 0.8 2040 1 US-10-617-619-12 Sequence 12	0.8 2106 1 US-10-617-619-9 Sequence 9, 0.8 483 1 US-09-918-995-8429 Sequence 84,	0.8 1440 1 US-10-375-741-13 Sequence 13 0.7 1361 1 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 0.7 1361 US-10-382-248-35 Sequence 35 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUNEARAL INFORMATION:

JAPPLICANT: Alsobrook, et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

JELE REPERENES: 21402-568C

CURRENT APPLICATION NUMBER: 06/366,928

PRIOR PELING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-05

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR PILING DATE: 2002-03-19

PRIOR SEQ ID NOS: 92

SOFTWARE: CLRASEQLIST VERSION 0.1

LENGTH: 1361
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Sequence 2, Sequence 5, Sequence 6, Sequence 6, Sequence 7, Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 3,
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APPLICANT: CIRCH, ALL
APPLICANT: CIRCH, ALL
TILLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: ALPHA GALACTOSIDASE A
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FILLE OF INVENTION: GALACTOSIDASE A
FILLE OF INVENTION: GALACTOSIDASE A
CURRENT APPLICATION NUMBER: US 60/324,692
PRIOR APPLICATION NUMBER: US 60/324,692
PRIOR PILING DATE: 2001-10-19
PRIOR FILLING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-16
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APPLICANT: Neose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Defrees, Shawn
APPLICANT: Bayer' Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: 104083-01-5053
CURRENT FILE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE PEPERENCE: 104083-01-5053
CURRENT FILING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
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0.8%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 4.9;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10411026
Publication No. US20040063911A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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      TITLE REFERENCE: 040833-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-0-19
PRIOR FILING DATE: 2002-06-07
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PRIOR PILING DATE: 2002-06-16
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Matches 35; Conservative (
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ORGANISM: Homo sapiens
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IIILE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSES LEGUIDLE STATES, AND APPLICANT: BEFREES, Shawn APPLICANT: BOFFEES, Shawn APPLICANT: Zopf, David APPLICANT: Bayer, Robert APPLICANT: Bayer, Robert APPLICANT: Hakes, David APPLICANT: Hakes, David APPLICANT: Chen, Xi APPLICANT: Chen, Xi APPLICANT: Chen, Xi TITLE OF INVENTION: GINCOCONJUGATION OF G-CSF TITLE OF INVENTION: GINCOCONJUGATION OF G-CSF TITLE OF INVENTION: GINCOCONJUGATION OF G-CSF CURRENT APPLICATION NUMBER: US 60/328,523 PRIOR FILING DATE: 2001-10-10 PRIOR PAPLICATION NUMBER: US 60/344,692 PRIOR FILING DATE: 2001-10-10 PRIOR PAPLICATION NUMBER: US 60/387,292 PRIOR PAPLICATION NUMBER: US 60/387,292 PRIOR FILING DATE: 2002-06-07 PRIOR PAPLICATION NUMBER: US 60/391,777 PRIOR FILING DATE: 2002-06-16 PRIOR PAPLICATION NUMBER: US 60/404,249 PRIOR FILING DATE: 2002-09-16 PRIOR FILING DATE: 2002-09-16 PRIOR PAPLICATION NUMBER: US 60/407,527 PRIOR FILING DATE: 2002-09-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING DATE: 2002-08-16 PRIOR FILING PRIOR FILING DATE: 2002-08-16 PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIO
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0.8%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 4.9;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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US-10-410-962-7/c
Sequence 7, Application US/10410962
Publication No. US2004007783641
GENERAL INFORMATION:
APPLICANT: Noses Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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; ORGANISM: Homo sapiens
US-10-410-962-7
.; ORGANISM: Homo sapiens
US-10-411-026-7
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Matches 35; Conserv
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bowe, Caryn
ITILE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
ITILE OF INVENTION: BETA: US/10/410,930
CURRENT APPLICANTON NUMBER: US/00/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLING DATE: 2001-10-19
PRIOR PLING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PLING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PLING DATE: 2002-09-16
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### APPLICANT: DeFrees, Shawn
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### APPLICANT: Bowe, Caryn
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Sequence 7, Application US/10287994
Publication No. US20040137557A1
GENERAL INFORMATION:
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Matches 35; Conservative
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; ORGANISM: Homo sapiens
US-10-411-012-7
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CORGANISM: Homo sapiens
US-10-287-994-7
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
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APPLICANT: Chen, Xi
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APPLICANT: Chen, Xi
APPLICANT: Bayer, Robert
APPLICANT: Bost, Caryn
TITLE OF INVENTION: FOLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONUUGATION OF
TITLE OF INVENTION: FOLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONUUGATION OF
TITLE OF INVENTION: FOLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONUUGATION OF
TITLE OF INVENTION: FOLICLE STIMULATING HORMONE: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-08-16
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PRIOR FILING DATE: 2002-08-16
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                                                                                                                                                                 876 IICAAITGICITITAICIGICGAGACIIGCITITGITIGAAAIAIGIAITCAAITITGG 934
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Query Match

O.8%; Score 20.6; DB 1; Length 1332;
Best Local Similarity 59.3%; Pred. No. 4.9;
Matches 35; Conservative 0; Mismatches 24; Indels 0
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Sequence 7, Application US/10411012
Fublication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Caryne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10410997; Publication No. US20040126838A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-410-997-7
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US-10-617-619-12/c

Sequence 12, Application US/10617619

Sequence 12, Application World10929A1

CENNERAL INFORMATION:

APPLICANT: Nicolaisen, Else M

APPLICANT: Nicolaisen, Else M

TITLE OF INVENTION: TF Binding Compound

FILE REFERENCE: 6455.200-US

CURRENT APPLICATION NUMBER: US/10/617,619

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: US 003-07-12

PRIOR APPLICATION NUMBER: US 004-04,568

PRIOR PILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-08-19

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.2

SEQ ID NO 12

LENGTH: 2040

TVPE: NATAL

LENGTH: 2040

LENGTH: 2040

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LENGTH: 2040

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APPLICANT: Bjorn, Soren B
APPLICANT: Bjorn, Soren B
APPLICANT: Nicolaisen, Blse M
APPLICANT: Orogensen, Anker S
TITLE OF INVENTION: TP Binding Compound
FILE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/10/617,619
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1440;
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0.8%; Score 20.6; DB
Best Local Similarity 59.3%; Pred. No. 6.8;
Matches 35; Conservative 0; Mismatches
                  PRIOR APPLICATION NUMBER: CO. PRIOR FILING DATE: 1997-01-27
PRIOR FILING DATE: 1997-01-22
PRIOR FILING DATE: 1997-01-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 1440
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Publication No. US20040110929A1
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FILING DATE: 1997-03-27
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CORGANISM: Homo sapiens
US-10-375-741-13
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APPLICANT: Chen, XI
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GLYCOCONUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE REPERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PLING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-17
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PRIOR PLING DATE: 2002-06-17
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Sequence 13, Application US/10375741
GENERAL INFORMATION:
APPLICANT: Thorbo, Philip E
APPLICANT: King, Steven W
APPLICANT: King, Steven W
APPLICANT: King, Steven W
APPLICANT: TISSUE PACTOR METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR TITLE OF INVENTION: TREATMENT
FILE REFERENCE: 4001.001999
CURRENT APPLICATION NUMBER: 08/10/375,741
CURRENT APPLICATION NUMBER: 09/573,835
PRIOR APPLICATION NUMBER: 6,156,321
PRIOR APPLICATION NUMBER: 6,156,321
PRIOR APPLICATION NUMBER: 6,156,321
PRIOR APPLICATION NUMBER: 6,1456,321
PRIOR APPLICATION NUMBER: 60/042,427
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                                                                        876 TICAATIGICITITAICIGICGAGACTIGCITIGITITIGAAATAIGIATICAATITIGG 934
                                                                                                                              558 TTGCTGGCATTTCTTTTTTTTAGGTATTTTTTCCACATGGATATTCAACTGTGG 500
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       24; Indels
   0; Mismatches
                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10410913
Publication No. US20040112856A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Expf. David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 59.3%;
Matches 35; Conservative (
       35; Conservative
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CRGANISM: Homo sapiens
US-10-410-913-7
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US-10-375-741-13/c
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US-10-410-913-7/c
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              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JAPRICANT: Alsobrook, et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE PERERENCE: 21402-568C
CURRENT APPLICATION NUMBER: US/10/382,248
CURRENT FILING DATE: 2003-03-05
PRIOR PELLING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-06
PRIOR PRILING DATE: 2002-03-06
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0.8%; Score 20.4; DB 1; Length 1440;
Best Local Similarity 65.2%; Pred. No. 6.1;
Matches 30; Conservative 0; Mismatches 16; Indels 0
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0.7%; Score 19.4; DB 1; Length 1361;
Best Local Similarity 55.1%; Pred. No. 12;
Matches 38; Conservative 0; Mismatches 31; Indels 0
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Sequence 2, Application US/09782587B
Sequence 2, Application US/09782587B
PUBLICATION OF US20030096338A1
GENERAL INFORMATION:
APPLICANT: PEDERGEN, ANDERS H.
APPLICANT: ANDERSON, KIM V.
APPLICANT: BORNAES. CLAUS
TITLE OF INVENTION: RACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT APPLICATION NUMBER: US/09/782,587B
; PRIOR FILING DATE: 1997-01-27; PRIOR PELING DATE: 1997-01-22; PRIOR FILING DATE: 1997-01-22; NUMBER OF SEQ ID NOS: 27; SOFTWARE: Patentin version 3.1; SEQ ID NO 13; LENGTH: 1440; TYPE: DNA; TYPE: DNA; CRGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/10382248
Publication No. US20040058347A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS;
; LOCATION: (45)..(1301)
US-10-382-248-35
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US-10-382-248-35/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           876 TTCAATTGTCTTTTATCTGTCGAGACTTGCTTTTGAAATATGTATTCAATTTTGG 934
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0.8%; Score 20.6; DB 1; Length 2106;
Best Local Similarity 59.3%; Pred. No. 7;
Matches 35; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8429, Application US/09918995

Publication No. US2003007362341

GENERAL INPORMATION:

APPLICANT: Hyeeq. Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIERARIES

FILE REFERENCE: 20411-756

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/918,995

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FESTSEQ for Windows Version 3.0

SEQ ID NO 8429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 ACAGGCATGGCCATGGCTCCAGAGATTGCCTCTTCCAGGTGCAGGC 419
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Best Local Similarity 65.2%; Pred. No. 2.3;
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8429
                                   SOFTWARE: Patentin version 3.2
SEQ ID NO 9
                                                                                                                                                                                                                                     , OTHER INFORMATION: Synthetic US-10-617-619-9
   NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                      TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-918-995-8429
                                                                                                      2106
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US-10-375-741-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619 GACCTGCCAGGGCACTCCCCCTTAGGGCAGACCTTCCCGCCGACGATCCGGCCCTGGG 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19.2; DB 1; Length 1338;
Pred. No. 14;
0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOSTICAL-2014-4/C
Sequence 4, Application US/09782587B
FUDICATION No. US20030096338A1
GENERAL INFORMATION:
APPLICANT: PEDERREN. ANDERS H.
APPLICANT: PEDERREN. ANDERS H.
APPLICANT: BORNAES, CLAUS
TILE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
TILE REFERENCE: 31-001100US
CURRENT FILING DATE: 2002-03-26
FRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-22
FRIOR FILING DATE: 2000-02-22
FRIOR FILING DATE: 2000-02-22
FRIOR FILING DATE: 2000-02-22
FRIOR PELICATION NUMBER: 60/184,036
FRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 4
LENGTH: 1357
TAVER: NANA
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CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: PA 2000 00218
PRIOR FILING DATE: 2000-02-11
PRIOR PAPPLICATION NUMBER: 60/184,036
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR PILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 2
LENGTH: 1338
TYPE: DNA
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 48; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (115)..(1332)
US-09-782-587B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
US-09-782-587B-4/c
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GREREAL INFORMATION:

APPLICANT: Neces Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, David
APPLICANT: DeFrees, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Ghen, Xi
APPLICANT: Hakes, David
APPLICANT: Dave, Carry
TILLE OF INVENTION: ALFAH GALACTOSIDASE A
FILE REFERENCE: 040853-01-508
CURRENT FILING NATE: 2003-04-09
FRIOR FILING DATE: 2003-04-09
FRIOR APPLICATION NUMBER: US 60/384,692
FRIOR FILING DATE: 2001-00-19
FRIOR PAPLICATION NUMBER: US 60/387,292
FRIOR FILING DATE: 2002-06-07
FRIOR APPLICATION NUMBER: US 60/387,292
FRIOR FILING DATE: 2002-06-07
FRIOR APPLICATION NUMBER: US 60/387,292
FRIOR FILING DATE: 2002-06-16
FRIOR APPLICATION NUMBER: US 60/396,594
FRIOR PAPLICATION NUMBER: US 60/404,249
FRIOR PAPLICATION NUMBER: US 60/407,527
FRIOR APPLICATION NUMBER: US 60/407,527
FRIOR PLING DATE: 2002-08-16
FRIOR PLING DATE: 2002-08-28
FRIOR FILING DATE: 2002-08-28
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Bovid
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
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0.7%; Score 18; DB 1; Length 1332;
Best Local Similarity 45.7%; Pred. No. 28;
Matches 63; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10411026 Publication No. US20040063911A1 GENERAL INFORMATION:
Sequence 7, Application US/10411037
Publication No. US20040043446A1
GENERAL INFORMATION:
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US-10-411-037-7
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Robert
APPLICANT: Hakes, David
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Publication No. US20040082026A1
GENERAL INFORMATION:
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       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-962-7
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US-10-411-049-7
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Best Local S
Matches 63
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TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REPERENCE: 040985-01-054
CURRENT PRILING DATE: 2003-04-09
PRIOR PLLING DATE: 2001-0-10
PRIOR PLLING DATE: 2001-10-10
PRIOR PLLING DATE: 2001-10-10
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PRIOR PLLING DATE: 2001-0-25
PRIOR PLLING DATE: 2002-06-25
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PRIOR PLLING DATE: 2002-06-26
PRIOR PLLING DATE: 2002-06-26
PRIOR PLLING DATE: 2002-06-26
PRIOR PLLING DATE: 2002-06-26
PRIOR PLLING DATE: 2002-08-16
PRIOR PLLING DATE: 2002-08-16
PRIOR PLLING DATE: 2002-08-28
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PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR PELICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10410962
PUBLICATION NO. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Unc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Hakes, David
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SEQ ID NO 7
LENGTH: 1332
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CORGANISM: Homo sapiens
US-10-411-026-7
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Bowe, Caryn
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APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
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APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, David
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                    CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-07
PRIOR PILING DATE: 2002-06-07
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Publication No. US20040132640A1
GENERAL INFORMATION:
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US-10-410-997-7
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US-10-410-930-7

Sequence 7, Application US/10410930

Publication No. US20040115168A1

GENERAL INFORMATION:

APPLICANT: Neces Technologies, Inc.

APPLICANT: Neces Technologies, Inc.

APPLICANT: Neces Technologies, Inc.

APPLICANT: Sequence 1

APPLICANT: Neces Technologies, Inc.

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Sobrid

APPLICANT: Bowe, Caryn

ITILE OF INVENTION: UNRERENCE 105/10-410-9

FILES REFERENCE: 40893-01-5056

CURRENT APPLICATION NUMBER: US 60/328,523

PRIOR PELING DATE: 2001-60-19

FRIOR APPLICATION NUMBER: US 60/389,222

REIOR APPLICATION NUMBER: US 60/399,777

PRIOR FILING DATE: 2002-06-27

PRIOR FILING DATE: 2002-06-27

PRIOR FILING DATE: 2002-06-27

PRIOR FILING DATE: 2002-06-27

PRIOR PELING DATE: 2002-08-16

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Sequence 7, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION C
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680 TCTCCGCGCCCACTGTT 697
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CORGANISM: Homo sapiens
US-10-410-930-7
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US-10-410-997-7
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APPLICANT: Defrees, Shawn
APPLICANT: Defrees, Shawn
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APPLICANT: Beyer, Robert
APPLICANT: Beyer, Robert
APPLICANT: Beyer, Robert
APPLICANT: Beyer, Bowid
APPLICANT: Bewer, Caryn
APPLICANT: Brow, Caryn
TITLE OF INVENTION: WITHOUS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: WITHOUS BETTO BE CURRENT APPLICATION NUMBER: US (0/228,523)
FILE REFRENCE: C040853-01-5081
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-08-28
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45.7%; Pred. No. 28;
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Publication No. US20040110929A1
GENERAL INFORMATION:
APPLICANT: Bjorn, Soren E
APPLICANT: Nicolaisen, Else M
APPLICANT: Orgensen, Anker S
TITLE OF INVENTION: TF Binding Compound
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Publication No. US20040142856A1
GENERAL INFORMATION:
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US-10-617-619-12
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Publication No. US20040137557A1
Publication No. US20040137557A1
APPLICANT: Neose Technologies, Inc.
APPLICANT: Zopf, David
APPLICANT: Bayer, Nobert
APPLICANT: Bayer, Nobert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-00
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Pred. No. 28;
0; Mismatches 75; Indels
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CURRENT APPLICATION NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/347,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
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PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
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                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-287-994-7
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Best Local Similarity
Matches 63; Conserv
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Best Local Similarity
Matches 63; Conserv
                                                                                                                           LENGTH: 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10617619; Sequence 9, Application US/10617619; Publication No. US20040110928A1
GENERAL INFORMATION.
JEDELICANT: Bjorn, Soren E
APPLICANT: Diogasen, Anker S
TITLE OF INVENTION: TF Binding Compound
TITLE OF INVENTION: TF Binding Compound
TITLE REFERENCE: 6455.200-US
CURRENT FILING DATE: 2003-07-11
PRIOR PLILING DATE: 2002-07-12
PRIOR PLILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 2106
TYPE: NNA
FILE REFERENCE: 6455.200-US
CURRENT APPLICATION NUMBER: US/10/617,619
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/404,568
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ 1D NOS: 13
SOFTWARE: PATCHIN VERSION 3.2
SEQ 1D NO 12
LENGTH: 2040
TYPE: DAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.7%; Score 18; DB 1; Length 2040; Best Local Similarity 45.7%; Pred. No. 23; Matches 63; Conservative 0; Mismatches 75; Indels
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, OTHER INFORMATION: Synthetic US-10-617-619-12
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COTHER INFORMATION: Synthetic US-10-617-619-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial
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US-10-617-619-9
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280 GATCACTCCTCCAGGAGCAGGCAGG-GAAGAGCCTCAGGTGATTGCTCCTCTAGATGCTG 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Expression; OTHER INFORMATION: cassette for expression of FVII in mammalian cells US-09-782-587B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 17.1; DB 1; Length 1357; Best Local Similarity 62.7%; Pred. No. 35; Matches 42; Conservative 0; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09782587B;
Sequence 2, Application US/09782587B;
Sequence 2, Application 0. US20030096338A1
GENERAL INFORMATION:
APPLICANT: PEDERSEN, ANDERS H.
APPLICANT: BORNAES, CLAUS
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
CURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT APPLICATION NUMBER: US/09/782,587B
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/241,916
PRIOR APPLICATION NUMBER: 60/241,916
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARCELLING OF SEQ ID NOS: 19
SEQ ID NOS: 19
RESULT 30
US-09-782-587B-4

j Sequence 4, Application US/09782587B

j Publication No. US20030096338A1

j GENERAL INFORMATION:
   APPLICANT: PEDERSEN, ANDERS H.
   APPLICANT: BORNAES, CLAUS
   TILLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
   TILLE OF INVENTION: PACTOR VII OR VIIA-LIKE MOLECULES
   TILLE OF INVENTION: PACTOR VII OR VIIA-LIKE MOLECULES
   TILLE OF INVENTION PACTOR VII OR VIIA-LIKE MOLECULES
   TILLE OF INVENTION NUMBER: US/09/782,587B
   CURRENT FILING DATE: 2000-02-11
   PRIOR PILING DATE: 2000-02-11
   PRIOR APPLICATION NUMBER: 60/184,036
   PRIOR PILING DATE: 2000-02-11
   PRIOR APPLICATION NUMBER: 60/184,036
   PRIOR PILING DATE: 2000-10-18
   NUMBER OF SEQ ID NOS: 19
   SOFTWARE: PATENTIN VET: 2.1
   SEQ ID NO 4
   LENGTH: 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (115)..(1332)
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ORGANISM: Homo sapiens
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464 TCTGAGGCTCCAATGGTT 481

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GETILE REPERENCE: AEOMICA-X-2
CURRENT PAPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARST FILING DATE: AGUING ELISTING ENGINE VEFS. 1.1
SEQ ID NO 9623
LENGTH: 555
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                                                                                                                                                       Gaps
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OTHER INFORMATION: MAP TO CHRI3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: SXPISSPROT HIT: PO8709, EVALUE 7.00e-63
OTHER INFORMATION: NT HIT: J02933.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: ALS31727.1, EVALUE 5.00e-76
US-10-029-386-9623
; OTHER INFORMATION: EST HUMAN HIT: ALE31727.1, EVALUE 3.00e-26; CTHER INFORMATION: SMISSPROT HIT: POR709, EVALUE 3.00e-37 US-10-029-386-23323
                                                                                                      Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 555;
                                                                                                 Query Match 0.5%; Score 14.8; DB 1; Length 2: Best Local Similarity 53.4%; Pred. No. 1e+02; Matches 31; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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56.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9623, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Conservative
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Best Local Similarity
Matches 28; Conserv
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US-10-029-386-9623
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LENGTH: 555
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ADONIGA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILLNG DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 23323
LENGTH: 222
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                                                   DB 1; Length 1338;
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US-09-918-995-8429/c
| Jequence 8429/ Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT PILING DATE: 2001-07-30
| PRIOR FILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFUMARE: FastSEQ for Windows Version 3.0
| LENGTH: 483
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: ASPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: NT HIT: G114783796, EVALUE 1.00e-122
                                                                                                      Indels
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                                                                                                                                                       310 GCCTCAGGTGATTGCTCCTCTAGATGCTGGCAGGCC 345
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0.6%; Score 16.4; DB 1;
Best Local Similarity 55.2%; Pred. No. 52;
Matches 32; Conservative 0; Mismatches 26;
                                                                                                                                                                                                     0.6%; Score 16.8; Dilarity 66.7%; Pred. No. 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23323, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8429
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                           Local Similarity
les 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-029-386-23323/c
  JS-09-782-587B-2
                                                      Query Match
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Matches
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, CURRENT FILING DATE: 2002-10-11

; PRIOR APPLICATION NUMBER: 09/69
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US-10-273-321-22/c

i Sequence 22, Application US/10273321
; Publication No. US20030180749A1
; Genemce 22, Application No. US20030180749A1
; Genemce 22, Application No. US20030180749A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO TITLE OF INVENTION: GENETIC MARKERS
; FILE REFERENCE: 24736-2033B
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR PAPLICATION NUMBER: 60/127,658
; PRIOR PAPLICATION NUMBER: 60/129,176
; PRIOR PAPLICATION NUMBER: 60/129,176
; PRIOR APPLICATION NUMBER: 60/129,176
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SEQ ID NO 22
; LENGTH: 60
; SEQ ID NO 22
; LENGTH: 60
; LENGTH: 60
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62.9%; Pred. No. 58;
tive 0; Mismatches
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0.5%; Score 14.2; D
Best Local Similarity 62.9%; Pred. No. 58;
Matches 22; Conservative 0; Mismatches
    PRIOR APPLICATION NUMBER: 00/687,483
PRIOR PILLING DATE: 2000-07-10
PRIOR PELICATION NUMBER: 60/217,658
PRIOR PELICATION NUMBER: 60/159,176
PRIOR PELICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR PELICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 09/663,968
PRIOR PELICATION NUMBER: 09/663,968
PRIOR PELICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOCTWARB: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 60
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US-10-272-756-22/c
; Sequence 22, Application US/10272756
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Best Local Similarity 62.99
Matches 22, Conservative
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; OTHER INFORMATION: Probe
US-10-272-665-22
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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US-10-020-3323

US-10-022-3323

Sequence 23323, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.

TITLE OF INVENTION: USANDARS.

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 23233

LENGTH: 222
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Sequence 22, Application US/10272665

Publication No. US20030180748A1

GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: GENERALIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
FILE REPERENCE: 24736-2033E

CURRENT APPLICATION NUMBER: US/10/272,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 CAGGCAGGCCCATGCCTCTGGTGATCACTCTAGTGAAAGGTGGGGGTCTGAGGCT 472
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OTHER INFORMATION: MAP TO CRR13.3
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.006-12
OTHER INFORMATION: EST HUMAN HIT: PO8709, EVALUE 3.006-27
US-10-029-386-23323
PEATURE:
OTHER INFORMATION: MAP TO CHR13.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACEWIA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: STRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: STRESSED IN HEART, SIGNAL = 0.95
OTHER INFORMATION: STRESSED IN HEART, SIGNAL = 0.95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 555
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Matches 21; Conservative
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Sequence 107, Application US/10272665
Fublication No. US2033180748A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POIL
TITLE OF INVENTION: METHOD STORE 102-10-15
FILE REPRENCE: 24736-2033E
CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-07-10
PRIOR PELING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFFWARE FEALESED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Braun et al.
APPLICANT: Braun et al.
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI
TITLE OF INVENTION: GENETIC MARKERS
TILE REFERENCE: 24736-2033B
CURRENT PELLICATION NUMBER: US/10/23,321
CURRENT FILING DATE: 2002-10-15
FRIOR PELLOATION NUMBER: 09/687,483
FRIOR FILING DATE: 2000-07-10
FRIOR FILING DATE: 2000-07-10
FRIOR FILING DATE: 1999-10-13
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                     Sequence 107, Application US/10273321 Publication No. US20030180749A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-10-272-665-107
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; ORGANISM: Homo sapien
US-10-273-321-107
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Best Local Similarity
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US-10-272-665-107/c
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GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: MENERS
FILE REFREBENCE: 2476-2013
CURRENT APPLICATION NUMBER: 09/687,483
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR APPLICATION NUMBER: 60/17,658
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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Pred. No. 58;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 60
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Best Local Similarity 62.9%;
Matches 22; Conservative
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Best Local Similarity 62.9
Matches 22, Conservative
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Sequence 106, Application US/10272665
Publication No. US20030180748A1
GENERAL INFORMATION:
I TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO
ITILE OF INVENTION: GENETIC MARKERS
I CURRENT APPLICATION NUMBER: US/10/272,665
CURRENT FILING DATE: 2000-07-10
PRIOR PAPLICATION NUMBER: 60/217,658
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PLING DATE: 2000-07-10
PRIOR PELICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 60/217,251
PRIOR PELICATION NUMBER: 09/663,968
PRIOR PILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
IDENGER: 100
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j Sequence 106, Application US/10273321

j Publication No. US20030180749A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO.

ITILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PO.

ITILE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033B

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR APPLICATION NUMBER: 60/119,176

PRIOR APPLICATION NUMBER: 60/119,176

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PELING DATE: 2000-07-10

PRIOR PELING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/119,176

PRIOR APPLICATION NUMBER: 09/663,968

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PRIOR APPLICATION NUMBER: 09/663,968

PRIOR APPLICATION NUMBER: 09/663,968

PRIOR PILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARR: FESTER FOR MAINGOWS VERSION 4.0

SEQ ID NO 106

LENGTH: 100
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                    Query Match 0.5%; Score 14.2; DB 1; Length 100; Best Local Similarity 62.9%; Pred. No. 91; Matches 22; Conservative 0; Mismatches 13; Indels (
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Best Local Similarity 62.9%; Pred. No. 91;
Matches 22; Conservative 0; Mismatches 13;
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US-10-272-665-106
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| Sequence 100, Application US/10272756 |
| Sequence 107, Application US/10272756 |
| Publication No. US2003190644A1 |
| GENERAL INFORMATION: |
| APPLICANT: Braun et al. |
| APPLICANT: Braun et al. |
| TITLE OF INVENTION: GENETIC MARKERS |
| TITLE OF INVENTION: GENETIC MARKERS |
| TITLE OF INVENTION: GENETIC MARKERS |
| TITLE OF INVENTION: GENETIC MARKERS |
| TITLE OF INVENTION: GENETIC MARKERS |
| FILE REPERENCE: 24736-2033C |
| CURRENT APPLICATION NUMBER: 09/687,483 |
| PRIOR APPLICATION NUMBER: 09/687,483 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-09-19 |
| NUMBER OF SEC ID NOS: 118 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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| Sequence 107, Application US/10273228
| Publication No. US20030207297A1
| GENERAL INFORMATION:
| APPLICANT: Braun et al. |
| TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC TITLE OF INVENTION: METHODS FOR US/10/273,228
| FILE REFERENCE: 24736-2033D |
| CURRENT APPLICATION NUMBER: 09/687,483 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
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| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-07-10 |
| PRIOR PILING DATE: 2000-09-19 |
| PRIOR PILING DATE: 2000-09-19 |
| NUMBER OF SEQ ID NOS: 118 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 107 |
| LENGTH: 100
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Pred. No. 91;
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13; Indels
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US-10-273-228-107
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, ORGANISM: Homo sapien
US-10-272-756-107
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Sequence 8. Application US/09951121A
GENERAL INFORMATION:
APPLICANT: Persson. Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT FILING DATE: 2001-09-13
PRIOR PELLING DATE: 2000-09-13
PRIOR PELLING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 36
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Pred. No. 83;
0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 106
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
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OTHER INFORMATION: Synthetic
US-09-951-121A-8
                                                                                          ; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-228-106
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US-10-272-756-106/C

Sequence 106, Application US/10272756

Publication No. US20030190644A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENETIC MARKERS

FILE REFERENCE: 24736-2033

CURRENT APPLICATION NUMBER: US/10/272,756

CURRENT PILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/217,658

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

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Publication No. US2003020729741

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING POTTINE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING POTTINE OF INVENTION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GEN
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                            ; ORGANISM: Homo sapien
US-10-273-321-106
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ORGANISM: Homo sapien
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Matches 22; Conserv
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US-10-281-727-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII
US-10-255-032-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, 4/201625032
| Sequence 9, 4/201625032
| Publication No. US20030100075A1
| GENERAL INFORMATION:
| APPLICAMT: No. US20030100075A10 No. US20030100075A1disk A/S
| TITLE OF INVENTION: HUWAN COAGULATION FACTOR VII POLYPEPTIDES
| TITLE OF INVENTION HUMBER: US/10/255,032
| CURRENT APPLICATION NUMBER: US/10/255,032
| CURRENT APPLICATION NUMBER: DK PA 2001 01413
| PRIOR PILING DATE: 2001-09-27
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: Patentin version 3.1
| LENGTH: 36
                                                                                                                                                                                                                                                                       | Sequence %, Application US/10255032
| Sequence %, Application US/1025032
| Publication No. US20030100075A1
| GENERAL INFORMATION:
| APPLICATI NO. US20030100075A1C NO. US20030100075A1disk A/S
| TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
| PILE REPERENCE: 6337-MO
| CURRENT APPLICATION NUMBER: US/10/255,032
| CURRENT APPLICATION NUMBER: DK PA 2001 01413
| PRIOR PILING DATE: 2001-09-27
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: PATENTIN VERSION 3.1
| SEQ ID NO 8
| LENGTH: 36
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                                         DB 1; Length 36;
                                                                                  3; Indels
                                         Score 13.2; D
Pred. No. 83;
0; Mismatches
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ORGANISM: Artificial Sequence
                                         Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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US-10-255-032-9/c
US-09-951-121A-9
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US-10-255-032-8
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; Sequence 9, Application US/10295682
; Publication No. US20030100740A1
; GENERAL INFORMATION:
; APPLICANT: Person, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Variants
; FILE REFERENCE: 6224.700-US
; CURRENT APPLICATION NUMBER: US/10/295,682
; CURRENT PILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PA 2000 01361
; PRIOR PILING DATE: 2000-09-13
; PRIOR FILING DATE: 2000-09-13
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NOS: 17
; SEQ ID NOS: 17
; SEQ ID NOS: 17
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US-10-295-682-8
US-10-295-682-8

JOS-10-295-682-8

Sequence 8, Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Disen, Joe Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 36
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Pred. No. 83;
0; Mismatches
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83.3%; Pred. No. 83;
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic US-10-295-682-8
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Best Local Similarity 83.33
Matches 15; Conservative
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Polypeptides

8 8 ö OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII , OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII US-10-281-727-3 . Length 36; 0.5%; Score 12.8; DB 1; Length 36; 87.5%; Pred. No. 1.2e+02; iive 0; Mismatches 2; Indels Query Match 0.5%; Score 12.8; DB 1; Length 3
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT APPLICATION NUMBER: PA 2001 01627
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
LENGTHRE: FastSEQ for Windows Version 4.0
SEQ ID NO 5 Sequence 3, Application US/10281727
Publication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
FILE REFERENCE: 6410.200-US CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0 406 TTCCAGGTGCAGGCAG 421 Query Match Best Local Similarity 87.5 Matches 14; Conservative TYPE: DNA ORGANISM: Unknown TYPE: DNA ORGANISM: Unknown US-10-281-727-2 FEATURE: FEATURE: RESULT 56 ò

ö Gaps ö Length 32 ; OTHER INFORMATION: DNA primer for preparation of S314E-FVII US-10-281-727-6 FEATURE:
; OTHER INFORMATION: DNA primer for preparation of S314E-FVII US-10-281-727-7 APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT FILING DATE: 2002-10-28
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-05
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7 Score 12.6; DB 1; Pred. No. 1.2e+02; 0; Mismatches FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
SOFTWARE: FastSEQ for Windows Version 4.0 290 CCAGGAGCAGGCAGGAAG 308 Sequence 7, Application US/10281727 Publication No. US20030130191A1 GENERAL INFORMATION: 2 ccrecadcadeaaceaad 20 0.5%; Query Match
Best Local Similarity 78.9
Matches 15; Conservative TYPE: DNA ORGANISM: Unknown TYPE: DNA ORGANISM: Unknown US-10-281-727-7/c SEQ ID NO 6 LENGTH: 32

Gaps . Indels Query Match 0.5%; Score 12.6; DB 1; Best Local Similarity 78.9%; Pred. No. 1.2e+02; Matches 15; Conservative 0; Mismatches 4; 290 CCAGGAGCAGGCAGGAAG 308

31 cercesácadeaacedaag 13 RESULT 59 US-10-349-858-8/C ð

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406 TICCAGGIGCAGGCAG 421

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Sequence 8, Application US/10349858
Publication No. US20930220247A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Children's Hospital of Philadelphia
APPLICANT: CAMIRE, RODNEY M.
APPLICANT: LARSON, PETER J.
APPLICANT: STAFFORD, DARREL W.
TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT CI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 11.8; DB 1; Length 5. Best Local Similarity 69.6%; Pred. No. 3.4e+02; Matches 16; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT:
    APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT APPLICATION NUMBER: PA.2001 01627
; FRIOR APPLICATION NUMBER: PA.2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; SEQ ID NO 6
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Publication No. US20030130191A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT PILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
FILLE OF INVENTION: FACTORS
FILE REFERENCE: 018743-0301425
CURRENT PELLING DATE: 2033-01-22
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR APPLICATION NUMBER: 60/124,609
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-10-349-858-8
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ORGANISM: Unknown
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APPLICANT: Nicolaisen, Else Marie
APPLICANT: Nicolaisen, Lars Soegaard
APPLICANT: Nicolaisen, Lars Soegaard
TITLE OF INVENTION: Method for the Production of Vitamin K-Dependent Proteins
FILE REFERENCE: 6270.204-US
CURRENT FILING DATE: 2003-109-02
FRIOR APPLICATION NUMBER: Danish application PA 2000 00456
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: Danish application PA 2001 00430
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/271, S81
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/276, 322
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: DNA primer for preparation of S314E-FVII
US-10-281-727-7
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PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 32
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US-10-398-422A-20
US-10-398-422A-20
Sequence 20, Application US/10398422A
Publication No. US20040058413A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
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LENGIH: 38
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Best Local Similarity 56.8
Matches 21, Conservative
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; OTHER INFORMATION: Probe
US-10-272-665-22
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ORGANISM: Homo Sapien
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                             APPLICANT: NOTE TO THE STATE APPLICANT: NOTE APPLICANT: NOTE APPLICANT: NOTE APPLICANT: Klausen, Niels K
APPLICANT: Klausen, Niels K
FILE OF TUNENTYNON: Factor VII Glycoforms
FILE REFERENCE: 620'.510-US
CURRENT APPLICATION NUMBER: US/09/969,357
CURRENT APPLICATION NUMBER: Danish Application No. PA 2000 01456
PRIOR FILING DATE: 2000-10-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
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Pred. No. 3.7e+02;
0; Mismatches 11; Indels
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0.4%; Score 11.4; DB 1; Length 38;
Best Local Similarity 62.1%; Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 11; Indels
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GENERAL INFORMATION:
APPLICANT: KONGRATION:
TITLE OF INVENTION: Method for Production of Recombinant
TITLE OF INVENTION: Proteins in Bukaryote Cells
TITLE OF INVENTION: Proteins in Bukaryote Cells
TITLE CE INVENTION: Proteins in Bukaryote Cells
FILE REFERENCE: 6480.500-US
CURRENT APPLICATION NUMBER: US/10/254,394
CURRENT APPLICATION NUMBER: PCT/DK01/00632
PRIOR APPLICATION NUMBER: PCT/DK01/00634
PRIOR FILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: PA 2002 00460
PRIOR APPLICATION NUMBER: PA 2002 00460
PRIOR PILING DATE: 2002-10-04
NUMBER OF SEC ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEC ID NOS: 2
LEAST AND SEC ID NOS: 2
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Novo Nordisk Pharmaceuticals, Inc.
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Publication No. US20030096366A1
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Best Local Similarity 62.1%;
Matches 18; Conservative
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Sequence 22, Application US/10272665
Fublication No. US20030180748A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
ITILE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POINTER. SPILORATION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POINTER. SPILORATION UMBER: US/10/272,665
CURRENT APPLICATION NUMBER: US/10/272,665
FRICE REFERENCE: 24736-20336
FRICE REPERIORS: 2002-01-15
FRICE APPLICATION NUMBER: 09/687,483
FRICE RELING DATE: 2000-07-10
FRICE FILING DATE: 2000-07-10
FRICE RELING DATE: 1999-10-13
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Sequence 22, Application US/10273321

Sublication No. US20030180749A1

SEMERAL INFORMATION:

APPLICANT: Braun et al.

ITILE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING POINTER. RILENGE INVENTION: GENERAL STACKERS

TITLE OF INVENTION: WETHODS (SENERATING DATABASES FOR IDENTIFYING POINTER. RILENGE AFFORCED: 10/2/23331

CURRENT APPLICATION NUMBER: US/10/273,321

CURRENT FILING DATE: 2000-07-10.

PRIOR FILING DATE: 2000-07-10.

PRIOR PLING DATE: 1999-10-13

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

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PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR PRIOR APPLICATION NUMBER: 60/217,251

PRIOR PRIOR PRIOR APPLICATION NUMBER: 09/663,968

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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 107, Application US/10273321
Sequence 107, Application US/10273321
Publication No. US20030180749A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033B
FILE REFERENCE: 24736-2033B
CURRENT APPLICATION NUMBER: US/10/273,321
CURRENT APPLICATION NUMBER: 09/687,483
FRIOR FILING DATE: 2002-07-10
FRIOR PAPLICATION NUMBER: 60/159,176
PRIOR PAPLICATION NUMBER: 60/159,176
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0.4%; Score 11.4; DB 1; Length 100;
Best Local Similarity 56.8%; Pred. No. 4.5e+02;
Matches 21; Conservative 0; Mismatches 16; Indels
                                                                                                                                                            Query Match 0.4%; Score 11.4; DB 1; Length 60; Best Local Similarity 56.8%; Pred. No. 4.6e+02; Matches 21; Conservative 0; Mismatches 16; Indels
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                                                                                          ; OTHER INFORMATION: Probe US-10-273-228-22
                      TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
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Sequence 22, Application No. US2000207297A1

GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERIC MARKERS
FILE REFERENCE: 2436-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 00/663,968
PRIOR APPLICATION NUMBER: 00/663,968
PRIOR APPLICATION NUMBER: 00/663,968
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US-10-272-756-22

Sequence 22, Application US/10272756

Fublication No. US20030190644A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERALIC, MARKERS

TITLE OF INVENTION: GENERALIC, MARKERS

TITLE OF INVENTION OF GENERALIC, MARKERS

FILE REFERENCE: 24736-2033C

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 09/687,483

PRIOR PLING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PLING DATE: 2000-09-19

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SEQUID NO 22

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Query Match

0.4%; Score 11.4; DB 1;
Best Local Similarity 56.8%; Pred. No. 4.6e+02;
Matches 21; Conservative 0; Mismatches 16;
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ORGANISM: Homo Sapien
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NUMBER OF SEQ ID NOS: 118 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 22 LENGTH: 60

Length 60;

; OTHER INFORMATION: Probe US-10-273-321-22

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RESULT 73

US-10-272-665-106

US-10-272-655-106

Sequence 1066, Application US/10272665

Publication No. US20030180748A1

GENERAL INFORMATION:

ITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POINTER. TELLING DATE: 2003-10-15

CURRENT FILING DATE: 2003-10-15

FILE REFERENCE: 24736-2033E

CURRENT TAILNG DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 09/687, 483

PRIOR APLICATION NUMBER: 60/217, 658

PRIOR PLING DATE: 2000-07-10

PRIOR PLING DATE: 2000-07-10

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PRIOR APPLICATION NUMBER: 09/663.968

PRIOR PLING DATE: 2000-07-10

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PRIOR APPLICATION NUMBER: 09/663.968

PRIOR PLING DATE: 2000-07-10

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Pred. No. 4.5e+02;
0; Mismatches 16;
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 100
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Best Local Similarity 56.8%;
Matches 21; Conservative
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US-10-273-228-107
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Publication No. US20000190644A1

GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERATIC MARKERS
FILE REFERENCE: 24736-2033C
CURRENT APPLICATION NUMBER: US/10/272,756
CURRENT FILING DATE: 2000-10-15
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,176
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
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NUMBER: 09/663,968
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Pred. No. 4.5e+02;
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Pred. No. 4.5e+02;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 100
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   PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/217,251
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-19
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1 Similarity 56.8%;
21; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapien
US-10-273-321-107
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; ORGANISM: Homo sapien
US-10-272-756-107
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Best Local Similarity
Matches 21; Conserva
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US-10-272-756-107
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US-10-273-228-107
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; Sequence 106, Application US/10273321 ; Publication No. US20030180749A1 ; GENERAL INFORMATION: RESULT 74 US-10-273-321-106

APPLICANT: Braun et al. TITLE OF INVENTION: MENTIC MARKERS TITLE OF INVENTION: GENETIC MARKERS FILE REFERENCE: 24736-2033B

APPLICANT: Braun et al.
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
FILE REFERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483

; Sequence 107, Application US/10273228 ; Publication No. US20030207297A1 ; GENERAL INFORMATION:

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GENETIC MARKERS

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; Sequence 14, Application US/09951121A
; Publication No. US20030104978A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Ole Hvisted
; TILE OP INVENTION: Human Casqulation Factor VII Variants
FILE REFERENCE: 6224.200-US
; CURRENT APPLICATION NUMBER: US/09/951,121A
; CURRENT APPLICATION NUMBER: EA 2000 01361
; PRIOR FILING DATE: 2000-09-13
; PRIOR PILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2598 CAGGGCCTATTGTAATAGGGTTTTAGCAGGGACATAT 2634
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                                                                   CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 2002-10-15
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PRIOR APPLICATION NUMBER: 60/127,658
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 106
LENGTH: 100
                                                                CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT FILING DATE: 2002-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: Synthetic US-09-951-121A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapien
US-10-273-228-106
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Sequence 106, Application US/10272756
Publication No. US20030190644al
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERATION DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENERAL OS/10/272,756
FILE REFERENCE: 2436-2033C
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 1999-10-13
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
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108-10-273-228-106
108-10-273-228-106
1 Sequence 106, Application US/10273228
2 Publication No. US20030207297A1
2 GENERAL INFORMATION:
1 APPLICANT: Braun et al.
2 TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/687,483
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
SOUTHWARE: FASTESE 2000-09-19
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; ORGANISM: Homo sapien US-10-272-756-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapien
US-10-273-321-106
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                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Persson, Bgon
ITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286,200-US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE PASSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 35
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Sequence 6, Application US/10109498

Publication No. US20030044908A1

GENERAL INFORMATION:
TILE OF INVENTION: Coagulation Factor VII Derivatives

FILE REFERENCE: 6286.200-US

CURRENT APPLICATION NUMBER: US/10/109,498

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                          Query Match

0.4%; Score 11.2; DB 1;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 CAGAGATTGCCTCTTCCAGGTGCAGGCAGGGC 424
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PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  1837 IGCAGIAGICIGGCCIGACAICIG 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10109498; Publication No. US20030044908A1; GENERAL INFORMATION:
                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                  FEATURE:

OTHER INFORMATION: Synthetic
US-10-295-682-15
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US-10-109-498-5/c
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10S-10-295-682-15
11S-20-205-682-15
1 Publication No. US20030100740A1
1 CENERAL INFORMATION:
1 APPLICANT: Person, Egon
1 TITLE OF INVENTION: Human Coagulation Factor VII Variants
1 FILE REFERENCE: 6224.200-US
1 CURRENT FILIATION NUMBER: US/10/295,682
1 CURRENT FILIATION NUMBER: BA 2000-1361
1 PRIOR APPLICATION NUMBER: 2002-11-15
1 PRIOR FILING DATE: 2000-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Person, Egon
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
TILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR PELING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PELING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PRIOR DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION WUMBER: US/09/951,121A
CURRENT APPLICATION WUMBER: US/09/13
PRIOR APPLICATION WUMBER: PA 2000 01361
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1837 TGCAGTAGTCTGGCCTGACATCTG 1860
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Publication No. US20030100740A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Synthetic US-09-951-121A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic US-10-295-682-14
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Matches 16; Conserv
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US-10-295-682-14/c
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LENGTH: 33
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Indels
13;
0; Mismatches
19; Conservative
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283 CACTCCTCCAGGAGCAGGCAGGGAAGAGCCTC 314 2 cacrecegrecadecrecadeaceaecre 33 TYPE: DNA ORGANISM: Artificial Matches g à ö 셤 ö Gaps 0 ö Query Match 0.4%; Score 11.2; DB 1; Length 42; Best Local Similarity 59.4%; Pred. No. 4.5e+02; Matches 19; Conservative 0; Mismatches 13; Indels Length 35; Ouery Match
0.4%; Score 11.2; DB 1; Length 3
Best Local Similarity 59.4%; Pred. No. 4e+02;
Matches 19; Conservative 0; Mismatches 13; Indels ; OTHER INFORMATION: Protein C mutagenic oligonucleotide US-09-803-810-8 Sequence 8, Application US/09803810; bublication No. US20010018414A1
GENERAL INFORMATION:
APPLICANT: VALSectuen, Gary L.
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT; TITLE OF INVENTION: POLYPEPTIDES; FILE REFERENCE: 09531/00201
CURRENT APPLICATION NUMBER: US/09/803,810
CURRENT FILING DATE: 2001-03-12; NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 42 US-10-296-330-8
Sequence 8, Application US/10298330
Sequence B. Application US/10298330
publication No. US20030100506A1
GENERAL INFORMATION:
TITLE OF INVENTION: Modified Vitamin K-Dependent
TITLE OF INVENTION: Modified Vitamin K-Dependent
TITLE OF INVENTION: Modified Vitamin K-Dependent
CURRENT APPLICATION NUMBER: US/10/298,330
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
SPRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0 283 CACTCCTCCAGGAGCAGGGAAGAGCCTC 314 393 CAGAGATTGCCTCTTCCAGGTGCAGGCAGGGC 424 ) ORGANISM: Artificial Sequence FEATURE: ) OTHER INFORMATION: Nucleotide Primer US-10-109-498-6 TYPE: DNA ORGANISM: Artificial Sequence RESULT 83 US-09-803-810-8

RESULT 85

US-10-398-422A-20/c

1 Sequence 20, Application US/10398422A

2 Publication No. US20040058413A1

3 GENERAL INCORMATION:
APPLICANT: Wiclaisen, Else Marie
APPLICANT: Wiclaisen, Else Marie
APPLICANT: Wiclaisen, Else Marie
APPLICANT: Wiclaisen, Else Warie
APPLICANT: Wiclaisen, Else Warie
APPLICANT: Wiclaisen, Else Warie
APPLICANT: Wiclaisen, Else Warie
APPLICANTON WHERE: 2004-05

CURRENT FILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
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PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRI ö Sequence 2, Application US/09969357

Publication No. US2002013767341

GENERAL INFORMATION:

APPLICANT: Pingel, Hans K

APPLICANT: Pingel, Hans K

APPLICANT: Pingel, Hans K

APPLICANT: Riamsen, Miels K

APPLICANT: Reper Number Niels K

TILE REFERENCE: 6207.510-US

CURRENT APPLICATION NUMBER: US/09/969,357

CURRENT APPLICATION NUMBER: Danish Application No. PA 2000 01456

PRIOR PILING DATE: 2000-10-02

PRIOR PLICATION NUMBER: Danish Application No. PA 2001 00262

PRIOR FILING DATE: 2001-02-16

PRIOR PLICATION NUMBER: Danish Application No. PA 2001 00430

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14

PRIOR PLING DATE: 2001-03-14 .. 0 Length 38; 0; Indels Query Match 0.4%; Score 11; DB 1; L. Best Local Similarity 100.0%; Pred: No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; CTHER INFORMATION: synthetic US-10-398-422A-20 285 CICCICCAGGA 295

Score 11.2; DB 1; Pred. No. 4.5e+02;

0.4%;

Query Match Best Local Similarity

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

; OTHER INFORMATION: Primer US-10-298-330-8

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280 GATCACTCCTCCAGGAGCAGGCAGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GAGTÁCCCCTCATGGCACCGACAGG 3
   PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-951-121A-14

. Sequence 14, Application US/09951121A
. Publication No. US20030104978A1
. GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
, OTHER INFORMATION: Synthetic
US-09-951-121A-14
                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-122-4
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Matches 13; Conserv
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LENGTH: 33
TYPE: DNA
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Sequence 4, Application US/10017122
GENERAL INFORMATION:
APPLICANT: MCCARCHY, Jeanette
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MM-007
CURRENT APPLICATION NUMBER: US/10/017,122
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 11; DB 1; Length 38; Best Local Similarity 100.0%; Pred. No. 4.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/254,394
CURRENT FILING DATE: 2002-09-25
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2002-03-66
PRIOR PILING DATE: 2002-04-66
PRIOR PILING DATE: 2002-06-67
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Best Local Similarity 100.0%; Pred. No. 1..
Matches 11; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/238,944
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/271,581
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 2
SOFWARE: Patentin version 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10254394
Publication No. US20030096366A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic US-09-969-357-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 CTCCTCCAGGA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 CTCCTCCAGGA 20
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial
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Gaps
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Sequence 15, Application US/09951121A
Sequence 15, Application US/09951121A
Sequence 15, Application US/09951121A
Sequence 15, Application No. US2030104978A1
GENERAL INFORMATION: Human Coagulation Factor VII Variants
TITLE OF INVONTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: BA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT Olsen, Ole Hvilsted
APPLICANT Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A
CURRENT PILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 333
      Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.4%; Score 10.6; DB 1; Length 33; 1 Similarity 76.5%; Pred. No. 5.9e+02; 13; Conservative 0; Mismatches 4; Indels
Query Match
0.4%; Score 10.6; DB 1;
Best Local Similarity 64.0%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 9;
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Gaps

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Score 10.6; DB 1; Length 33; Pred. No. 5.9e+02; 0; Mismatches 4; Indels

261 TGGAGGCTATGGCTCCT 277

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22 rescesceaeseacrecr

RESULT 93 US-09-951-121A-8/c

Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative

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ORGANISM: Artificial Sequence
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ö RESULT 91
US-10-295-682-14
i Sequence 14, Application US/10295682
sequence 14, Application US/10295682
sequence 14, Application US/10295682
sequence 14, Application Sequence 14
APPLICAMT: Persson, Egon
APPLICAMT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFREENCE: 6224-200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2000-11-15
PRIOR PELICATION NUMBER: PA 2000 01361
PRIOR PELICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 2355
SEQ ID NO 14
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TENEMEN OF Query Match 0.4%; Score 10.6; DB 1; Length 33; Best Local Similarity 76.5%; Pred. No. 5.9e+02; Matches 13; Conservative 0; Mismatches 4; Indels 261 TGGAGGCTATGGCTCCT 277 22 regececcaaecacrecr 6 TYPE: DNA ORGANISM: Artificial Sequence ; OTHER INFORMATION: Synthetic US-10-295-682-14 ) OTHER INFORMATION: Synthetic US-09-951-121A-15 Query Match ò

## Sequence 8, Application US/09951121A
## Sequence 8, Application US/09951121A
## CENERAL INFORMATION:
## APPLICANT: Person. Egon
## TITLE OF INFORMATION: Human Coagulation Factor VII Variants
## TITLE OF INFORMATION: Human Coagulation Factor VII Variants
## CURRENT FILING DATE: 2000-09-13
## PRIOR FILING DATE: 2000-09-13
## PRIOR PELICATION NUMBER: G6/236,455
## PRIOR FILING DATE: 2000-09-29
## PRIOR PELICATION NUMBER: G6/236,455
## PRIOR FILING DATE: 2000-09-29
## NUMBER OF SEQ ID NOS: 17
## SOFTHARE: EastSEQ for Windows Version 4.0
## SEG ID NO 8
## ILING DATE: AUTHOR OF SEG ID NOS: 17
## ILING DATE: 2000-09-29
## SOFTHARE: RestSEQ for Windows Version 4.0
## ILING DATE: 3000-09-29
## ILING DATE: 2000-09-29
## SEQ ID NO 8

0.4%; Score 10.6; DB 1; Length 33; 76.5%; Pred. No. 5.9e+02; tive 0; Mismatches 4; Indels 261 TGGAGGCTATGGCTCCT 277 12 resceecaaedacreer 28 Best Local Similarity 76.5 Matches 13; Conservative à

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Gaps

.. 0

Length 36; Indels

Query Match

0.4%; Score 10.6; DB 1;
Best Local Similarity 76.5%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 4;

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

; OTHER INFORMATION: Synthetic US-09-951-121A-8

2438 CACTITCAGGICCIGAA 2454

33 cacgrigaddaccrada 17

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8

Sequence 15.7

Sequence 15. Application US/10295682

Publication No. US20030100740A1

GENERAL INFORMATION:
APPLICANT: Person. Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/10/295,682

CURRENT FILING DATE: 2002-11-15
PRIOR PELING DATE: 2000-09-13
PRIOR PELING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17

SOFTWARE: FRASEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 33 RESULT 92 US-10-295-682-15/c

TYPE: DNA ORGANISM: Artificial Sequence

; OTHER INFORMATION: Synthetic US-10-295-682-15

NS-09-951-121A-9
; Sequence 9, Application US/09951121A
; Sequence 9, Application US/09951121A
; Publication No. US20030104978A1
; GENERAL INFORMATION:
 APPLICANT: OS 105en, Ole Hvilsted
 TILLE OP INVENTION: Human Coagulation Factor VII Variants
 FILE REPERENCE: 6224.200-US
; CURRENT APPLICATION NUMBER: US/09/951,121A
; CURRENT FILING DATE: 2001-09-13
; PRIOR PILING DATE: 2000-09-13
; PRIOR PILING DATE: 2000-09-29
; NUMBER: OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9: LENGTH: 36

Query Match
0.4%; Score 10.6; DB 1; Length 36;
Best Local Similarity 76.5%; Pred. No. 6.1e+02;
Matches 13; Conservative 0; Mismatches 4; Indels à

ORGANISM: Artificial Sequence

TYPE: DNA FEATURE:

OTHER INFORMATION: Synthetic

US-09-951-121A-9

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Gaps

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2438 CACTITCAGGICCTGAA 2454

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; TITLE OF INVENTION: Human Coagulation Factor VII Variants; FILE REFERENCE: 6224.200-US
; CURRENT APPLICATION NUMBER: US/10/295,692
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PA 2000 01361
; PRIOR APPLICATION NUMBER: PA 2000 01361
; PRIOR APPLICATION NUMBER: 0A/236,455
; PRIOR PILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO
; LENGTH: 36
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic US-10-295-682-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: DNA primer for preparation of E296V/M298Q-FVII US-10-255-032-9
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) Publication No. US20030100075A1
) Publication No. US20030100075A1
) GENERAL INFORMATION:
APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S
) TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
) FILE REPERENCE: 6157-WO

CURRENT APPLICATION NUMBER: US/10/255,032
) CURRENT APPLICATION NUMBER: DS PRIOR PRIOR DATE: 2001-09-27
) PRIOR FILING DATE: 2001-09-27
) NUMBER: OF SEQ ID NOS: 9
) SOFTWARE: Patentin Version 3.1
) SEQ ID NOS: 9
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TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
FILE REFRENCE: 6357-W0
CURRENT APPLICATION NUMBER: US/10/255,032
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: DK PA 2001 01413
PRIOR PILING DATE: 2001-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 10.6; DB 1; Length 36; Best Local Similarity 76.5%; Pred. No. 6.1e+02; Matches 13; Conservative 0; Mismatches 4; Indels
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                                                                                                        RESULT 95
US-10-255-032-8/c
Sequence 8, Application US/10255032
Publication No. US20030100075A1
GENERAL INFORMATION:
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US-10-295-682-8/c
S-quence 8, Application US/10295682
Publication No. US20030100740A1
GENERAL INPORMATION:
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       cacerreaddaccreda 20
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APPLICANT: Olsen, Ole Hvilsted
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ORGANISM: Artificial Sequence
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US-10-255-032-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8
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US-10-272-665-23
US-10-272-665-23
Sequence 23, Application US/10272665
Publication No. US20030180748A1
GENERAL INFORMATION:
APPLICANT: Braun et al.
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING FOR TITLE OF INVENTION: GENETIC MARKERS
TITLE OF INVENTION: GENETIC MARKERS
TITLE OF PLICATION UNMER: US/10/272,665
CURRENT PELING DATE: 2002-10-15
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; Sequence 9, Application US/10295682
; Publication No. US20030100740A1
; GENERAL INFORMATION:
    APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Variants
; FILE REFERENCE: 6224.200-US
; CURRENT APPLICATION NUMBER: US/10/295,682
; CURRENT FILING DATE: 2002-11-15
; PRIOR PLLING DATE: 2000-09-13
; PRIOR PLLING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 17
; SOFFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
LENGTH: 36
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     Length 36;
Query Match 0.4%; Score 10.6; DB 1; Length 36 Best Local Similarity 76.5%; Pred. No. 6.1e+02; Matches 13; Conservative 0; Mismatches 4; Indels
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Generace 23, Application US/10273321

Sequence 23, Application No. US20030180749A1

GENERAL INFORMATION:

APPLICATION NO. US20030180749A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PO

TITLE OF INVENTION: GENETIC MARKERS

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TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

TITLE OF INVENTION: GENETIC MARKERS

FILE REPRENCE: 24736-2033B

CURRENT FILING DATE: 2002-10-15

PRIOR PELICATION NUMBER: 60/217,658

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PELING DATE: 1999-10-10

PRIOR PELING DATE: 2000-07-10

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0.4%; Score 10.6; DB 1; Length 60;
Best Local Similarity 53.7%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 19; Indels
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Pred. No. 6.7e+02;
0; Mismatches 4;
                   CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 29061,483
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR PELING DATE: 2000-07-10
PRIOR PELING DATE: 2000-07-10
PRIOR PELING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 23
LENGTH: 60
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; Sequence 23, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION;
; APPLICANT: Braun et al.
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Best Local Similarity 76.5%;
Matches 13; Conservative
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US-10-273-321-23
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ORGANISM: Homo sapien
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Sequence 23, Application US/10272665

Publication No. US20031080748A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC

TITLE OF INVENTION: GENERAL MARKERS

FILE REPERINCE: 24736-2033E

CURRENT APPLICATION NUMBER: US/10/272,665

CURRENT APPLICATION NUMBER: US/10/210,665

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: 60/159,176

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 23

LENGTH: 60

LENGTH: 60
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Sequence 23, Application US/10273321
Sequence 23, Application World Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color Color
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0.4%; Score 10.6; DB 1; Length 60;
Best Local Similarity 53.7%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 19; Indels
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 1099-10-13
PRIOR PLING DATE: 1999-10-13
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-07-10
PRIOR PLING DATE: 2000-09-19
PRIOR PRIOR DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 60
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US-10-272-665-23
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; ORGANISM: Homo sapien
US-10-272-665-23
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US-10-272-665-23/c
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JURILICANT: Braun et al.

JITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PORTITE OF INVENTION: GENERATING DATABASES AND DATABASES FOR IDENTIFYING PORTITE OF INVENTION: GENERATING MARKERS
FILE OF INVENTION: GENERATION MARKERS
FILE REFERENCE: 24736-2033D
CURRENT APPLICATION NUMBER: US/10/273,228
CURRENT APPLICATION NUMBER: 0202-10-15
PRIOR APPLICATION NUMBER: 60/217,658
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/159,16
PRIOR APPLICATION NUMBER: 60/159,16
PRIOR APPLICATION NUMBER: 60/159,16
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
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PRIOR FILING DATE: 2000-09-10
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PRIOR FILING DATE: 2000-09-10
PRIOR FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR PRIOR FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-10
PRIOR APPLICATION NUMBER: 09/663,968
PRIOR FILING DATE: 2000-09-10
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Outs, Score 10.6, DB 1;
Best Local Similarity 76.5%; Pred. No. 6.7e+02;
Matches 13; Conservative 0; Mismatches 4;
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Pred. No. 6.7e+02;
0; Mismatches 19;
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                  US20030207297A1
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0.4%;
Best Local Similarity 53.7%;
Matches 22; Conservative 0
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; ORGANISM: Homo sapien
US-10-273-228-23
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US-10-273-228-23
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US-10-273-228-23/c
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LENGTH: 60
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; Sequence 23, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
    APPLICANT: Braun et al.
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
    TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING PC
    TITLE OF INVENTION: GANCE: 2002-10-15
    FILE REPREMENT 2000-07-10
    PRIOR APPLICATION NUMBER: 09/687, 483
    PRIOR FILING DATE: 2000-07-10
    PRIOR PLILING DATE: 2000-07-10
    PRIOR PLILING DATE: 2000-07-10
    PRIOR PLILING DATE: 2000-07-10
    PRIOR PLILING DATE: 2000-07-10
    PRIOR PLILING DATE: 2000-07-10
    PRIOR FILING DATE: 2000-07-10
    PRIOR FILING DATE: 2000-07-10
    PRIOR FILING DATE: 2000-09-19
    NUMBER OF SEC ID NOS: 118
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 23
    LENGTH. 6.0
TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
TITLE OF INVENTION: GENETIC MARKERS
FILE REFRENCE: 24796-2033C
CURRENT APPLICATION NUMBER: U5/10/272,756
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 23
LENGTH: 60
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US-10-273-228-23
; Sequence 23, Application US/10273228
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Best Local Similarity 76.5
Matches 13; Conservative
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ORGANISM: Homo sapien
US-10-272-756-23
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ORGANISM: Homo sapien
US-10-272-756-23
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Best Local Similarity
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US-10-272-756-23/c
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Sequence 23, Application US/10273228

FUDICATION OF US20030207297A1

GENERAL INFORMATION:

APPLICANT: Braun et al.

TITLE OF INVENTION: METHODS FOR GENERATING DATABASES FOR IDENTIFYING FOR TITLE OF INVENTION: GENERATING DATABASES FOR IDENTIFYING FOR TITLE OF INVENTION: GENERAL OSCIOLAGE

FILE REFERENCE: 24736-2033D

CURRENT APPLICATION NUMBER: US/10/273,228

CURRENT APPLICATION NUMBER: US/01/615

FRIOR APPLICATION NUMBER: 60/169,176

FRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-10

FRIOR PAPLICATION NUMBER: 60/159,176

FRIOR PLING DATE: 2000-07-10

FRIOR PLING DATE: 2000-07-10

FRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 118

SOFTWARE FRIENG DATE: 2000-09-19 ö Gaps .. 0 Indels

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3; Indels
Publication No. US20030044908A1
GENERAL INFORMATION:
APPLICANT: Perseno.
TITLE OF INVENTION: Cagulation Factor VII Derivatives
FILE REFERENCE: 6286.200 US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR APPLICATION NUMBER: PA 2001 00477
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FREASEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 35
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0.4%; Score 10.2; DB 1;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 12; Conservative 0; Mismatches 3;
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US-10-109-498-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10349858; Publication No. US20030220247A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: DNA primer for preparation of $314E/K316H-FVII
VS-10-281-727-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: DNA primer for preparation of S314E/K316H-FVII US-10-281-727-3
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0.4%; Score 10.4; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
0.4%; Score 10.4; DB 1; Length 36;
Best Local Similarity 70.0%; Pred. No. 7e+02;
Matches 14; Conservative 0; Mismatches 6; Indels
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Publication No US20030130191A1
GENERAL INFORMATION:
APPLICANT: Person, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: BOJYpeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: DA 2001 01627
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 3
IENGTHALS: FastSEQ for Windows Version 4.0
SEQ ID NO 3
IENGTHALS: AUGUSTANIA CONTRACTION OF SEQ ID NO 3
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APPLICANT: Person, Egon
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281,727
CURRENT PILING DATE: 2002-10-28
PRIOR PILING DATE: 2001-11-02
PRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
MANUAL HORSEN AND ADDITION NUMBER: PA 2001 11-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
MANUAL HORSEN AND ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDITION NUMBER ADDI
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US-10-109-498-5
; Sequence 5, Application US/10109498
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                                                                                                        ; Sequence 2, Application US/10281727; Publication No. US20030130191A1; GENERAL INFORMATION:
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ORGANISM: Unknown
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ORGANISM: Unknown
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US-10-281-727-3/c
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US-10-109-498-6/C

Sequence 6, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
APPLICANT: Persson, Egon
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286 200-US
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-03
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2001-04-03
; PRIOR PILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 10.2; DB 1;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 12; Conservative 0; Mismatches 3;
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Publication No. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Persion. Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPRENCE: 6224.200-US
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US/09/951,121A
PRIOR FILING DATE: 2000-09-13
PRIOR PLING DATE: 2000-09-13
PRIOR PAPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LEMOTH: 34
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APPLICANT: Olsen, Ole Hvisted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PA. 2000 01361
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                         ch 0.3%; Score 9.2; DB 1; 1 Similarity 63.6%; Pred. No. 1.2e+03; 14; Conservative 0; Mismatches 8;
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Pred. No. 1.2e+03;
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                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 63.6%;
Matches 14; Conservative
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                                                                    FEATURE:
// OTHER INFORMATION: Synthetic
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Best Local Similarity
Matches 14; Conserva
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TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT CITLE OF INVENTION: PACTORS
FILE REPERENCE: 01943-0301425
CURRENT APPLICATION NUMBER: US/10/349,858
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 09/526,947
PRIOR APPLICATION NUMBER: 06/124,609
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
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; Sequence 4, Application US/10017122
; Publication No. US2030087244A1
; Publication No. US20330087244A1
; GENERAL INFORMATION:
    APPLICANTY MCCARLEY, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-007
    CURRENT APPLICATION NUMBER: US/10/017,122
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/327,487
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; SEQ ID NO 4
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Pred. No. 8.3e+02;
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Best Local Similarity 61.5%;
Matches 16; Conservative
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Matches 13, Conservative
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; ORGANISM: Homo sapiens
US-10-349-858-8
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US-10-017-122-4
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                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 54
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US-10-298-330-8
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publication No. US20030100740A1
general invermation.
General invermation.
APPLICANT: Person, Egon
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2000-13-15
PRIOR APPLICATION NUMBER: PA 2000 01361
PRIOR PILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
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Query Match 0.3%; Score 9.2; DB 1; Length 34; Best Local Similarity 63.6%; Pred. No. 1.2e+03; Matches 14; Conservative 0; Mismatches 8; Indels
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0.3%; Score 9.2; DB 1; Length 34;
Best Local Similarity 63.6%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 8; Indels
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; Publication No. US20010018414A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
    TITLE OF INVENTION: POLYPEPTIDES
    FILE REPERENCE: 09531/002001
    CURRENT APPLICATION NUMBER: US/09/803,810
    CURRENT FILING DATE: 2001-03-12
    NUMBER OF SEQ ID NOS: 18
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 8
    LENGTH: 42
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US-09-803-810-8/c
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US-10-295-682-3/c
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Sequence 2, Application US/0995121A

Publication Wo. US20030104978A1

GENERAL INFORMATION:
APPLICANT: Olsen, Olsen, District Capulation Factor VII Variants
TITLE OF INVENTION: Human Casqulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT APPLICATION NUMBER: US/09/951,121A

CURRENT FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-13

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEC ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2:
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.3%; Score 8.8; DB 1; Length 42; Best Local Similarity 57.1%; Pred. No. 1.2e+03; Matches 16; Conservative 0; Mismatches 12; Indels
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Sequence 8, Application US/10298330
| Publication No US20030100506A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: Modified Vitamin K-Dependent
| TITLE OF INVENTION: POLIPSPICAGE
| FILE REFERENCE: 09531-127001
| CURRENT FILING DATE: 2002-11-18
| PRIOR FILING DATE: 2000-02-03
| PRIOR FILING DATE: 1999-04-29
| PRIOR FILING DATE: 1999-04-29
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Pred. No. 1.4e+03;
0; Mismatches 14
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Best Local Similarity 54.8%;
Matches 17; Conservative
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        Sequence 1, Application US/09951121A
Sequence 1, Application US/09951121A
Senemal INFORMATION:
GENERAL INFORMATION:
APPLICANT: Persson, Egon
APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVANTION: Human Coagulation Factor VII Variants
FILE REFERENCE: 6224.200-US
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: DA 2000 01361
PRIOR APPLICATION NUMBER: EA 2000 01361
PRIOR PILING DATE: 2000-09-13
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LEMOTH: 34
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APPLICANT: Olsen, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII Variants
FILE REPERENCE: 6224.200-u8
CURRENT APPLICATION NUMBER: US/10/295,682
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 60/236,455
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 17
SOPTWARE: FastSEQ for Windows Version 4.0
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0.3%; Score 8.6; DB 1; Length 34;
Best Local Similarity 54.8%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 14; Indels
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Publication No. US20030100740A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-295-682-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic
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US-09-951-121A-3
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Sequence 3, Application US/10295682 Publication No. US20030100740A1

US-10-295-682-3

GENERAL INFORMATION: APPLICANT: Persson, Egon

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### APPLICANT: Olsen, Ole Hvilsted
### TITLE OF INVENTION: Human Cagulation Factor VII Variants
### CURRENT PRINTON: Human Cagulation Factor VII Variants
### CURRENT APPLICATION NUMBER: US/10/295,682
### CURRENT PLING DATE: 2002-11-15
### PRIOR PILING DATE: 2002-11-15
### PRIOR FILING DATE: 2000-09-13
### PRIOR FILING DATE: 2000-09-29
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### NUMBER OF SEQ ID NOS: 17
### SOFTWARE: FastSEQ for Windows Version 4.0
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## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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August 9, 2004, 15:31:08 ; Search time 4 Seconds (without alignments) 3.740 Million cell updates/sec
nucleic search, using sw model
OM nucleic
                                            Run on:
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us-10-664-775-1 2715 1 ctgcaggaagaggcgacagg......ttgtaattctaggtgctgat 2715

Perfect score:

Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 Gapop 10.5 4 seqs, 2755 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 250 summaries

rstdb:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ACCESSION: AL531727	ACCESSION:A1116939	ACCESSION: AL531727	ACCESSION: AI099321	ACCESSION: AI116939	ACCESSION: AU099140	ACCESSION: AI099321	ACCESSION: AU099140
ai ai	AL531727	AI116939	AL531727	AI099321	AI116939	AU099140	AI099321	AU099140
DB	н	Н	Н	Н	Н	Н	Н	н
Query Match Length DB ID		645	1201	609	645	300	609	300
- 1		0.7	0.7	9.0	9.0	9.0	9.0	0.5
Score		19.8	18	17.2	17.2	17	16.3	14
Result No.	c C	2	٣	4	Ŋ	y	7	8 0

## ALIGNMENTS

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RESULT 1 AL531727/c LOCUS	AL531727 1201 bp mRNA linear EST 23-MAY-20
DEFINITION	AL531727 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODM003Y101 5-PRIME, mRNA secuence.
ACCESSION	AL531727
VERSION	AL531727.2 GI:31069559
KEYWORDS	BST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1201)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12795220.
	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - France

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases I to 645)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 02-SEP-1998
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The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
MAGE Consortium (info@image.llnl.gov) for further information.
MGI:930178
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/mol Lype="makan" darkers
/clone="CSODMON3Y101"
/tissue Lype="FETAL LIVER"
/dev stage="fetal"
/dev stage="fetal"
/dev stage="fetal"
/dev stage="fetal"
/dev stage="fetal"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Livitrogen. This sequence belongs to sequence cluster 7252.f For
more information about this cluster, sequence cluster 7252.f For
thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DW003AE01QPi&cluster=7252.f. Contact :
feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DM003AE01QPI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All16939 G45 bp mRNA linear EST 02-SI ue29908.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481822 5' similar to gb:Ml3232 COAGULATION FACTOR VII PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 20.6; DB 1; Length 1201;
59.3%; Pred. No. 0.31;
ative 0; Mismatches 24; Indels 0.
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/organism="Mus musculus"
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High quality sequence stop: 483.
Location/Qualifiers
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/clone="IMAGE:1481822"
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Mus musculus
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Best Local Similarity
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Gaps

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13; Indels

7; Mismatches

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AI099321
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/lab_host="DH10B"
/clone lb="Sugano mouse liver mlia"
/clone lb="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: liver; Vector: pME18S-FL3; Site_1: Brand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGG, 3' site CACTGTGG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCCACA."
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/dev_tsage="FETAL LIVER"
/dev_tsage="FETAL LIVER"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a Not1-cligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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BP 191 91006 EVRY cedex - France
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.8; DB 1;
Pred. No. 0.97;
0; Mismatches 12;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AL531727.2 GI:31069559
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Best Local Similarity 69.2<sup>3</sup>
Matches 27; Conservative
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AL531727
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Score 18; DB 1; Length 1201; Pred. No. 1.5;

0.7%;

Query Match Best Local Similarity

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/noce="Organ: liver; Vector: pWE185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pWE185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 609)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                               ue37b03.yl Sugano mouse liver mila Mus musculus cDNA clone
IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unpublished (1996)
Unpublished (1996)
Contact: Marka M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Email: mouseest@watson.wustl.edu
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2113 TCTCAAGGTTAGGAAATTTTTCTTTTTTGGTTTTCTTGAAAA 2154
                                     1148 TCCCAAAWHAGGAKAATTTTTTTKCGGTWWTYGAWGGAAA 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 GGCTATGGCTCCTTTGATCACTCCTCCAGGAGCAGGCA 302
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65.8%; Pred. No. 4.5;
tive 0; Mismatches
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High quality sequence stop: 289.
Location/Qualifiers
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/clone="IMAGE:1482509"
                                                                                                                                                                                                                                                                                                                                                                                           AI099321.1 GI:3448846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
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Best Local Similarity 65.8)
Matches 25, Conservative
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9 17:46:42 2004
Mon Aug
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RESULT 5 AI116939 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: ysuzuki@ina.u-cokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
                                                                                                                                                                        Eukaryotani, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (basea, 1 to 300.

1 uta, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S., In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2197 ICCTITGGITTITGCATAGIGICTCTGGCTTCCTGGATGTTTTATGCCT 2245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; Score 17; DB 1; Length 300; Best Local Similarity 59.2%; Pred. No. 10; Matches 29; Conservative 0; Mismatches 20; Indels
clone lambda-HVII2463, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                 AU099140
AU099140.1 GI:13550269
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo-capping method
Unpublished (2001)
                                                                                                                   Homo sapiens (human)
Homo sapiens
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/lab_host="DH10B"
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(CACTCTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
/ATGTGCCTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG); XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencings 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 645)
Marram, Hillier, L., Allan, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R. Tyle, I., Leunon, G., Soares, B., Wilson, R. and Waterston, R. The Washu-HHMI Mouse EST Project
Unpublished (1956)
Contact: Marza M/Mouse EST Project
Vashu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Fashington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseestGwatson.wustl.edu
This clone is available royalty-free through LINL; contact the
This clone is available royalty-free through LINL; contact the
MGI:930178
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                                                                                         EST 02-SEP-1998
                                                                            All16939
ue29908.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481822 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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Ouery Match
Best Local Similarity 65.8%; Pred. No. 4.3;
Matches 25; Conservative 0; Mismatches
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High quality sequence stop: 483.
Location/Qualifiers
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FEATURES

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Gaps

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Mus musculus (nouse mouse)

Mus musculus (nouse mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammallai, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 609)

8 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,C., Norris,M.,

Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra W/Mouse EST Project

WashU-HMI Mouse EST Project

WashU-HMI Mouse EST Project

WashU-HMI Mouse EST Project

WashU-HMI Mouse EST Project

WashU-HMI Mouse EST Project

The 114 286 1800

Fax: 314 286 1810

Email: mouseest@wastson.wustl.edu.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:930865 EST 20-AUG-1998 A1099321
ue37503.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1482509 5' similar to gb:M13232 COAGULATION FACTOR VII
PRECURSOR (HUMAN);, mRNA sequence.

LOCUS

RESULT 6 AU099140

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9 17:46:42 2004

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/lab_host="DH10B"
/clone llb="Sugano mouse liver mlia"
/clone llb="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (s' site CACTGTGTG, 3' site ACACATGTG)
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencings: 5' end primer CTTCTGCTCTRAAAAGCTGCG and 3' end
primer CGACCTGCAAGCACA."
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hef-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ilma.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
Ilength-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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L (bases, I to 300, T. Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S., Inmana, A. and Sugano, S., Inmana, A. and Sugano, S., Inman mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
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Ouery Match.

Best Local Similarity 63.5%; Pred. No. 6.5;
Matches 40; Conservative 0; Mismatches
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18;
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Job time : 4 secs
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## ALIGNMENTS

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I (bases I to 289)
Szostak, J. W., Roberts, R. W. and Liu, R.
Method for selection of proteins using RNA-protein fusions
Patent: US 6288558-A 17 10-JUL-2001;
Location/Qualifiers
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PAT 17-0CT-2001
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Szostak,J.W., Roberts,R.W. and Liu,R.
Szostak,J.W., Roberts,R.W. and Liu,R.
Mucleic acid-protein fusion molecules and libraries
Patent: US 6281344-A 17 28-AUG-2001,
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                                                                                           Unknown.
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                                                                                                                                            AUTHORS
TITLE
JOURNAL
FEATURES
                        LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                       ORGANISM
                                                                                                                                 REFERENCE
RESULT 2
AR166614
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1356 AGTGAGAAATAGATTTAAGGGCCTAGATCTGATAGACAGAGTACCTAATGAACTATGGAC 1415 9 Ouery Match 1.1%; Score 39.4; DB 1; Length 289; Best Local Similarity 12.9%; Pred. No. 0.0023; Matches 37; Conservative 100; Mismatches 150; Indels

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Gaps

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1535 1536 GAAAAGCAAAGGAAAAAAAGGAAAGATAAAAAGCATCTGAATGCAGAGTTCCAAAGAACTTC 1595 BC040125 Innear PRI 26-NOV-2002 Homo sapiens, similar to coagulation factor X, clone IMAGE:5764698, found 2898 TITITARCITITATGITATTATTAATTTIGGGATTITAACTATITCTAAAG 2957 1416 AGAGGTTCATGACATTGTACAGGAGACAGGGATCGAGACCATCCCCATGGAAAAGAAATG 1475 ö 61 RSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNR 120 121 RSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRN 180 Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: m Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961350.

Location/Qualifiers Craniata, Vertebrata, Euteleostomi; Catarrhini; Hominidae; Homo. Strausberg,R.

Direct Submission
Submitted (22-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, 191 RSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRCRARGRCRTRGRCRGRTRARA 1476 CAAAAAAGCAAAATGGCTGTCTGGGGAGGCCTTACAAATAGCTGTGAAAAGAAGAAGT Gaps WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anurad
Anup Madan, Jessica Pahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting / ... 1573 /organism="Homo sapiens" /mol_baref="taxon:9606" /clone="IMAGE:5764698" /clone="IMAGE:5764698" /clone="tibe"NH MGC_114" /lab_hos="tibe"NH MGC_114" /note="Vector: pGWV-SPORT6" .. 0 1596 CAGTIGITCAAGCIGGITITAGAAAAGICAGAGGAACCAGAGACCAA 1642 Length 1573; Indels 44: 1.1%; Score 37.6; DB 1; ilarity 59.3%; Pred. No. 0.01; Conservative 0; Mismatches 44; Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates, 1 (bases 1 to 1573) BC040125 BC040125.1 GI:25455627 Homo sapiens (human) Homo sapiens Query Match Best Local Similarity Matches 64; Conserv BC040125/c LOCUS SOURCE ORGANISM source DEFINITION REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS REMARK COMMENT FEATURES 8 a à 셤 δ g à g ò g

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VRT 25-JUL-2001

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NADSYMCLCAPGFSGRHCEQSIGDVLDSCLHDNGGCEHFCTEQDGRRNCSCADGYYLD
NSGQKCRSHEVFPCGKVPLLQAGKAADHQVDLRSRIVGGSECPKGHCPWQVLLKYGEK
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VSETADSDIALLRLRTPIVYSVYAVPVCLPLREMAERELWAVSKHTVSCWGKRSEDGP
TSRILRRLLVPRIRTQECVQVSNLTLISNMFCAGYIEGRQDSCKGDSGGPLVTRYRDT
                                                                                                                                                                                                                              Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cyprinidae, Danio.

1 (base 1 to 1671)

8 beeban, J. Templer, M., Gregory, M., Hanumanthaiah, R., Troyer, D., Phan, T., Thankavel, B. and Jagadeeswarn, P. Demonstration of the extrinsic coagulation pathway in teleostei: Bencillication of zebrafish coagulation factor VII

1353085
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Sheehan, J., Templer, M., Gregory, M., Hanumanthaiah, R., Troyer, D., Phan, T., Thankavel, B. and Jagadeeswaran, P.
Direct Submission
Submitted (14-JUN-2001) Cellular and Structural Biology, Universof Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229, USA
Location/Qualifiers
1. 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1473 GICTIGGATAATTAAAGTAATCGCCGICACTICATAATTAATATAAATTTTITTTATTTT
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/product="coagulation factor VII"
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Sequence 17 from patent US 6258558.
AR162089
AR162089.1 GI:16229155
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                                                                                                                        GI:15020317
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1 (bases 1 to 289)
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Direct Submission
Submitsed (14-JUN-2001) Cellular and Structural Biology, University
of Texas Health Science Center at San Antonio, 7703 Floyd Curl
Drive, San Antonio, TX 78229, USA
Location/Qualifiers
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Gypriniformes; Cyprinidae; Danio.

1, (bases 1 to 1671)

Sheehan,J., Templer,M., Gregory,M., Hanumanthaiah,R., Troyer,D., Phan,T., Thankavel,B. and Jagadeeswaran,P.

Demonstration of the extrinsic coagulation pathway in teleostei: identification of zebrafish coagulation factor VII

Proc. Natl. Acad. Sci. U.S.A. 98 (15), 8768-8773 (2001)
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Sheehan, J., Templer, M., Gregory, M., Hanumanthaiah, R., Troyer, D.,
Phan, T., Thankavel, B. and Jagadeeswaran, P.
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Danio rerio coagulation factor VII mRNA, complete cds.
AY040345
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Best Local Similarity 46.7%;
Matches 106; Conservative (
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Szostak,J.W., Roberts,R.W. and Liu,R.
Method for selection of proteins using RNA-protein fusions
Patent: US 625858-A 17 10-JUL-2001;
Location/Qualifiers
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12.7%; Pred. No. 0.54;
tive 89; Mismatches 151; Indels
                                                                                                                                          Query Match 0.8%; Score 30.2; DB 1; Length 2 Best Local Similarity 12.7%; Pred. No. 0.54; Matches 35; Conservative 89; Mismatches 151; Indels
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Szostak, J.W., Roberts, R.W. and Liu, R.
Nucleic acid-protein fusion molecules and
Nucleic acid-protein fusion molecules and
Patent: US 6281344-A 17 28-AUG-2001,
Location/Qualifiers
1 . 289
/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 17 from patent US 6281344.
AR166614 GI:16242009
                                                                                       /organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 12.7
Matches 35; Conservative
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

It (bases 1 to 1792)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Mooret, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Abramson, R.D., Millahy, S.J., Bosak, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Shaiska, U., Smallus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

NET 2238827
                                                                                                           Homo sapiens protein C (inactivator of coagulation factors Va and VIIIa), mRNA (cDNA clone MGC:34565 IMAGE:5188604), complete cds. BC034377.1 GI:21707770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnardne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg,R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
46 TYAYAYTYTYGYTYAYAYAYAYTYAYGYTYAYAYAYTY 12
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Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: h Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506114.

Location/Qualifiers

/organism="Homo sapiens" /mol_type="mRNA" /db_Xref="texon:9606" /clone="MGC:34565 IMAGE:5188604"

source

FEATURES

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10664775-2.rge

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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramason, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchaz, A., Mhiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schnerch, A., Schlein, J.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

L. 2238257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email.nih.gov
Tissue Procurement.afrC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov
Series: IRAK Plate: 14 Row: 1 Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21614535.
Location/Qualifiers
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/product="protease, serine, 22"
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/db_xref="161:16370275"
/db_xref="LocusID:64063"
/translation="MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKP
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SVLIGAWVIGAPOGSRSGKVGVAWVEPHPVYSWKEGACADIALVRLERSIGFSERVLPI
CLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQ
GPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLLAGIISWGBGCAERNRPGVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (29-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186. .902
/note="Tryp_SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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/clone_lib="NIH_MGC_70"
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                        Lissue type="Colon, Kidney, Stomach, adult, whole pooled"
/olone_lib="NIH MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                               \label{eq:product} protein \ \texttt{C} \ (inactivator \ of \ coagulation \ factors \ Valla)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFLEELRHSSLERECTEELCDFEEAKEIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
SLCCGHGTCTDGIGSFSCDCRSGWEGSFCQREVSFLNGSLDNGGCTHYCLEEVGWRRC
SCAPGYKLGDDLLQCHBAVKSCRFWKRNSHLKRDTEDQEDQVDDFLLDGKWRR
RRGDSFWQVVLLLDSKKKLACGAVLIHPSWVLFPAHCMDESKKLLNYLGEYDLSRWEKW
BLDLDIKEVYHPNYSKSTDNDIALHLAQPATACQTIVPTCLPBGSGLAERELNQAG
QETLVTWGWYYNSEREAKRANFTVLNFIKTOVPAHCGENGNWSENMCAGILLG
DRQDACEGDSGGPWVASFHGTWFLVAFIKTOVPHAGGGGLACHTGGTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present in a large number of membrane bound and extracellular (mostly animal) proteins. Many of these proteins require calcium for their biological function and calcium-binding sites have been found to be located at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO Sapiens protease, serine, 22, mRNA linear PRI 12-NOV-2003 HOMO Sapiens protease, serine, 22, mRNA (cDNA clone MGC:9599 PANACE:38999480), complete cds.
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Eukarydea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukarydea; Metazoa; Chordata; Craniata; Hominidae; Homo.

I (bases I to 1403)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAH34377.1"
/db_xref==G1:2170771"
/db_xref==LocusID:5664"
/translation="MWQLTSLLLFVATWGISGTPAPLDSVFSSSERAHQVLRIRKRAN
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/note="EGF_CA, Region: Calcium-binding EGF-like domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692. .1399
/note="Tryp SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125. .316
/note="GLA; Region: Domain containing Gla
/gamma-carboxyglutamate) residues"
/db_xref="CDD:smart00069"
353. .451
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57.6%; Pred. No. 1.2;
live 0; Mismatches
                                                                                                                 note="Vector: pCMV-SPORT6"
                                                                                                                                                                     /gene="PROC"
/db_xref="LocusID:5624"
/db_xref="MIM:176860"
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Best Local Similarity 57.61
Matches 53; Conservative
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BC009726/c
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PRI 05-APR-1995

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1758 CTTTTTCATAAACAGAGTATCCCCCTCAACACACACACAGCTTTAGACCCCGCAAAACTTGG 1699
                                                                                                                                   3345 CITITGIACITGCATTTATTGAAGTTTATGATTTATGAATTATGATGCTTTTTTTGGG 3404
                                                                                                                                                   Mammalia; Butelaca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1843)

Beckmann, N.J., Sohmidt, N.J., Santerre, R.F., Flutzky, J.,

Crabtree, G.R. and Long, G.L.

The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of cloned human liver cDNAs

Nucleic Acids Res. 13 (14), 5233-5247 (1985)
                                                                       3285 GAAGTITIGACAATGCTTTGAGCAATAATTTAGGATATTTTTGAATGGTTCATGAGTATG
           TTAAAGAATGTCATTCTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="unnamed protein product; protein C precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (aa 1-45)"
                                                                                                                                                                                                                                                                                                    linear
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/note="signal peptide (aa -42 to -10)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Data kindly reviewed (27-MAR-1986) by G. Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="light chain (aa 1-155)"
224. .358
/note="gamma carboxylation domain
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/note="EGF-domain II (aa 92-137)"
653. .730
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/note="EGF-domain I (aa 46-91)"
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              GITCIATGGCTITAATAAAGTTTTTTTTTTTTTT
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Human liver mRNA for protein C.
X02750
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/note="propeptide (aa
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protein C; signal peptide.
Homo sapiens (human)
Homo sapiens
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Kurachi, K. and Kurachi, S.
Kurachi, K. and Kurachi, S.
Nucleotide sequences for gene regulation and methods of use thereof
Patent: US 6610906-A 49 26-AUG-2003;
Location/Qualifiers
1. .1843
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0.8%; Score 27.7; DB 1; Length 1843;
Best Local Similarity 50.3%; Pred. No. 3.7;
Matches 92; Conservative 0; Mismatches 88; Indels 3.
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/organism="Homo sapiens"
/Orl type="unassigned DNA"
/db xref="textran:9606"
/noTe="EMBL/GenBank Accession No. X02750"
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AX411026
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Best Local Similarity 50.3%; Pred. No. 3.7;
Matches 92; Conservative 0; Mismatches
 Mismatches
                                                                                                                              Sequence 49 from patent US 6610906.
                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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Homo sapiens
 Conservative
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Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1758 CTTTTTCATÀAACAGAGTATCCĆCCTCÁACACACACAGCTTTAGACCCCGCÁAAACTTGG 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                      3345 CTTTTGTACTTGGCATTTATTGAAGTTTATGATTTATGAATTATGATGCTTTTTTTGGG
                                                                                                                                                                                                                                                                  Gaps
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0
'note="activation peptide region (aa 144-169)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3247 TITITITITITITITITAAAGAATGTCATICTITGTGAAGTTTTGA 3294
                                                                                                                                                                                                             Length 1843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             riririririririririciaakcagargcarriraargggaarcriaa 340
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                                                                                                   /note="serine protease region (aa 170-419)
1759. .1764
/note="polyA signal"
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                                                                                                                                                                                                                                                               88; Indels
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1 (bases 1 to 364)

Edwards, L.B.D.M., Jobert, S. and Giordano, J.-Y.

BST's and encoded human proteins

Patent: US 6639063-A 17202 28-OCT-2003;

Location/Qualifiers
                                                                                                                                                                                                          Score 27.7; DB 1;
Pred. No. 3.7;
0; Mismatches 88;
                           695. .1531
/note="heavy chain (aa 57-419)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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0.8%; Score 27.2; Di
Best Local Similarity 72.9%; Pred. No. 3.4;
Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease homologs
Patent: US 6331427-A 41 18-DEC-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/wol_type="genomic DNA"
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AR425705.1 GI:40180815
                                                                                                                                                                                                             0.8%;
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Robison, K.E.
                                                                                .1531
                                                                                                                                                                                                                                      Best Local Similarity 50.3
Matches 92; Conservative
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                                                                                misc_feature
                                                                                                                                  misc_feature
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SOURCE
ORGANISM
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AR425705
LOCUS
DEFINITION
ACCESSION
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AR263863/C
LOCUS
DEFINITION
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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TITLE
JOURNAL
FEATURES
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PAT 18-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                   134 YRKYRSRGMCCAMCAGSGMCYSRSAGSRYSKKGSRGRWYWKKGCSRATSKKGRMMMKKG 193
                                                                                                                                                                                                                                                                                 310 AGAAGGGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTATGAAA 369
                                                                                                                                                                                                                                                                                                                                                                                 370 AGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTGCCCCATATGCT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CI2N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 AGAAGGGAATGCAAACCACTTCAGTATTCTTGCCTTGAGAACCCCATGAACAGTATGAAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 SRRRATSRYGMYSSMYGASKRMSSACTRMSGASCMMYMMSAGSYASCAWKMSKRR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0S-AUG-1999 US 60/147499
JEAN BAPUTIST DUWAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE
                                                                                                                                                                                                                                                                                                              194 SRRRATSRYGNMSSMYGASKRMSSMCSASTRMSSASCMMYMYMSAGSYASCAWKMSKYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 TGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGTGGTCCACTGG
                                                                                                                                                                               250 TGGGGCAACCCAAGATGGGCAGGTCATGGTGGAGAGATCTGACAGAATGTGGTCCACTGG
                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 26.6; DB 1; Length 364;
15.7%; Pred. No. 4.8;
tive 76; Mismatches 80; Indels
                                                                               DB 1; Length 364;
                                                                                                                               80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 364)
Edwards, J.B.D.M., Jobert, S. and Glordano, J.E.
EST and encoded human protein
GENETH: JP 2002010789-A 13335 15-JAN-2002;
GENSET CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST and encoded human protein
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                             ch 0.7%; Score 26.6; Di
1 Similarity 15.7%; Pred. No. 4.8;
29; Conservative 76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .364
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/organism="unknown"
/wol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
JP 2002010789-A/13335
15-JAN-2002
07-AN-2000 JP 2000280889
05-AUG-1999 US 60/147499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded human protein.
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BD121258
BD121258.1 GI:23216168
JP 2002010789-A/13335.
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REFERENCE
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                                                              COMMENT
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E40671.
E40671.1 GI:18625105
UP 2000135094-A/1.
Sus scrofa (pig)
EURATOOLOGY
ENGLISH (pig)
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                                                                                                                                                                                                                                                                                                                                                                              AY022485 230 bp DNA linear PLN 07-FEB-2001 Oryza sativa microsatellite MRG4810 containing (AGG)X10, genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
Direct Submission.

Bundited (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
Slud, Creve Coeur, MO 63167, USA
Derived Irom rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Oryza sativa
Coryza sativa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Valoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (Dases I to 230)
Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G.F.
Simple sequence repeats from Monsanto rice genomic sequences
Unpublished
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370 AGGCAAAATGATAGGATACTGAAAGAGGAACTCCCCAGGTCAGTAGGTGCCCCATATGCT 429
                                        254 CAKWSCTYSWYMRASMKKSKYCAWSRKGSKCCMYSRKGSKSCYCCWGGSCCCCGCCAGCA 313
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Yamashita, M., Iida, K. and Kido, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2588 TGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGAAGGGGACGACGACAGAGA
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/organism="Oryza sativa"
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1. .230
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                                                                                                                                       430 ACTGG 434
                                                                                                                                                                                                      314 GCAGG 318
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Mus musculus (house mouse)

Mus musculus

ENKaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa (Chordata; Sciurognathi; Muridae; Murinae; Musculus

Enkaryota, Feingold, E.A., Grouse, L.H., Derge, J.G.,

I (bases 1 to 829)

Straubsborg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collinhs, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieb, F.,

Diatchenko, L., Marusina, K., Fermer, A.A., Burg, J., Haieb, F.,

Diatchenko, L., Marusina, K., Bomaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Moriey, K.C., Hale, S., Garcia, A.M., Morkan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Worley, K.C., Hale, S., Garcia, A.M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Youndh, Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC061135 829 bp mRNA linear ROD 25-NOV-2003 Mus musculus trypsin 4, mRNA (cDNA clone MGC:74265 INAGE:30306436), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 Aggecerragadeadeadearecareageaaaagaaageceeragacaaagageeer 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12P21/08, (C12N15/09, C12R1:91), (C12N1/21, C12R1:19), (C12N9/64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 1GCTGGTGCTGGCGCTGCCCCTCCTGGTGAGCCTGGTCCACACGGCCCCCGCCCCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2594 AGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGGAGGACGACAGAGAGATGAGAT
                                                                                                                                                                                                                                                                                                                                          MAKOTO YAMASHITA, KENJI IIDA, HIROSHI KIDO
CIZNI5/09, CO7K16/40, CIZN1/21, CIZN9/64, CIZQ1/70, G01N33/15,
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(1) . (825)
(2) peptide (1) . (805)
(1) peptide (91) . (825) .

Location/Qualifiers

1 . 828
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
Patent: JP 2000135094-A 1 16-MAY-2000;
SANKYO CO LTD
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0.7%; Score 26.2; DE
Best Local Similarity 49.6%; Pred. No. 7.5;
Matches 67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12R1:19),
C12N15/00, (C12N15/00,C12R1:91)
                                                                                            Sus scrofa (pig)
JP 2000135094-A/1
16-MAY-2000
24-AUG-1999 JP 1999236296
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mat_peptide
                                                                                                  Sus scr

PN JP 2000

PN 16-MAY-

PF 24-AUG-

PR MAKCTO

PC C12N15/

G01N33/50//

PC C12P21/

PC C12P21/

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BC061135/c
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VERSION
KEYWORDS
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Page 10

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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%;
Best Local Similarity 70.8%;
Matches 34; Conservative
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                                                                                                     GI:589297
                                                                                                                                                                                  Unclassified.
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                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: o Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755892. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHFCGGSLINDWWVSAAHCYKSRIOVRLGEHNINVLEGNBOFVNSAKIIKHPNFNSR
TLANDIMLIKLASPVTLNARVATVALPSSCAPAGTQCLISGWGNTLSFGVNNPDLLQC
LDAPLLPQADCEASYPGKITNNMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRALLFLALVGAAVAFPVDDDDKIVGGYTCRENSVPYQVSLNSG"
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                                                                                                   Strausberg, R.

Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="Tryp_SPc; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein / Ted Usdin
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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/db_xref="LocusID:22074"
/db_xref="MGI:102757"
                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .829
/organism="Mus musculus"
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                                                                                  (bases 1 to 829)
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morernon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC061149 11869 bp mRNA linear ROD 25-NOV-2003 Wus musculus coagulation factor VII, mRNA (cDNA clone MGC:74281 IMAGE:30305571), complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1869)
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Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2438)
Hagen, F.S., Murray, M.J., Busby, S.J., Berkner, K.L., Insley, M.Y., Woodbury, R.G. and Gray, C.L.
Expression of factor VII and IX activities in mammalian cells Patent: EP 0200421-A2 6 10-DEC-1986;
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Pred. No. 14;
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/wol_type="unassigned DNA"
107991 2438 bp
Sequence 6 from Patent BP 0200421.
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NIH-MGC Project URL: http://mgc.nci.nih.gov

REMARK

768 C 768

PAT 27-MAR-2003

linear

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Padigaru, M., Li, L., Zerhusen, B.D., Casman, S.J., Shenoy, S., Spytek, K.A., Zhong, M., Gangolli, B.A., Burgess, C.E., Patturajan, M., Ventet, C.A., Taylor, S., Tchernev, V.T., Miller, C.E., Guo, X., Boldog, F.L., Grosse, M.M., Alsobrook, J.P., Gerlach, V., Malyankar, S., Rothenberg, M.B., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and Stone, D.J.
                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO 02055704-A 33 18-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
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                                                                                                                                 AX675583.1 GI:29333568
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
B. K. M. Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 53 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753805.

Location/Qualifiers
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CGAVLLDARTUTAAHCFDNIRYWGINITVWGEHDFSEKDGDEQVRRYTQVIMPDKYI
RGKINHDIALLRALRPVFTDVVVPLCLPEKSFSENTLARIRFSRVSGWGQLLDRGAT
ALELMSIEVPRLMTQDCLEFAKHSSNTPKITENMFCAGYMDGTKDAGKGDSGGPHATH
YHGTWYLTGVVSWGEGCAAIGHIGVYTRVSQYIDMLVRHMDSKLQVGVFRLPLL"
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/db_xref="CDD:cd00190"
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                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein / Ted Usdin
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/lab host="DH108"
/note="Vector: pDNR-LIB"
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db_xref="MGI:109325"
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Contact: MGC help desk
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Best Local Similarity 78.9
Matches 30; Conservative
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2620 GGCAGGAGGAGAAGGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG 2679
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Query Match 0.7%; Score 25; DB 1; Length 882; Best Local Similarity 50.0%; Pred. No. 15; Matches 86; Conservative 0; Mismatches 80; Indels
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Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 65,9063-A 17202 28-OCT-2003;
Location/Qualifiers
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Sequence 17202 from patent US 6639063.
AR425705
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RESULT 21

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2730 TCCTGCGGCGATTCATGGGGTC 2751
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AY083553.1 GI:20146915
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                                                                                                                                                                                                                               Oryza sativa
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AY083553/c
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SOURCE
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AY022941/c
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                                                    2610 AGGGATTGGGGGCAGGAGAAGGGGACAACAGAGATGAGATGGCTGGATGGCATCAC 2669
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198 TYYYSCMMKWKKYCMMSATYSGCMMWRWYCYSCMMSRYSCTSYSRGKGSCTGWKGKCYG
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                                                                                                                                           : :::: : : | :::: : : | 138 -----YRMYRGRWWYYRMSRGARRYTKRSRGWCRSTKRYRKTCASWGAKGTKWCCMRMGS 84
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Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent; JP 2002010789-A 13335 15-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 364;
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Orange Deal Similarity 12.2%; Professional Similarity 12.2%; Professional Similarity 12.2%; Professional Similarity 11.3%; Professional Similarity 11.3%; Mismatches 108; Indels Matches 132; Conservative 117; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                     linear
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Kev Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     DNA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002010789-A/13335
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/14749
                                                                                                                                                                                                                                                                                                                   364 by
EST and encoded human protein.
BD121258
                                                                                                                                                                                              2730 TCCTGCGGCGATTCATGGGGTC 2751
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                                                                                                                                                                                                                BD121258.1 GI:23216168
JP 2002010789-A/13335.
Homo sapiens (human)
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source
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PC C12N1
C12N1/21,
PC C12N5/00
CC C12N15/00
CC EST at
FH Key
FT SOULC
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BD121258/c
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2 (bases 1 to 251)
Norgren,R.B. Jr., Zink,M.A., Jia,Y., Ojeda,S.R. and Spindel,B.R.
Direct Submission
Submitted (11-MAR-2002) Molecular and Cellular Biology Core, Oregon
Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
                                                                                                                                                   AY022941 227 bp DNA linear PLN 07-F5B-2001
Oryza sativa microsatellite MRG5266 containing (CTC)X9, genomic
sequence.
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gene, 3' UTR.
                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
Sukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae, Oryzae; Oryza.
Enrhartoideae, Oryzae; Oryza.
I Chases 1 to 227)
Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G.F.
Simple sequence repeats from Monsanto rice genomic sequences
Unphilished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tao, N., Barbaruk, W.B., Liu, J., Wu, K. and Barry, G.F.
Direct Submission
Submission
Submission
Submission
Blyd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
thtp://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
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1 (bases 1 to 251)
Norgren, R. B. Jr., Zink, M.A., Jia, Y., Ojeda, S.R. and Spindel, E.R. Construction of a targeted rhesus macaque microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2595 GACCCTGATGCTGGGAGGGATTGGGGGCCAGGAGGAGGAGGGACGACAGAGGATGAGATG
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/mol type="genomic DNA"
/db_rref="taxon:4530"
1. .227
/note="microsatellite MRG5266"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 24.8; Di
Best Local Similarity 63.3%; Pred. No. 12;
Best Ches 38; Conservative 0; Mismatches
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Macaca mulatta
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23 CTCCMGGCGGYTYCMKSCSRYY
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2957 GACTIGTATTTCTAATATTTACTTATTCTATTTTACTTTAATTGCACTTATTTTATTGA 3016

474 GACTGTTTTTCCTGATGTGGACTATGTAATTCTACTGAAGCTGAAACCATTTTGGATAA

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Gaps .. 0

37; Indels

Pred. No. 17; 0; Mismatches

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Best Local Similarity 56.0%;
Matches 47; Conservative (
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E01075/c
LOCUS
DEFINITION
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/db_xref="GB8:G00-119-900"
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/translation="NANKILNRPERY"
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PPDDVYVNSTERATILDNITGSTQSFNDFTRVVGGEDAKPGOPPWQVYLNGKVDAFCG
GSIVNEKMIVTAAHCVFTGVKITVVAGEHNIBETEHTEOKRNVIRIIPHHNYNAAINK
YNHDIALLEDDEPLY
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                                                                                                                                                                                                                                                                                                   3172 TTATTTTTGTAAATTAGCTCTTTAAATTCATTATTCTTTGATAACAGCTTCAGTTCTAT 3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 01-NOV-1994
                                                                                                                                                                                                                                                                                                                                    190 TCATCATTACCAAAAACTCGCCATAACAACACCCAAGAAAAAATGTTTAAGCCACAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                       3232 GGCTTTAATAAAGTTTTTTTTTTTTTTTTTTTAAAGAATGTCATTCTTTGTGAAGTTT
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jagadeeswaran, P., Lavelle, D.E., Kaul, R., Mohandas, T. and
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Location/Qualifiers
                                                                                                                                                                                                                                Length 251;
                                                                                                                                                                                                                                                              72; Indels
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                                                                                                                                                    /product="growth associated protein 43" <1. .>251
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Human coagulation factor IX mRNA, partial cds.
                                                                                                                                                                                                                                DB 1;
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M35672.1 GI:180287
coagulation factor IX; serine protease.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="coagulation factor IX"
                                                                                                                                                                                                                            Query Match
0.7%; Score 24.8; D
Best Local Similarity 48.6%; Pred. No. 13;
Matches 68; Conservative 0; Mismatches
                l. .251
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                                                /mol_type="genomic DNA"
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Location/Qualifiers
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                                                                                                                      <1. .>251
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                                                                                                      /gene="GAP43"
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/gene="F9"
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HUMCFIX
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         PAT 29-SEP-1997
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Purederitsuku, E.H., Maaku, J.M., Shiyaaron, J.B., Kiyasuriin, E.B., Burederitsuku, E.H., Michiyaado, J.U. and Chiyaaruzu, E.G. DNA ENCODING FACTOR VI. 106-JAN-1987;
PARCOLING FACTOR VI. 106-JAN-1987;
PHEMOJIENETITSUKUGU INC NIPPON SODA CO LTD, NISSAN CHEM IND LTD, TOYO SODA MFG CO LTD
OS Human {Homo sapiens}
PN JP 1987000283-A/1
PD 06-JAN-1987
PD 106-JAN-1987
PD 106-JAN-1987
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*source: library=cDNA library, lambdagt11 cDNA library; CC
rce: clone=lambdaVII 2115, lambdaVII 1923; FH Key
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PR 17-ARE-1985 US 85 724311, 16-DEC-1985 US 85 810002 P
FUREDERITSUKU ESU HAAGEN, MAAKU JIEI MARII,
PI SHIYAARON JIEI BAZUBII,
PI KIYAAROD JII UYSUDOBRII,
CHIYAAROD JII UYSUDOBRII, CHIYAARUZU ERU GUREI PC
CLANI5/00, AGIKZ7/465, CI2NS/00, CI2N9/50, (CI2N9/50, CI2R1:91); CC
strandedness: Double;
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/product='factor VII peptide'
         linear
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Human S protein-alpha (PS-alpha) gene, exon 2.
M57841 J02917
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Pred. No. 21;
CDNA sequence of factor VII fragment.
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Location/Qualifiers
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/organism="unidentified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            topology: Linear;
hypothetical: No;
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                                                         E01075.1 GI:2169334
JP 1987000283-A/1.
unidentified
unclentified
unclassified.
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ilarity 72.7%;
Conservative
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FH
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FT exon
FT 3'UTR
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HUMPS02/c
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0.7%; Score 24.8; DB 1; Length 873,

Query Match

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AX697671 1378 bp D
Sequence 262 from Patent WO0104311.
AX697671.1 GI:29498757
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Homo sapiens serine protease PRSS22 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (14-NOV-2000) Rheumatology, Immunology and Allergy,
Brigham and Women's Hospital, Harvard Medical School, 1 Jimmy Fund
Way, Boston, MA 02115, USA
Location/Qualifiers
                                                                                     Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 352)
Schmidel, D.K., Tatro, A.V., Phelps, L.G., Tomczak, J.A. and Long, G.L. Organization of the human protein S genes
Biochemistry 29 (34), 7845-7852 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 1332)

Wong, G.W., Yasuda, S., Madhusudhan, W.S., Li, L., Yang, Y.,

Krilis, S.A., Sali, A. and Stevens, R.L.

Krilis, S.A., Sali, A. and Stevens, R.L.

16p13.3 family of human serine proteases expressed in airway epithelial cells
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 M57841.1 GI:190535
S protein; anticoagulant cofactor; vitamin K-dependent protein.
2 of 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          /gene="PS-alpha"
order(MS7840.1:913. .1014,1. .134)
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                                                                                                                                                                                                                                                                                                                                                              /tiŝsue_type="liver"
join(M57840.1:837. .912,135. .181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 276 (52), 49169-49182 (2001)
                                                                                                                                                                                                                                    Original source text: Human liver DNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
0.7%; Score 24.6; Di
Best Local Similarity 51.4%; Pred. No. 16;
Matches 57; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                       Homo sapiens (human)
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                                                                            Homo sapiens
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/ Lissue Lype="pancreas"

18. .971
/ Cissue Lype="pancreas"

18. .971
/ Codon_start=
/ product="eerine protease PRSS22"
/ protein id="AAG35070.1"
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CLPDASSHLEPWICAGYTLEGERSDACLGDSGGPLMCQVDGAMLAG1ISWGEGCAERNRPGYZI
SLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGGSGAAARS"
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Sakhenazi,A., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N., Filvaroff,E., Fong,S., Gao,W.-Q., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Stlavin,L.J., Mather,J.P., Pani,J., Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding
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0.7%; Score 24.6; DB 1; Length 1:
Best Local Similarity 53.7%; Pred. No. 21;
Matches 51; Conservative 0; Mismatches 44; Indels
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Location/Qualifiers
1. 1378
/organism="unknown"
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Best Local Similarity 53.7%; Pred. No. 22;
Matches 51; Conservative 0; Mismatches
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PF 18-DEC-2
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17-SEP-1997 U
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21-OCT-1997
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                                                                            Ashkenazi, A.J., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E., Goddard, E., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding
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             Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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60 (059112,17-52F-1997 W
60 (059113,17-52F-1997 W
60 (059266,15-00T-1997 W
60 (062287,17-00T-1997 W
60 (063287,17-00T-1997 W
60 (063120,24-00T-1997 W
60 (063329,27-00T-1997 W
60 (063329,27-00T-1997 W
60 (063329,27-00T-1997 W
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OS Home sapiens (human)
PD 02-OCT-2001
PD 02-OCT-2019
PP 16-SEP-1998 JP 2000511867
PP 17-SEP-1997 US 60/059115,17-SEP-
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60/063704,29-OCT-1997
60/064215,29-OCT-1997
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60/063544, 28-OCT-1997
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/db_xref="taxon:9606"
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Location/Qualifiers
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JP 2001516580-A/214.
Homo sapiens (human)
Homo sapiens
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Secreted and transmembrane polypeptides and nucleic acids encoding
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C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
C12N1/19,
C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, P
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Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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       60/063870 | 60/064809 | 60/065846 | 60/066120 | 60/066772 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/066770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/06770 | 60/067
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          1332 ATTTATTCCTCCAATTTCAATAAATTATTATTCT 1366
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33.7%; Pred. No. 22;
ve 0; Mismatches 44;
60/064103,31-OCT-1997 U.
60/065186,17-NOV-1997 U.
60/065186,17-NOV-1997 U.
60/06563,21-NOV-1997 U.
60/066364,24-NOV-1997 U.
60/066466,24-NOV-1997 U.
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6()059113,17-SEP-1997 US
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6()05926,15-0CT-1997 US
6()062287,17-0CT-1997 US
6()063486,24-0CT-1997 US
6()063120,24-0CT-1997 US
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GENENTECH INC
S Home 200223786-A/214
PD 13-AUG-2002
PP 18-DEC-2001 JP 2001385135
PR 17-SEP-1997 US 60/059115,17-SEP-
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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C12N15/00,C12N5/00
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JP 2002223786-A/214.
Homo sapiens (human)
Homo sapiens
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Secreted and transmembrane polypeptides and nucleic acids encoding the same.
BD173079.1 GI:28414388
JP 2002238587-A/214.
Homo sapiens (human)
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C12N1S/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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1 (bases 1 to 1378)
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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0.7%; Score 24.6; D
Best Local Similarity 53.7%; Pred. No. 22;
Matches 51; Conservative 0; Mismatches
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Secreted and transmembrane polypeptides and nucleic acids encoding
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1378)
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OS Homo sapiens (human)
PN JP 2002238586-A/214
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059113,PR
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C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21,
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                    60/063327 PR
60/063541 PR
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1. .1378
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        27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/06354, 28-OCT-1997 US 60/06354, 28-OCT-1997 US 60/06354, 28-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063370, 23-OCT-1997 US 60/063370, 23-NOV-1997 US 60/063870, 03-NOV-1997 US 60/0653870, 03-NOV-1997 US 60/0653870, 03-NOV-1997 US 60/0653870, 03-NOV-1997 US 60/0653870, 03-NOV-1997 US 60/065120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066120, 21-NOV-1997 US 60
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Best Local Similarity 53.7%; Pred. No. 22;
Matches 51; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD172760.1 GI:28414064
JP 2002238586-A/214.
Homo sapiens (human)
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FH Key
FT source
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BD172760
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Secreted and transmembrane polypeptides and nucleic acids encoding
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PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
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60/062816 E
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                                                                                             US 60/059115,17-SEP-1997 US 60/05912,17-SEP-1997 US 60/05912,17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059266,15-OCT-1997 US 60/059266,15-OCT-1997 US 60/063129,24-OCT-1997 US 60/063129,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/06350,24-OCT-1997 US 60/063870,03-NOV-1997 US 60/064809,12-NOV-1997 US 60/066120,21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066772,24-NOV-1997 US
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Patent: JP 2002238587-A 214 27-AUG-2002;

GENENTECH INC

OS Homo sapiens (human)

PD 27-AUG-2002

PP 27-AUG-2002

PP 18-DEC-2001

PP 18-DEC-2001

PP 17-SEP-1997 US 60/059115,17-SEP-1
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0.7%; Score 24.6; Dest Local Similarity 53.7%; Pred. No. 22;
Matches 51; Conservative 0; Mismatches
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1. 1378
/ Organism="Hono sapiens"
//mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD173398
BD173398.1 GI:28414709
JP 2002238588-A/214.
Homo sapiens (human)
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17. SEP-1997 US
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BD173398
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DEFINITION
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17-1997 US 60(05246).1.

21-077-1997 US 60(06248).1.

22-077-1997 US 60(062120,24-07-1-2).

22-077-1997 US 60(063120,24-07-1-2).

22-077-1997 US 60(063120,24-07-1-19).

22-077-1997 US 60(063120,24-07-1-19).

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25-077-1997 US 60(063120,24-07-1-19).

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                                                                                                                                                                                   encoding
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1378) Mood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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Secreted and transmembrane polypeptides and nucleic acids
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Pred. No. 22;
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OS Homo sapiens (human)
PN JP 200223888-A/214
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059122.17-SIP-1997 US 60/059113,17-SI
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1272 TTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGTAACCCTGCCCACATATCTT 1331
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53.7%; Pred. No. 22;
tive 0; Mismatches
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C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
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C12D21/08, (C12N1/19,C12R1:645), (C12N1/21,C12R1:19), (C12N5/10,
                                                                                  Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1378)

                                                                                                                                          Yuan,J.
Secretory and transmembrane polypeptide and nucleic acid encoding
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: A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066710 PR 60/066770,24-NOV-1997 US 60/066710 PR ELLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, JIAN ZHENG,
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                                                                                                                        Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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C12N15/00,C12NS/00,A61K37/02,(C12N5/00,C12R1:91) CC
Ctory and transmembrane polypeptide and nucleic acid
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60/059263
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Pred. No. 22;
0; Mismatches 44; Indels
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6() 059113, 17-5EP-1997 U

6() 05926, 15-0CT-1997 U

6() 062287, 17-0CT-1997 U

6() 063814, 24-0CT-1997 U

6() 063145, 24-0CT-1997 U

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6() 063120, 24-0CT-1997 U

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6() 063129, 28-0CT-1997 U

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6() 063124, 28-0CT-1997 U

6() 063124, 28-0CT-1997 U
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GENENTECH INC
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60/064215, 29-OCT-1997
60/063732, 31-OCT-1997
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                                                                                                                                                                                                                                                    8-DEC-2001 JP 2001385319
7-SEP-1997 US 60/0591:
                                                                                                                                                                                                         Homo sapiens (human)
JP 2002253280-A/214
10-SEP-2002
           BD175432
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JP 2002253280-A/214.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1378)

Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chul,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagis,A., Vandien,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yis,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P. Zhang,M., Zhang,Z.,
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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Homo sapiens clone DNA43318 PRSS22 (UNQ302) mRNA, partial cds.
AY358396
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ISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSSQGSGAAARS
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Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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SE (Lases I to 1403)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer (C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,
Diatchenko, L., Marushana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skaiska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

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Contact: MGC help desk
Email: cgapbbs-r@mail.nih.gov
Email: cgapbbs-r@mail.nih.gov
Tissue Procurement: ATGC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgo.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: 1 Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21614535. Location/Qualifiers
     Honors agiens protease, serine, 22, mRNA linear PRI 12-NOV-2003 IMAGE:3899480), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-UNN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC009726.1 GI:16307274
                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
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RESULT 39
BC009726
                                                                                                                     ACCESSION
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COMMENT
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REFERENCE

TITLE

gene

FEATURES

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: m Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961350. Location/Qualifiers
                                                                                                                                                                        /product="protease, serine, 22"
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CLPDASIHLPPNTHOWT SGWSGJOGVPLPHPQTLQKLKVPIIDSBVCSHLWRGAGG
GPITEDMLCAGYLEGERDACLGGDSGGPLMCQVDGAWLLAGIISWGEGCAERNRPGVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1253 irrrengranaraangrangarrangarringrangerarringrancergeceaegararer 1312
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Homo sapiens, similar to coagulation factor X, clone IMAGE:5764698,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1573)
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Direct Submission
Submitted (22-NOV-2002) National Institutes of Health, Mammalian
Submitted (22-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (WGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186. .902
/note="Tryp_SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:cd00190"
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Contact: MGC help desk
Email: cgapbs.rémail..ih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
gene="PRSS22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 24.6; DB 1; Length 1403; Best Local Similarity 53.7%; Pred. No. 22; Matches 51; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGAAARS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC040125
BC040125.1 GI:25455627
                                                                                                             39.7.992
/codon_start=1
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Homo sapiens
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20

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AF318182
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ACCESSION
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KEYWORDS
SOURCE
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|protein_id="AAA31031.1"
|db_xref="GI:164451"
|translation="SHSPTILTRABIIFSNMDYENSTEVEPILDSLTESNQSSDDFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVGGENAKFOGFFWOVLLNGKIDAFCGGSIINEKWVVTAAHCIEFGVKITVVAGEYNT
EETEPTERKINJIRALPHHSYNATVNKYSHDIALELEBDETLINBSYPPEICIADKEYT
NIFIKFGSGYVSGWAVFNRRASTILOZLKVPLVDRATCLRSTKVITYSNMFCAGFH
EGGKDSCLGDSGGPHVTEVEGTSFLTGIISWGEBCAVKGKYGIYTKVORYVNN
                                                                                                                                                                              1499 GGGAGCCTTACAAATAGCTGTGAAAAGAAGAAGAAGAAAAGCAAAGGAAAAAAAGGAAA 1558
                                                                                                                                                                                                               linear MAM 27-APR-1993
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Draft entry and computer-readable sequence for [1] kindly provided
by G.Sarkar, 18-JUL-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
I (bases 1 to 813)
Sarkar,G., Koeberl,D.D. and Sommer,S.S.
Direct sequencing of the activation peptide and the catalytic Gomain of the factor IX gene in six species
Genomics 6 (1), 133-143 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GATTATTTTTCCAACATGGACTATGAAATTCTACTGAAGTTGAACCAATTTTGGATAG 92
                                                                                                                                            Gaps
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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                                                                                                                                          43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 0.7%; Score 23.8; DB 1; Length 8 1 Similarity 55.4%; Pred. No. 31; 46; Conservative 0; Mismatches 37; Indels
                                                                                                      Query Match 0.7%; Score 24.2; DB 1; Best Local Similarity 53.8%; Pred. No. 28; Matches 50; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                 1559 GATAAAAGCATCTGAATGCAGAGTTCCAAAGAA 1591
                                                                                                                                                                                                                                                                                    1530 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1562
                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                         PIGFIXA 813 bp
Pig factor IX mRNA, partial cds.
M26235
 clone="IMAGE:5764698"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3017 ITTICIAATAAATCCAGICCT 3039
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/note="factor IX"
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factor IX.
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Sus scrofa
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Best Local Similarity
Matches 46; Conserv
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PIGFIXA
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PCCGHGTCIDGIGSFSCSCDKGWEĞKFCĞQEIRFQDCRVNNGGCLHYCLEESNGRCA
CAPGYELADDHMRCKSTVNFPCGKLGRWIEKKRKILKRDTDLEDELEPDPRIVNGTLT
KQGDSFWQAILLDSKKKLACGGVLIHTSWVLTNAHCYBGTKTTVRLGEYDLERRDHW
ELDLI KEILVHPNYTRSSDNDIALLELAQPATSKTIVPICLPNNGLAQELTQAGG
ETVYTGWGYQSDRINGTRIFILIFIRIPLADEN BEVARNEVYSENMLCAGIGE
TRDACDGDSGGPMVVPFRGTWFLVGLVSWGEGCGHTNNYGIYTKVGSYLKWIHSYIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="anticoagulant protein C"
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FLEEMRPGSLERECMEEICDLEEAQEIFQNVEDTLAFWIKYFDGDQCSAPPLDHQCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 15-AUG-2001
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Compounds for immunotherapy and diagnosis of colon cancer and methods for their use
Patent: WO 0149716-A 931 12-JUL-2001;
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                          Washington University, 4444
63108, USA
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mRNA"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-NOV-2000) Genetics,
Forest Park Avenue, St. Louis, MO
Location/Qualifiers
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Pred. No. 40
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                                Complete sequence of UC72A01
                                            Mus musculus (house mouse)
Mus musculus
AF318182.1 GI:12802522
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Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                          Korf, I.
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DB 1; Length 596;

Score 23.4; I Pred. No. 36;

0.7%;

Query Match Best Local Similarity

LOCUS AF318182 14-FEB-2001 DEFINITION Mus musculus anticoagulant protein C mRNA, complete cds.

AF318182/c

RESULT 42

2620 GGCAGGAGGAGAAGGGGACGACAGGATGAGATGGCTGGATGGCATCACTGACTCGATG 2679 27-MAR-2003 PAT 25-SEP-2002 1, 537 geccacarida con contra de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contración de la contrac 477 riczadecadecagardagicegareragegegagagereardargegeretegiegagi 418 Padigaru, M., Li, L., Zerhusen, B.D., Casman, S.J., Shenoy, S., Spytek, K., Zhonog, M., Gangolli, E.A., Burgess, C.E., Patturajan, M., Vernet, C.A., Taylor, S., Tchernev, V.T., Miller, C.E., Guo, X., Boldog, F.L., Grosse, W.M., Alsobrook, J.P., Gerlach, V., Edingermark, S., Rothenberg, M.E., Ellerman, K., Macdougall, J., Malyankar, U., Millet, I., Peyman, J., Smithson, G., Gunther, E. and Stone, D.J. 101 recadegadecadardedecegareracededadadeerdarederecedaderedade 160 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 2620 GGCAGGAGGAGAAGGGGACGACAAGAGGATGAGATGGCTGGATGGCATCACTGACTCGATG Gaps Gaps G-----ACGIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAGGGAGG 2725 2680 G----ACGIGAGICIGGGIGAACICCIGGAGIIGGIGAIGGACAGGGAGG 2725 417 GAGTGCAATGTCGCCCTGGGGAGCCTCCTGGAGGTAGCTGGGGGTGGGGGATG 366 161 GAGTGCAATGTCGCCCTGGAGCCCTCCTGGAGGTAGCTGGGGTGGGGGATG 212 PAT . 9 Length 1142; 81; Indels linear 81; Indels linear DB 1; DNA 1 (bases 1 to 1142)
Darrow,A., Qi,J. and Andrade-Grodon,P.
Zymogen activation system
Patent: US 6420157-A 8 16-JUL-2002;
Location/Qualifiers Query Match 0.7%; Score 23.4; D Best Local Similarity 49.4%; Pred. No. 42; Matches 85; Conservative 0; Mismatches AX675581 1161 bp D Sequence 31 from Patent WO02055704. AX675581 Mismatches 1142 bp Sequence 8 from patent US 6420157. AR219285 AR219285.1 GI:23320255 /organism="unknown" /mol_type="genomic DNA" ., AX675581.1 GI:29333567 Homo sapiens (human) Homo sapiens 1. .1142 Conservative Unclassified. Unknown Unknown 85; 2680 RESULT 45 AX675581/c LOCUS DEFINITION KEYWORDS SOURCE ORGANISM RESULT 44 AR219285/c LOCUS DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES ACCESSION VERSION REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE Matches d à g ò g g ò g ò à

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Proteins, polynucleotides encoding them and methods of using the

Patent: WO 02055704-A 31 18-JUL-2002;

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                             2560 GGCCACCTGATCAGAAGAGCTGACTCGCAAAAGACCCTGATGCGGAGGGATTGGG
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9.4%; Pred. No. 42;
ve 0; Mismatches 81;
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Darrow,A., Qi,J. and Andrade-Grodon,P.
Zymogen activation system
Patent: US 6420157-A 7 16-UUL-2002;
Location/Qualifiers
                                                                                                  O.7%; Score 23.4; E. Similarity 49.4%; Pred. No. 42; 35; Conservative 0; Mismatches
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Sequence 81 from Patent WO03038129.
AX774765
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Seguence 7 from patent US 6420157.
AR219284
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Curagen Corporation (US)
Location/Qualifiers
1. .1161
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Messier, T.L., Pittman, D.D., Long, G.L., Kaufman, R.J. and Church, W.R. Cloning and expression in CoS-1 cells of a full-length cDNA encoding human coaquiation factor X

Gene 99 (2), 291-294 (1991)
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/gene="F10"
/note="putative VECTOR sequence Bacteriophage lambda
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Human coagulation factor X (F10) mRNA, complete cds.
M57285
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Methods for assessing and treating leukemia
Patent: WO 03038129-A 81 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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Best Local Similarity 81.8%; Pred. No. 44;
Matches 27; Conservative 0; Mismatches
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81.8%; Pred. No. 44;
rative 0; Mismatches
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1. .1507
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Matches 27; Conservative
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Schelecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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                                                                                                                                                                                                                                                                                                                                                                                    / trainslation="MGRPLHIVILSASLAGLILLIGESLFIRREQANNILARVTRANSF
LEEMKKGHLERECMEETCSYEEAREVFEDSDKTUNEFWNKYKOGDOGETSPCONGGKCK
DGLGEYTCCLLEGFEGKNCELFTRKICSLDNGDCOPCHEEQNSVCCSCARGYTLADN
GKACIFTGPY PCGCYLERRRRSVAQATSSSGEAPDSITWRYDAADLDFTENFFILL
DFNQTQPERGUNNLTRIVGGOECKDGECPWQALLINEENEGFCGGTILSEFYILTAAH
CLYQAKR KKWVQDRANEGEGGEAAHNEVEVYTKHRRFFYERYDFDIAVLRKFTITF
RMNVAPACLEBRDMAESTLMTQVTGTVSGFGRTHEKGRGSTRLKMLEVPEDTANGKKK
SSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYG
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//note="GLA; Region: Domain containing Gla
//note="GLA; Region: Domain containing Gla
dgamma-carboxyglutamate) residues. A hyaluronan-binding
domain found in proteins associated with the extracellular
matrix, cell adhesion and cell migration"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. \
1 (bases 1 to 1792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 .401
/note="EGF; Region: EGF-like domain. There is no clear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738. 1424
/note="Tryp SPc; Region: Trypsin-like serine protease"
/db_xref="CDD:smartC0020"
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81.8%; Pred. No. 44;
iive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                      /product="coagulation factor X precursor"
(protein id="AAH46125.1"
db_xref="G1:28374356"
/db_xref="LocusID:2159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"
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                             note="Vector: pCMV-SPORT6"
                                                                                                                 note="synonyms: FX, FXA"
db_xref="LocusID:2159"
db_xref="MIM:227600"
'lab_host="DH10B"
                                                                                                                                                                                                                                      codon_start=1
                                                                                       gene="F10"
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Homo sapiens
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Best Local Similarity 81.8
Matches 27; Conservative
                                                       .1541
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BC034377
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/db_xref="Locusid:5644,"
/translation="WWQLTSLILFVATWGISGTPAPLDSVFSSSERAHOVLATRKRAN
StreELRHSTSLERECIEDFEAKETPQVVDDTLAFWSKHVDGDQCLVLPLEHPCA
SLCCGHGTCLDGFSCDCRSGWEGRFCQFBVSFLNCSLDNGGCTHYCLEEVWRRC
SCAPGYKLGDDLLQCHPAVKPPCGRPWRAMEXKRSHLKRDTEDQBDQVDPALIDGKWT
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//organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/clone="MGC:3455 F188604"
/tissue type="Colon, Kidney, Stomach, adult, whole pooled"
/clone_lib="NIH MGC_116"
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ELDDIKEVPHPRYSKSTTDNDIALHLAQPATASQTIV PICLDPSGABREIMQAG
DETLYTGWGYHSSRERAKRRPTVLAFIK IPVVPHNECSEVMSNWSENMLOAGILG
DRQDACEGDSGOPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 50 Row: h Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506114.

1. 1792
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, K., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whithing, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schwutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Oby: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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/note="GLA, Region: Domain containing Gla
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/note="Vector: pCMV-SPORT6"
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/db_xref="G1:21707771"
/db_xref="Locmeth.eff"
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/db_xref="MIM:176860"
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/codon start=1
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Strausberg, R.
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1690 AAACATCTATTTCTGCTTTATTGACTATGCAAAAGCCTTTGACTGTGGGGGTCACAATAA 1749
                                                    1750 ACTGTGGAAAATTCTGAAAG 1769
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/note="factor IX"
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                                                                              241 AATTCTTCAGTACCTTAAAG
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Best Local Similarity
Matches 46; Conserv
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                                     Felis catus coagulation factor IX (F9) gene, partial cds.
AF459806.1 GI:27462785
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/protein_id="AAO15585.1"
/db_xref="G1:27462786"
/db_xref="G1:27462786"
/Tanslation="EHTEQ786"
TPICVADREYINTFIKEGYGYVSGWGKVFNKCRPATLLQYLKVPLVDRATCLRSTKFT
IYNNMFCAGFHEGGKDSCQGDSGGPHVTEVEGINFLTGII"
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Felis.
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Susoft, E.E., Rollo,W.A., Venta,P.J. and Ewart,S.L.
Direct Submission
Submitted (18-DEC-2001) Large Animal Clinical Sciences, Michigan
State University, B36H National Food Safety & Toxicology Center,
East Lansing, MI 48824-1302, USA
                                                                                                                                                                                                                                       Gaps
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Susoct.E.B., Rollo, W.A., Venta, P.J. and Ewart, S.L. Characterization of 8 Feline Type I Markers
                                                                                                                                                                                                            21; Indels
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(gamma-carboxyglutamate) residues'
db_xref="CDD:smart00069"
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/mol type="genomic DNA"
/db_xref="taxon:9685"
order(AF459805.1:<1. .336,1.
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1 Similarity 63.2%; Pred. No. 46;
36; Conservative 0; Mismatches
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illarity 47.9%;
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Felis catus
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121 AAACAGCTACGTAACGCCTATTGCGTTGCCGACAGGGAATACACGAAACACCTTCCTCAA 180

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Oryza sativa microsatellite MRG5565 containing (GGA)X8, genomic
sequence.
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Cyzza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Bummalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae, Caprinae, Ovis.

1 (bases 1 to 823)

Sarkar,G., Koeberl,D.D. and Sommer,S.S.

Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species
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Draft entry and computer-readable sequence for [1] kindly provided by G.Sarkar, 18-JUL-1989.
Location/Qualifiers
181 ATTTGGATATGGCTACGTGAGTGGCTGGGGGAAAGTCTTCAACAAAGGGCGACCGGCTAC 240
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Pred. No. 44
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            Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
Simple sequence repeats from Monsanto rice genomic sequences
Unpublished
L pupublished
Tao N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.
Direct Submission
Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-JAN-1996) R. Blasczyk, Bloodbank, Dep. of Internal Medicine, Division of Hematology and Oncology, Virchow-Klinikum, Humboldt-University, Augustenburger Platz 1, Berlin, 13353, FRG Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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HLA-B gene; human leukocyte antigen; major histocompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Length 224;
Pred. No. 36;
0; Mismatches 40; Indels
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Best Local Similarity 54.0%;
Matches 47; Conservative
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Direct Submission
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HSB4901/c
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                                                                                                                                                                                               2691 GGGTGAACTCCTGGAGTTGGTGATGGACAGGGCCTGTCCTGCGGCGATTCATGGGGT 2750
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
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                                                                                                                                                                                                                                                      851 AGAAGGGCAATGTCATGGTTGTACTTATTAATAGCTGCATTGTAGTTGTGGTGAGGAATA
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Warren, S.T.
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Score 23; DB 1; Length 244;
Pred. No. 37;
0; Mismatches 25; Indels
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0.6%; Score 23; DB 1; Length 873;
Best Local Similarity 45.0%; Pred. No. 50;
Matches 86; Conservative 0; Mismatches 105; Indels
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Human coagulation factor IX mRNA, partial cds.
M35672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serine protease.
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//organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="XQ26.3-q27.1"
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coagulation factor IX,
Homo sapiens (human)
Homo sapiens
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/gene="F9"
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Query Match
Best Local Similarity 60.33
Matches 38; Conservative
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/EC number="3.4.21.21"
/function="serum prothrombinconversion accelerator"
/note="vitamin K dependent serine protease, similar to
factor VII precursor; synthesized in liver; similar to
Fugu rubripes FVII and FVIIB; contains 2 EGF-like domains;
member of peptidase family S1/trypsin family"
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TSSDKOLAMLKLHRPYKLGLYVVPICLBAQNSTISRTLANIRGSTVSGWGRLSRFGPP
ATILQRLTLPRVPLQECRLHTKLNITRNMLCAGLKTGGRDACEGDSGGPLVTYYEKTW
FLTGVVSWGKGCANENLYGVYVRVTNFLDWIGNIIAIN"
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                                                                                                                                                 1293 bp mRNA linear VRT 02-FEB-2003
Pakifugu rubripes coagulation factor VIIc precursor, mRNA, complete
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1 (bases 1 to 1293)
Davidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G., Tuddenham, E.G.D. and McVey, J.H.
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
Unpublished
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Sequence 6 from Patent EP 0200421,
I07991,1 GI:589297
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Takifugu rubripes
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/db_xref="taxon:31033"
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      TCATTAACGAT 661
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AUTHORS
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NARUKI KURAMITSU, SHIGEYUKI YOKOYAMA
C12N15/09,C12N15/09,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC
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Thermus thermophilus
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
1 (bases 1 to 2438)
Hagen, F.S., Murray, M.J., Busby, S.J., Berkner, K.L., Insley, M.Y., Woodbury, R.G. and Gray, C.L.
Expression of factor VII and IX activities in mammalian cells Patent: EP 020421-AZ 6 10-DEC-1986;
Location/Qualifiers
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Kuramitsu.N. and Yokoyama.S.

Highly thermophilic bacterium-derived protein and gen Highly thermophilic bacterium-derived protein and gen Patent: JP 2002325574-A.665 12-NOV-2002;

THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH OS Thermus thermophilus PN JP 200232574-A.665

PD 12-NOV-2002

PP 23-FEBA-2001 JP 2001116171

PP 73-FEBA-2001 JP 2001116171

PP C 212N1S/09,C12N1S/09,C07K14/195,C12N1/15,C12N1/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 2438;
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Pred. No. 42;
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/organism="Thermus thermophilus"
/mol_type="genomic DNA"
/db_xref="taxon:274"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 23; DB
50.5%; Pred. No. 61;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1). .(264).
Location/Qualifiers
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1 Similarity 54.9%;
45; Conservative
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86 GCCTTTCCGGCTACGCCGAGAA 107

L0664//5-2.rge

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/rans ö 2651 GATGGCTGGATGGCATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGG 2710 MAM 27-APR-1993 The sequence reported in [1] included homopolymeric tails on the 5' and 3' ends (not shown here).

Location/Qualifiers
1. .1373 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 (bases 1 to 1373)

Long, G.L., Belagaje, R.M. and MacGillivray, R.T.

Cloning and sequencing of liver cDNA coding for bovine protein C Proc. Natl. Acad. Sci. U.S.A. 81 (18), 5653-5656 (1984) Original source text: Bovine liver, cDNA to mENA, clones pBC-2 and pBC-7. 25 ö Query Match 0.6%; Score 22.8; DB 1; Length 1373; Best Local Similarity 56.8%; Pred. No. 61; Matches 42; Conservative 0; Mismatches 32; Indels 0; 588. .1367 product="protein C inactive heavy chain" 630. .1367 /product="protein C active heavy chain" linear K02435.1 GI:163486
autoprothrombin IIA; protein C; serine protease.
Bos taurus (cow)
Bos taurus /lote="protein C signal peptide" 117. 581 /product="protein C light chain" 588. 1367 mRNA /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" ďq 1373 BOVPBC Bovine protein C mRNA. K02435 2711 TGATGGACAGGGAG 2724 sig_peptide mat_peptide mat_peptide mat_peptide ACCESSION VERSION KEYWORDS SOURCE ORGANISM source LOCUS AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT RESULT 59 BOVPBC/c REFERENCE CDS FEATURES ò 8

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0; Gaps

881 AAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCA 940

0.6%; Score 22.6; DB 1; Length 535; 52.7%; Pred. No. 56; ative 0; Mismatches 44; Indels

Query Match Best Local Similarity 52.77 Matches 49; Conservative

355 AAGCTGCAGTGCTTGAACATCCTGTCCTTCAAGGATTGTGACAACTCCTACCT 414

qq ò g

RESULT 61

REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL TITLE VRT 12-0CT-1998 DLAG882 535 bp mRNA line Dicentrarchus labrax mRNA for trypsin, partial. AJ006882 GI:3228220 trypsin. 

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

RESULT 60

g

DLA6882

c1. .. >533 / Codon start=1 / codon start=1 / product="trypsin" / protein id="CAA07315.1" / db xref="GOA:093594" / db xref="GOA:093594" / translation="QVSIASGYHFCGGSIVNENWVVSAAHCYKSRVEVRLGEHNIRVT ENTEQFISSRVIPHPRYSSYNIDNDIMLIKLSKPATINQYVQPVALPTSCAPAGTMC TVSGWGNTMSSTADRRNKLQCINIPPLISFKDCDNSYPGMITDAMFCAGYLEGGKDSCQG DSGGPVVCNGELQGCVVSW" Dicentrarchus labrax (European sea bass)
Dicentrarchus labrax
Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Percoidei; Moronidae; Dicentrarchus. Peres, A., Zambonino Infante, J.L. and Cahu, C.L.
Dietary regulation of activities and mRNA levels of trypsin and
amylase in sea bass (Dicentrarchus labrax) larvae
amylase. Isochem. 19, 145-152 (1998)
2 (bases 1 to 535)
Zambonino Infante, J.L.
Direct Submission
Submitted (11-JUN-1998) Zambonino Infante J.L., Unite Mixte
Inra-Ifremer de Nutrition des Poissons, Ifremer, BP 70, 29280 /organism="Dicentrarchus labrax"
/mol_type="mRNA"
/db_xref="taxon:13489"
/dev_stage="larvae" Location/Qualifiers 1. .535 Plouzane, FRANCE ORGANISM JOURNAL REFERENCE AUTHORS AUTHORS TITLE TITLE JOURNAL REFERENCE FEATURES

Sukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa, Rognathae; Galliformes; Phasianidae; Archosauria; Aves: Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1416)

1 Davidson, C.J., Hirr, R.P., Lal, K., Snell, P., Elgar, G., Congarative sequence analysis and molecular evolution of blood congulation genes from Gallus gallus and Fugu rubripes

1 Unpublished

2 (bases 1 to 1416)

3 McVey, J.H., Davidson, C.J., Lal, K., Snell, P. and Elgar, G.

Bircet Submission

L Submitted (04-JAM-2002) Haemostasis Group, MRC Clinical Sciences Centre, The Faculty of Medicine, Imperial College, Hammersmith AF465269 1416 bp mRNA linear VRT 02-FEB-2003 Gallus gallus coagulation factor IX precursor (F9) mRNA, complete AF465269.1 GI:28194009 Gallus gallus (chicken) Gallus gallus ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION TITLE JOURNAL AF465269

2895 1391

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source

FEATURES

gene

CDS

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/codon_start=1
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/product="coaqulation factor VII1"
/product=10=3AN71000.1"
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TGVVSWGRGCGPFGYYWIYTKVENFLIMMDTVMKTNTEDKSEQIANVSTFN
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In Chasses 1 to 2177)

Reagaretestucku,E.H., Maaku,J.M., Shiyaaron,J.B., Kiyasuriin,E.B., Magaretestucku,E.H., Richiyaado,J.U. and Chiyaaruzu,B.G.

DNA ENCODING FACTOR VII

DNA ENCODING FACTOR VII

TOYO SODA MFG CO LTD

OS Human (Homo sapiens)

PN JP 1987000283-A/1

PD 06-JAN-1986

PF 16-APR-1986 JP 1986087861

PR 17-APR-1986 US 85 724311, 16-DEC-1985 US 85 810002 PI

FUREDERINGUE BU BAAKUNAA, MAGARETSUTO WAI INSURE, PI

RIYAARON JIEI BAZUBII,

PI KIYAARON JIEI BAZUBII,

PI KIYAARON JIEI BAZUBII,

RICHIYAADO JII UTSUDOBERII, CHIYAARUZU ERU GUREI PC

CIZNIS/00,A6IK37/465,CIZNS/00,CIZNS/50,(CIZNS/50,CIZR1:91); CC

cc topology: Linear;

CC *Source: library-correliver;

CC *Source: library-correliver;

cc *Source: library-correlibrary, lambdagt11 cDNA library; CC

*source: clone=lambdaVII 2115, lambdaVII 1923; FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1392 GATTTCTGTGATGAGGTTTGCTTTAAGAAGGAAAATATGAGTTATGTGGGAAGTAAAGAGC 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3016 ATTITICIPATAAAATCCAGTCCTTGTTTTTAAAAAGACTTTAAAAATTATTAATTTCT 3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1452 CCTCAAACTCTTTACTTCCACCCTCATTCTGGATGGATAAATGCATATATAAATATAATT 1511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2896 GATTTTTATCTTTGATTTTTCTCTACTTATTTTAATTTTGGGATTTTAACTATTTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2956 TGACTTGTATTTCTAATATTTACTTATTCTATTTTACTTTAATTGCACTTATTTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2836 ATTTCATATGTATTCAAAATTATTTCATAATGTTGGTTAAGATAATAAGATTTTCAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1332 ATTGCTAATGTTTCCACTAAAATTGATGATTTAGTCCTAAAACAGATTAAAATGGCTGT
                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 22.5999; DB 1; Length 1722; 42.9%; Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2177 bp RNI
CDNA sequence of factor VII fragment.
E01075
note="clotting factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3076 CTTTAGTGTTTTACCAGTTCT 3096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1572 CTAAAGGTTAATTAATCTTCT 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E01075.1 GI:2169334 JP 1987000283-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1/
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DGVSSYECMCPPGYGGRNCEIDSTCATCAGGENFCRHUTPGACACCAGGATCHEDG
KSCKPAVPYPCGRITAPEMRGKVTRTENTIERWNITAHDEGDAHDEALDITEPPPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSAAPAKIVPITKNDTRVVGGYDSVKGQLPWQVHLVDSRGLGFCGGSIINEKWVTAA
HCLEPGDNYTRVARGEYNTKEDDHTEGRRQVVKLLLPYPTVRTRXHWHDTALLEDLOD
LTFRNSVTPLCIGSPD-TNNLLSNGPGTVSGWSSMLYRGRSAIVLQVLTVPFVDRYTC
LKSTSTTILLHSWFCAGYTAGGXDTCGGDSGGPYTNSIGETWFLIGUTSWGEBCAKPGK
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Comprehensive analysis of blood coagulation pathways in teleostei:
Evolution of coagulation factor genes and identification of
zebrafish factor VIII
Blood Cells Mol. Dis. (2002) In press
(Dases 1 to 1722)
Jagadeeswaran, P. and Hanumanthaiah, R.
                                                                                                                                                                                                                                                                                       /function="converts factor X to its active form in the presence of Ca++ ions, phospholipids, and factor VIIa" /note="vitamin X dependent serine protease; christmas factor; contains 2 EGF-like domains; member of peptidase family $1/trypsin family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (24-MAY-2002) Cellular & Structural Biology, University
of Texas Health Science Center at San Antonio, 7703 Floyd Curl
Drive, San Antonio, TX 78229, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Danio rerio coagulation factor VIII mRNA, complete cds.
AF515269
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u Cane Road, London W12 ONN, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                     /organism="Gallus gallus"
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1. .1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.6;
Pred. No. 69
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Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1722)
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27._.1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGIYTKVAKYVKWIRETTRLT"
                                                                                                                                                                                                                                                                        number="3.4.21.22"
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/gene="F9"
                                                                                                                                                                                           'gene="F9"
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Best Local Similarity 55.00
The A3; Conservative
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     Campus,
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DEFINITION ACCESSION VERSION

RESULT 62 AF515269 LOCUS

셤 ò KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE

TITLE JOURNAL AUTHORS

source

FEATURES

CDS

29

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AF011900.1
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Gallus gallus anticoagulant protein C precursor (FROC) mRNA,
complete cds.
AF465270
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human polymucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 3341 29-NOV-2001;
Curagen Corporation (US).
                                                                                                                                                                                     Length 2177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
0.6%; Score 22.4; DB 1; Length 186;
Best Local Similarity 53.4%; Pred. No. 49;
Matches 47; Conservative 0; Mismatches 41; Indels
                         13. .1128
/product='factor VII peptide' FT
2106. .2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                64; Indels
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                                                                                                                                                                                    0.6%; Score 22.6; L
48.8%; Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                            <1. .12
1129. .<2177.
Location/Qualifiers
1. .2177
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Location/Qualifiers
FH
FT CDS
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                                                                                                                                                                                        0.6
Best Local Similarity 48.8
Matches 61; Conservative
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                                                          polyA_signal
FT exon
FT 3'UTR
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AF465270
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NDIAMLHLABPWYNKYALPICLPTRDLABHELTTKGRQMLYTGWGSTSDEMRNYSAL
IGYTEIPIYUPKNECAQVMTKYSQYLEWIQHHINKKSGSWRG"
Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus:

I (Dasses It of 1302)

Tuddenham, E.G.D. and McVey, J.H.

Tuddenham, E.G.D. and McVey, J.H.

Tuddenham, E.G.D. and McVey, J.H.

Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes

Unpublished

L (Dasses It of 1302)

E (Dasses It of 1302)

Direct Submission

L Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences Centre, The Faculty of Medicine, Imperial College, Hammersmith Campus, Du Cane Road, London W12 DNN, UK

Location/Qualifiers
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Perromyzon marinus trypsinogen Bl (TRYPB1) mRNA, partial cds.
AF011900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="PROC"
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/EC_number="3.4.21.69"
/function="inactivates factors Va and VIIIa in the presence of Ca++ ions and phospholipids"
/note="vitamin K dependent serine protease; autoprochrombin IIa; coaqulation factor XIV; contains 2 EGF-like domains; member of peptidase family SI/trypsin family; synthesized in the liver and found in plasma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata, Craniata, Vertebrata, Hyperoartia, Petromyzontidae, Petromyzon.
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The Molecular Evolution of the Vertebrate Trypsinogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1302;
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56.9%; Pred. No. 76;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
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Eukaryota; Metazoa;
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1 (bases 1 to 832)
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Best Local Similarity 56.9
Matches 41; Conservative
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GCAWKNRPGVYTKVYNYVDWIKDTIAANS'
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70. .741
/product="mature enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%; Score 22; DB Best Local Similarity 63.0%; Pred. No. 86; Matches 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                         mesotrypsinogen; trypsin.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E01617.1 GI:2169870
JP 1988160582-A/1.
Homo sapiens (human)
                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 741)
Fukuoka, S.-I.
                                                                                                                             D45417.1 GI:644884
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mat_peptide
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E01617/c
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                                        RESULT 68
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NDDIMLIKLISSPATLMQYAQAVPLPSSCVGTGYMCTISGWGETQTSVGSPDVLMCVQ
APVISGTSCRNSYPGDITNNNICLGYLEGGKDSCQGDSGGPVVCNGQLQGIVSWGRGC
ALPNYPGVYTKVCNYNSWIASTWAAN"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                         Z vozec, J.C.
Direct Submission
Submitted (01-JUL-1997) Molecular Biotechnology, University of Washington, Seattle, WA 98195, USA
Location/Qualifiers
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Compositions and methods for the therapy and diagnosis of
parcreatic cancer
Patent: WO 021231-A 97 14-FEB-2002;
CORIXA CORPORATION (US)
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/organism="Petromyzon marinus"
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0.6%; Score 22.2; D
Best Local Similarity 77.1%; Pred. No. 78;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="trypsin bl"
/evidence=not_experimental

    534
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Sequence 97 from Patent WO0212331.
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                    (bases 1 to 832)
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Unpublished
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               PRI 10-FEB-1999
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
Fukuoka,S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
(Dases 1 to 711)
Takiguchi,H., Tani,T. and Kawashima,I.
NOVEL HUMAN PANCREATIC TRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-FEB-1995) Shin-Ichi Fukuoka, Kyoto University,
Research Institute for Pood Science; Gokanosho, Uji, Kyoto 611,
Japan (E-mail:fukuoka@soya.food.kyoto-u.ac.jp, Tel:0774-33-6905,
Fax:0774-33-3004)
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86;
               linear
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אנו אמאה קען 19 האוא בא
Human mRNA for mesotrypsinogen, partial cds.
מאסרובן אמריים
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Location/Qualifiers
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BC030238/c
                   source
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AUTHORS
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E15808/c
      FEATURES
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

B (Logas, 1.c. 744)

Takiguchi, H., Tani, T. and Kawashima, I.

NEW HUMAN.PANCEBATIC TRYPSIN

L. Patent: UP 1995184655-A 1 25-JUL-1995;
SANKYO CO LID

OS Homo sapiens (human)

PN 1995184655-A/1

PD 25-JUL-1995

PF 25-DEC-1986 JP 1994311512

PI TAKIGUCHI HIROSHI, TANI TOXIO, KAWASHIMA ICHIRO PC

C12NIS/09,C07H21/04,C12N5/10,C12N9/76//A6IK38/46; CC
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41
                                                                                                                                                                                                              peptide 1. .45
peptide 46. .741

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         94 CCTCACAGGTGTAGCCCCCAACAACTTGTCATCATCATCAAAGGGGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product='Spleen TrypsinogenIII'
                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 22; DB 1; Length 741;
llarity 63.0%; Pred. No. 86;
Conservative 0; Mismatches 20; Indels
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replace(743,'g').
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/organism='Homo sapiens'
/tissue_type='spleen'
1. 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA

    .741
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    /mol_type="genomic RNA"
    /db_xref="taxon:9606"

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Homo sapiens (human)
Homo sapiens
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Human mRNA for trypsinogen-like protein, complete cds.
E15808
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Nakanishi,J. and Koyama,J.
Nakanishi,J. and Koyama,J.
Patent: JP 1998099080-A 1 21-APR-1998;
SHISEIDO CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Momo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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JP 1998099080-A/1
21-APR-1998
26-SEP-1996
NAKANISHI JIYOUTAROU, KOYAMA JUNICHI
CI2NIS/09_C07H21/04,C07K14/47,C12N9/64//A61K38/43; CC
                                                                                                                                                                  921 CCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA
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Homo sapiens, clone IMAGE:4537998, mRNA, partial cds.
BC030238
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                                                                                 DB 1; Length 744;
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                                                                                                                           20; Indels
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1. .723
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                                                                                   Score 22; DB
Pred. No. 86;
0; Mismatches
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0.6%; Score 22; DB
Best Local Similarity 63.0%; Pred. No. 87;
Matches 34; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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/mol type="genomic RNA"
                          /mol_type="genomic RN.
/db xref="taxon:9606"
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CC topology: Linear,
FH Key L
                                                                                   Query Match
Best Local Similarity 63.0%;
Matches 34; Conservative
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Homo sapiens (human)
Homo sapiens
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TLSFGADYPDEHKCLDAPPVLYQAEGTASYPGKITNSMFCV9FLEGGKDSCQRDSGGPV
VCNGQLQGVVSWGHGCAMKNRPGVYTKVYNYVDWIKDTIAANS"
                                                                                                                                                                                                                        Direct Submission
Submitted (22-MAR-1993) U. Wiegand, Institut fuer Genetik der Univ.
Zu Koeln, Weyertal 121, 5000 Koeln 41, FRG
sequence revised by author 01-OCT-93
On Nov 26, 1998 this sequence version replaced gi:405754.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Parent: WO 0173002-A 2444 04-OCT-2001;
                                    Wiegand, U., Corbach, S., Minn, A., Kang, J. and Muller-Hill, B. Cloning of the CDNA encoding human brain trypsinogen and characterization of its product Gene 136 (1-2), 167-175 (1993)
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/cell_line="human brain poly(A)+ RNA"
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Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
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/note="allelic
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Best Local Similarity 63.0%;
Matches 34; Conservative
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/number=5
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/number=1
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/number=2
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/number=3
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/number=4
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AX265053
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                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcompgi.nih.gov/
Contact: nisc_mgcompgi.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gunn,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="PRVRARDADGCEALGTVAVPFDDDDKIVGGYTCEENSLPYQVS
INGSGHIGGGSLISEQWYVSAHCYKTRIQVRIGEBHIXVLYEGNBQFTHAAKIIHPR
YNRDTLDNUIMLIKLSSPAVINAKUSTISLPTAPPAAGTECLISGWGNYLLSFADYBD
ELKCLDAPVLIQAECKASYPGKIINSMFCVGFLEGGKDSCQRDSGGPVVCNGQLQGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found
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                                                                Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: RAK Plate: 62 Row: c Column: This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
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1 Similarity 63.0%; Pred. No. 87;
34; Conservative 0; Mismatches 20; Indels
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Homo sapiens mRNA for trypsinogen IV a-form.
X72781
                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs:r@mail.nih.gov
Tissue Proourement: DCTp/DTP
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'db_xref="G1:20988417"
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trypsin IV; trypsinogen; zymogen.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (clone="IMAGE:4537998"
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to 821)
                                         Direct Submission
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Best Local Similarity
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DEFINITION
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                                                                                                                                                                           785 GCAGTCTCAAAAACGACAGAATGATCTCTCTTTTGTTTCCAAGGCAAACCATTCAATATCA 844
                                                                                                                                                                                              50 GAAGTITITIGAAAACACTGAAAGAACAGTGAGTATITCCACATAATACCCTICAGATGCA 109
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                           Gaps
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002A 2445 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2448 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                 Sequence 2445 from Patent WO0173002. AX265054
                                                                                                            th 0.6%; Score 21.8; D Similarity 58.5%; Pred. No. 63; 38; Conservative 0; Mismatches
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UNIVERSITY OF DELAWARE (US)
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HSMYUBB. 170 bp DNA linear PRI 08-OCT-1996
H.sapiens gene encoding beta-myosin heavy chain, exon 3.
X04629
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lichter, P., Umeda, P.K., Levin, J.E. and Vosbarg, H.P.

Partial characterization of the human beta-myosin heavy-chain gene which is expressed in heart and skeletal muscle

Bur. J. Biochem. 160 (2), 419-426 (1986)
                                                                                                                                                                                                                                                                                                 52 GAAGTITITGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2449 04-OCT-2001,
UNIVERSITY OF DELAWARE (US)
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                                                                                                                                                    DB 1; Length 121;
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                                                                                                                                                  ; Score 21.8; DB; Pred. No. 63; 0; Mismatches
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AX265058
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Location/Qualifiers
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Best Local Similarity 58.5%;
Matches 38; Conservative
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Best Local Similarity
Matches 38; Conserv
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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MacGillivray, R.T., Degen, S.J., Chandra, T., Woo, S.L. and Davie, B.W.
Cloning and analysis of a cDNA coding for bovine prothrombin
Proc. Natl. Acad. Sci. U.S.A. 77 (9), 5153-5157 (1980)
81054926
                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              921 CCTTTTAGAACTAACACCCAAAAAAGATGTCCTTCTCATTATAGGGGACTG 971
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                                                                                                                                                  DNA
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Ouer Similarity 62.7%; Pred. No. 89;
Matches 32; Conservative 0; Mismatches
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Patent: WO 0212331-A 91 14-FEB-2002;
CORIXA CORPORATION (US)
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Sequence 91 from Patent W00212331.
AX527564
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    2653 TGGCTGGATGGCA 2665
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KST BTA. PROTHROMBIN.
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Bos taurus
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                                            95 AGTACGAAGGGGA
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Direct Submission
Submission
Submitted (10-JAN-2011) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Blvd., Creve Genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Hood
at the University of Washington in Seattle.
Location/Qualifiers
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1 (bases 1 to 227)
Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F. Simple sequence repeats from Monsanto rice genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GCATGGACCTGGAGCGAAGCGGAAGCTGGAGGGCGACCTGAAGCTGACCCAGGAGA 108
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                                                                                                                                                                                                                                                                                                                       Length 170;
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                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                         /gene="beta-myosin heavy chain"
see x04627-x04633 for beta-myosin gene.
Location/Qualifiers
1. .170
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Best Local Similarity 52.8%; Pred. No. 69;
Macches 47; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GCATCATGGACCTGGAGAATGACAAGCAG 137

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/db_xref="taxon:4530"
    .227

                                                              /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone="(lambda)gMHC-1"
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/rpt_unit="tcc"
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AY023453.1 GI:12706669
                                                                                                                                                                                                                                                                               /label=ex3
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                                                                                                                                                                                               .161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Best Local Similarity
Matches 41; Conserv
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AY023453/c
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RESULT 84
AY08353
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                                                                     1399 CCTAATGAACTATGGACAGGTTCATGACATTGTACAGGAGACAGGGATCGAGACATC 1458
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                                                                                                                                                                                                                                                             PAT 18-FEB-2003
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                                                                                                      439 CCTGAAGAAGTGGATACAGAAGGTCATTGATCGGTTAGGAAGTTAGGGAGCCACCACAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 ACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACGCAAGTACAAGCCAA 247
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 711)
Nakamura,Y., Sugano,S., Matsusue,T., Okamoto,A. and Okawa,K.
Novel serine profease MP493
Novel serine profease MP493
MOCHIDA PHARMACEUTICAL CO LTD,YUSUKE NAKAMURA,SUMIO SUGANO, TOMOXAZU MATSUSUE, ATSUSHI OKAMURA,SUMIO SUGANO, OS MOCHIDA PHOROSAZU PROMIDA PHOROSAZU PROMIDA PHOROSAZUPICAL CO LTD,YUSUKE NAKAMURA,SUMIO SUGANO, OS MO 02059295-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKAMOTO,
PI KAZUFUMI OKAWA
PC CINIS/09,C12N15/12,C12N9/64,C12N1/15,C12N1/19,C12N1/21 PC
C12N15/10,C07K16/40,
PC C12Q1/02
CC Novel serine protease MP493
FF Key
Location/Qualifiers
I . .TI
/organism='Homo sapiens (human)'.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-2002
23-ADA-2002 WO 2002JP000465
23-AN-2001 JP 01P 014563
YUSUKE NAKAMURA, SUMIO SUGANO, TOMOKAZU MATSUSUE, ATSUSHI
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   DB 1; Length 603;
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                                    Indels
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                                                                                                                                      1459 CCCATGGAAAAGAATGCAAAAAAGCAAA 1487
 0.6%; Score 21.8; D;
52.8%; Pred. No. 92;
iive 0; Mismatches
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                                                                                                                                                              499 TCCAAGGCTCCTCACTGCAAATCTCAGA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .711
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                               711 bp
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BD173590.1 GI:28414921
WO 02059295-A/3.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AGAGGCTGGGCAA 260
Query Match
Best Local Similarity 52.8'
Matches 47; Conservative
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BD173590
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E01189/c
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AY083553 251 bp DNA linear PRI 13-APR-2002 Macaca mulatta growth associated protein 43 (GAP43) gene, 3' UTR. AY083553
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Macaca mulatta
Macaca mulatta
Macaca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 251)
Norgren, R.B. Jr., Zink, M.A., Jia, Y., Ojeda, S.R. and Spindel, E.R. Construction of a targeted rhesus macaque microarray Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 251)
Norgren,R.B. Jr., Zink,M.A., Jia,Y., Ojeda,S.R. and Spindel,B.R.
Direct Submission
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/product='human protein C'
join(1503. .1508,1732. .1737)
1457. .1759.
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Oldery Match

Oldery Matches

Oldery Matches

Oldery Dred. No. 1.16+02;

Matches

Oldery Matches

Oldery Dred. No. 1.16+02;

Matches

Oldery Dred. No. 1.16+02;
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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3'UTR_
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AX524284.1 GI:25169380
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Matches 4
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AX553022
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Sphoeroides annulatus
Sphoeroides annulatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
Tetradontoidea; Tetraodontidae; Sphoeroides.
1 (bases 1 to 375)
1 (bases 1 to 375)
1 (bases 1 to 375)
1 Trypsin gene expression and enzymatic activity during embryonic and laryal development of the bullseye puffer (Sphoeroides annulatus)
Submitted (11-MAR-2002) Molecular and Cellular Biology Core, Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /produčt="trypsin precursor"
/protein id="AAO21468.1"
/db.xref="G1:27802524"
/tanslation="DIMLISKPATLNQYVQPVALPTSCAPAGTMCKVSGWGNTMSS
TADRAKLOCINIPLISDRDCKNSYPGMITDAMFCAGYLEGGKDSCGDSGGPVCNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sphoeroides annulatus trypsin precursor, mRNA, partial cds. AY179347
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                                                                                                                                                                                                                                                                                                                                                                          1522 AAAAGAAGAAGTGAAAAGCAAAGGAAAAAAGGAAAAGATAAAAGCATCTGAATGCAGAG 1581
                                                                                                                                                                                                                                                                                                                                                                                                           2 [bases 1 to 375]
Galaviz,M.A. and Garcia-Gasca,A.
Galaviz,M.A. and Garcia-Gasca,A.
Direct Submission
Submitted (13-NOV-2002) Molecular Biology, CIAD, Avenida Sabalo
Cerritos s/n, Mazatlan, Sin 82010, Mexico
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                                                                                                                                                                                                                                                                                                    Length 251;
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Best Local Similarity 52.2%; Pred. No. 93;
Matches 48; Conservative 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                     49; Indels
                                                                                                                                                                                                                            'product="growth associated protein 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 rrrrrgrrrcrrcrregrerrichrargeceachrirregram 184
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/mol_type="mRNA"
/db_xref="taxon:168377"
                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="intestine"
<1. .>375
/note="trypsinogen; protease"
                                                                                                                                                                                                                                                                                                  0.6%; Score 21.6; Dilarity 51.0%; Pred. No. 85; Conservative 0; Mismatches

    .251
    /organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"

                                                        Location/Qualifiers
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                                                                                                                                                                                       <1. .>251
/gene="GAP43"
                                                                                                                                                                       gene="GAP43"
                                                                                                                                                                                                                                                               /gene="GAP43"
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 51; Conserv
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AY179347
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ò Op ò g 881 AAGAAGCTGAAGTTGAACGGTCCTATGAAGACCTACAAGACCTTTTAGAACTAACACCCA 940

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. 3457 TGGCTTTAAAAAGTATTTGCTGCTATTAAACATGAATTAAAGTCTTATTTGCACTATAGTG 3516
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148 AAGCTGCAGTGCTGAATATCCCCATCCTGGGACAGGGACTGTAAGAACTCCTACCCA 207
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 recerecacadearerrereceaeaccacarrerreareaccrecadeacrearre 385
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Hoefer,M., Hofmann,M., Kaiser,C., Kranz,H., Loebbert,R. and
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Schlueter,T.
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0.6%; Score 21.6; DB 1; Length 427;
Best Local Similarity 53.6%; Pred. No. 96;
Matches 45; Conservative 0; Mismatches 39; Indels (
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Patent: WO 02074653-A 314 26-SEP-2002;
LION Bioscience AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlueter,T.
Gene library and method for its production
Patent: EP 1236798-A 314 04-SEP-2002;
LION Bioscience AG (DE)
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Sequence 314 from Patent WO02074953.
AX553022
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Sequence 314 from Patent EP1236798.
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/organism="Mus musculus"
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                                                                                     941 AAAAAGATGTCCTTCTCATTATAGGGGACTGG
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Mus musculus
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SOURCE ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS MEDLINE PUBMED

JOURNAL

TITLE

TITLE JOURNAL

FEATURES

CDS

RESULT 88 MUSBALB6/c DEFINITION

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셤 à ACCESSION VERSION KEYWORDS

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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 596)
Usuka,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A.,
McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
Unpublished (2003)
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Mus musculus (house mouse)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Musinae, Labases 1 to 1499)

Tada,N., Sato,M., Tsujimura,A., Iwase,R. and Hashimoto-Gotoh,T.

Isolation and characterization of a mouse protein C cDNA

Electric Constant (4), 491-495 (1992)
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Submitted (31-JAN-1992) Masahiro Sato, Hoechst Japan Co., Ltd.,
Pharma Research Laboratories; 1-3-2 Minamidai, Kawagoe, Saitama
350, Japan (E-mail:rkikuno@ddbj.nig.ac.jp, Tel:0492-43-6149,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 TGCCTGCACACATGTTCTCCGAGACCACATTCTTCATGACTCCACGCACTCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA 94024, USA Tel: 650855807
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted
Location/Qualifiers
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Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
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Fax:0492-41-6475)
Submitted (131-JAN-1992) to DDBJ by:
Baboratory for Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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D10445.1 GI:220385
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                                                                                                                                                                                                                                                                                                                                  Mouse gene for protein C (precursor of vitamin K-dependent serine protease), partial cds (catalytic region).
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Br. J. Haematol. 86 (3), 590-600 (1994)
326 TGCCTGCACACACATGTTCTCCGAGACCACATTCTTCATGACCTCCACGCACTCATTTC 385
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RPANMSEQ0005940 Roche Palo Alto Mus musculus STS genomic, sequence tagged site.
BV094002
BV094002.1 GI:37671481
STS.
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Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-DEC-1994) Masahiro Murakawa, Harasanshin General Hospital, Division of Hematology; 1-8 Taihaku-machi, Hakata-ku, Fukuoka, Pukuoka 812, Japan (Tel:092-291-3434, Fax:092-291-3266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vitamin K-dependent serine
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0.6%; Score 21.6; DB 1; Length 483;
Best Local Similarity 53.6%; Pred. No. 98;
Matches 45; Conservative 0; Mismatches 39; Indels 0; Gaps
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/function="regulation of blood coagulation"
/note="catalytic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                              D43755
D43755.1 GI:601897
protein C; serine protease zymogen;
protease; blood coagulation-related.
Mus musculus (house mouse)
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/strain="Balb/c"
                                                                       3517 GAGTCACAAAAGAGTTGGACATGA 3540
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Direct Submission
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ROD 01-FEB-2000

Masahiro Sato

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RESULT 89 BV094002/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1603)
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Pred. No. 1.2e+02;
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'product="activation peptide"
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rkikuno@ddbj.nig.jc.ap.
Location/Qualifiers
Reseaarch Baboratories
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                                  Hoechst Japan Co., Ltd.
1-3-2 Minamida, Kawagoe
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Best Local Similarity 53.6
Matches 45; Conservative
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Email:
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(gamma-carboxyglutamate) residues. A hyaluronan-binding domain found in proteins associated with the extracellular matrix, cell adhesion and cell migration"

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679476.
Location/Qualifiers
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Butterfield, Y.S., Kizywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-SEP-2001) National Institutes of Health, Mammalian
Submitted (07-SEP-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUL-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Lissue Pocurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadano@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/note="GLA; Region: Domain containing Gla
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/db_xref="LocusID:19123"
/db_xref="MGI:97771"
100-.1482
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/product="protein C"
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1007 CC:01:17 / Sau 11011
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1. .172 /
/note="exon 11"
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synthetic construct
artificial sequences.
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ilarity 55.3%;
Conservative
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Matches 42; Conserv
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AUTHORS
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AX565990
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AX814615
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/note="EGF; Region: EGF-like domain. There is no clear separation between noise and signal. pfam00053 is very similar, but has 8 instead of 6 conserved cysteines. Includes some cytokine receptors. The EGF domain misses the N-terminus regions of the Ca2+ binding EGF domains. The family is hard to model due to many similar but different sub-types of EGF domains. Pfam certainly misses a number of EGF domains. Pfam certainly misses a number of EGF domains.

/db_xref="CDD:pfam00008"
/note="TYPP SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:smart00020"
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/product="coagulation factor VIIi"
/product="coagulation factor VIII"
/product="coagulation.1"
/product="coagulation.1"
/db_xref="di.25005099"
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FMKGANLERECVERICDFEAREVFEDDDRTKQFWLSYSNKFPCLTNRGTCVYL
ADSYVCLCSEGYTEKVCRGLBETLKCOYVNGGCEOGCOGGARRSCSCAEGYALADD
GTSCVSQVDYPCGKIPVQKNTSQNQFLGGIHCPRGHCPWQVLIDYNGESVCGGALLEG
FWLITAAHCHORONTRELAYTGEHDDLANDGSEBPFEUSAYFIHPWYDPFTLDSDLA
LLELRVPVQSSLYAVPUCLFPPQLARSELWAARFFTLSGWGTRTAGHNLRREKGIKGP
ASGTLORLAVPLLPAAQCGNANTTANMFCAGYTEGDHASCRGHDGSPLVTRYGETSFL
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Danio rerio coagulation factor VIIi mRNA, complete cds.
AFS15269
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Submitted (24-MAY-2002) Cellular & Structural Biology, University of Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229, USA
Location/Qualifiers
1. 1722
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Pred. No. 1.2e+02;
0; Mismatches 94;
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/mol_type="mRNA"
/db_xref="taxon:7955"
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Best Local Similarity 45.3%;
Matches 78; Conservative
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TITLE
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                                            1487 CCATCCAGAATGAGGGTGGAAGTAAAAAGAGTTTGAGGGCTCTTTACTTCCACATAACTCAT 1428
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TICTAATATITIACTTATICTATITITACTTTAATIGCACTTATITITATITGATTTITCTAA
                                                                                              3026 TAAAATCCAGTCCTIGTTTTTTAAAAAGACTTTAAAATTATTAATTTCTCTTTAGTGTT
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Patent: WO 03064641-A 53 07-AUG-2003;
Geneprot, Inc. (CH)
Location/Qualifiers
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Pred. No. 1.2e+02;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid DNA pLN174"
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Patent: WO 02077218-A 2 03-OCT-2002;
NOVO NORDISK A/S (DK)
Location/Qualifiers
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Sequence 53 from Patent WO03064641.
AX814615.
AX814615.1 GI:39103828
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 2 from Patent WO02077218.
AX565990
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/translation="nylfogroecyafngtorflerylynreefvrfdsdygefrayt
Elgrpdeeywnsokdlleekravfdrmcrhnyelggpytlorr"
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                                                                                                                                                                                                            291 bp DNA linear PRI 22-WAR-2001
Homo sapiens MHC class II antigen (HLA-DPBI) gene, HLA-DPBI*5901
allele, exon 2 and partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished

[Dases 1 to 291)

[Liu,Z., Chen,W., Jia,Z., Pan,D. and Xu,A.]

Direct Submission
Submitted (16-JAN-2001) Biochemistry Department, Zhongshan (Sun Yat-sen) University, 135 W. Xingang Rd, Guangzhou, Guangdong 510275, P.R. China
Location/Qualifiers
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                               Length 243;
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HACVPTDPNPQEVVLGNVTENFNMGKNNMVEQMHEDI"
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                                   DB 1;
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/protein_id="AAK25784.1"
/db_xref="G1:13430240"
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; Pred. No. 99;
0; Mismatches
                                   Score 21.4; DB Pred. No. 95; 0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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/gene="HLA-DPB1"
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/gene="HLA-DPB1"
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AF336229.1 GI:13430239
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Best Local Similarity 46.9%;
Matches 67; Conservative C
                                     Query Match
Best Local Similarity 61.8%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.
1 (bases 1 to 243)
Fomsgaard,A.
Method for producing a nucleotide sequence construct with optimized codons for an HIV genetic vaccine based on a primary, early HIV isolate and synthetic envelope BX08 constructs
Patent: US 6649409-A 1 18-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /procein_id="CAC09208.1"
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/db_xref="REMTEMBL.6209208"
/tanslation="ASAADRLWVTVYKGVPVWKDATTTLFCASDAKAYDTEVHNVWAT
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Method for producing a nucleotide construct with optimised codons Method for producing a construct with optimised codons for an hiv genetic vaccine based on a primary, early hiv isolate and synthetic envelope bx08 constructs
and synthetic envelope bx08 constructs
Patent: WO 0029561-A 1 25-MAY-2000;
STATENS SERUMINSTITUT (DK); FOMSCAARD ANDERS (DK)
Location/Qualifiers
                                                                         21 GGAGAGGTACCTACCTCGTCCAAGGTAAGGAGCAGTAGCTGCGCGCTTTGCTGGAGCAGCC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1423 CATGACATTGTACAGGAGACAGGGATCGAGACCATCCCCATGGAAAAGAAATGCA 1477
                                           Gaps
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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         Length 172;
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/mol_type="unassigned DNA"
/db_xref="taxon:12721"
                                                                                                                                                                                                                                                                            linear
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                                         36; Indels
         DB 1;
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     Score 21.4; DB
Pred. No. 87;
0; Mismatches
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Sequence 1 from patent US 6649409.
AR430737.1 GI:40191666
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AX028553
AX028553.1 GI:10189710
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ilarity 54.4%;
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           Query Match
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                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 352)
Schmidel, D.K., Tatro, A.V., Phelps, L.G., Tomczak, J.A. and Long, G.L. Organization of the human protein S genes
Biochemistry 29 (34), 7845-7852 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petromyzon marinus (sea lamprey)
Petromyzon marinus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                          M57841 J02917
M57841.1 GI:190535
S protein; anticoagulant cofactor; vitamin K-dependent protein.
2 of 14
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Direct Submission
Submitted (25-JUN-1997) Molecular Biotechnology, University of Submitted, Seattle, WA 98185, USA
Mashington, Seattle, WA 98185, USA
Location/Qualifiers
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The molecular evolution of the vertebrate trypsinogense
Unpublished
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Petromyzon marinus trypsinogen Al mRNA, complete cds.
AF011352.1 GI:2293477
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Pred. No. 1e+02;
0; Mismatches 36; Indels (
                             HUMPSO2 352 bp DNA lir.
Human S protein-alpha (PS-alpha) gene, exon 2.
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order(MS7840.1:913. 1014,1. 1
                                                                                                                                                                                                                                                                                     source text: Human liver DNA. Location/Qualifiers
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/gene="PROS1"
/note="G00-120-721"
/number=2
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Best Local Similarity 54.4%;
Matches 43; Conservative (
                                                                                                                       Homo sapiens (human)
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E to 1329)

E bavidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G., Tudenham, E.G.D. and McVey, J.H.

Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes

L Unpublished

E (Nesses I to 1329)

McVey, J.H., Davidson, C.J., Lal, K., Snell, P. and Elgar, G.

Direct Submission

Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences Centre, The Faculty of Medicine, Imperial College, Hammersmith Location/Qualifiers
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| protein | id="hAA03389.1"
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1. .1329
/EC_number="3.4.21.21"
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/function="serum prothrombines protease; similar to frougu rubripes FVII; synthesized in liver; contains 2
EGF-like domains; member of peptidase family S1/trypsin
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Best Local Similarity 66.0%; Pred. No. 1.2e+02;
Matches 31; Conservative 0; Mismatches 16;

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    evidence=not_experimental

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/product="trypsin Al"
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GRQCIAEVEFPCGQLPPPETGPDQTVVGQTRLVGTNHCPKGECPWQVLVQLHQQSHCG
GVLIRPDWTTAAHCVTGKQPQHLSVYAGEHNLDNDOGTBGKFPVARFYSET
GDKDIALLHLNASVTLNRGVPVCLPYTKDLAERELLMTRYHTVSGWGKRTNGGNEDHG
VVNTAPVSPETARFSVPIIPRPOCSHRSQFNFTDNMFVAGYLEGNQQSCRGDDGSPLV
TLYGSTHFLIGVVGWGRGCPNPGYYGVYTNMGNFVDWANGIMMAANKKST"
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CGAVLLDTRAVIVTAAHCFDKFGKLVNTTVVLCEHDFSEKRGTFQVRLVBQVIRWNYT
RGRTDHDIALVALHRPVTFTDYVVPLOLEPRAFSENTLASIRFSRVSGWGQLLDRGAT
ALELWVIEVPRLMTODCLEHAKHSANTPRITENMFCAGYMDGTKDAGKGDSGCPHATH
YHGTWYLTGVVSWGGGCAAIGHIGVYTRVSQYIDWLVKYMDSKLRVGISRVSLL"
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LIEELWASSIERECNBERCSFBRARE IFKPPRRYKQFWTI SYGGDQCASDPCQNGGTC
QDHLKSYVCFCPLDFERRNCFKNKBQLI CANENGDCDQYCRDHYGRKTCSCHEDYV
LQPDBVSCKPKVEFPGGRI PVVBRRNFSRPQCRIVGGYVCPKGECPWQAVLKFNBALL
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Rattus norvegicus coagulation factor VII mRNA, complete cds.
emoggnikrecieeicnyeearevfeddaqtrkfwetynrhdpcsvmpconngvcvsm
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Murphy, K. and Ramaker, M.
Direct Submission
Submitted (24-UUL-2002) Biotechnology, Bristol-Myers Squibb,
Box 80336, Wilmingtion, DE 19880-0336, USA
Location/Qualifiers
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Murphy, K. and Ramaker, M.
Nuclectide sequence of the cDNA encoding rat coagulation
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Pred. No. 1.3e+02;
0; Mismatches 26; Indels 0
                                                                                                                                                                                   0.6%; Score 21.4; DB 1; Length 1329;
49.5%; Pred. No. 1.3e+02;
ive 0; Mismatches 56; Indels 0
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/protein_id="AAM95967.1"
/db_xref="G1:22347745"
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/mol_type="mRNA"
/srrain="Sprague-Dawley"
/db_xref="taxon:10116"
1. 1341
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Best Local Similarity
Matches 37; Conserv
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.3e+02;
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0.6%; Score 21.2; DB 1;
Best Local Similarity 47.1%; Pred. No. 1.3e+02;
Matches 65; Conservative 0; Mismatches 73;
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Nucleic acids encoding proteases
Patent: WO 03040393-A 37 15-MAY-2003;
Decode Genetics EHF. (IS)
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Protease homologs
Patent: US 6331427-A 43 18-DEC-2001,
Location/Qualifiers
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0.6%; Score 21.2; Di
Best Local Similarity 69.0%; Pred. No. 1.3e
Matches 29; Conservative 0; Mismatches
                       Sequence 43 from patent US 6331427.
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WO03040393.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 26 from Patent WO0200860.
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/mol_type="genomic DNA"
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AX763043
AX763043.1 GI:32257659
                                                                          AR263865.1 GI:28075869
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1 (bases 1 to 505)
Robison, K.E.
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RESULT 102
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Novel proteases
Patent: Wool Discousses Patent: Woll (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Darrow,A., Qi,J. and Andrade-Grodon,P.
DNA encoding the human serine protease
Patent: US 6456564-A 8 01-OCT-2002;
Location/Qualifiers
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1. 888
7. Coganism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 2 from patent US 6426199.
AR221273.1 GI:23328188
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Sequence 8 from patent US 6458564.
AR234337

    1130
/organism="unknown"
/mol_type="genomic DNA"

   AX360070.1 GI:18675696
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                                                                                    Homo sapiens (human)
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Unclassified.
                                                                                                                     Homo sapiens
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Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sess 1 to 252)
Noble,J.A., Cavalli,A.S. and Erlich,H.A.
DPB1*5901a: a novel HLA-DPB1 allele from a Caucasian family with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Human MHC class II antigen HLA-DP-beta (HLA-DPB1) gene, exon .
partial cds..
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                                                                                                                                                                                                                      Length 1166;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
1 (bases 1 to 1166)
Darrow,A., Qi,J. and Andrade-Grodon,P.
DNA
Patent: US 6426199-A 2 30-JUL-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coagulation factor vii derivatives
Patent: WO 02077218-A 2 03-OCT-2002,
NOVO NORDISK A/S (DK)
Location/Qualifiers
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Sequence 2 from Patent W002077218.
AX565990
                                                                                                                                            /organism="unknown"
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artificial sequences.
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10664775-2.rge

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<1...>255
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ELGRPDEEYWNSQXDLLEEKRAVPDRMCRHNYELGGPMTLQ"
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/Asolate="Indonesian 57"
/Ab xref="taxon:9606"
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/haplotype="DPB21"
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/organism="Homo sapiens"
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   /db xref="taxon:9606"
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/gene="HLA-DPB21"
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|gene="HLA-DPB21"
                                                                1. .255
/gene="HLA-DPB1"
                                     /chromosome="6"
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ELGRPDEEXWNSQKDLLEEKRAVPDRMCRHNYELGGFMTL"
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Human WHC class II antigen DPbetal gene (DPB1*5901 allele), partial
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Six new DPB1 alleles identified in a study of 1,302 unrelated bone marrow donor-recipient pairs
Tissue Antigens 49 (5), 512-516 (1997)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 255)

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Steiner, L., Begovich, A. and Noreen, H.
Direct Submission
Submitted (29-MAY-1996) Human Genetics, Roche Molecular Systems, 1145 Atlantic Avenue, Alameda, CA 94501, USA
Location/Qualifiers
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                                                                                                                         2 (bases 1 to 252)
Noble, J.A. and Erlich, H.A.
Direct Submission
Submitted (19-JUN-1995) Janelle A. Noble, Human Genetics,
Molecular Systems, 1145 Atlantic Ave., Alameda, CA 94501,
Location/Qualifiers
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insulin-dependent diabetes mellitus
Tissue Antigens 47 (2), 159-162 (1996)
                                                                                                                                                                                                                                                                                                               1. .252
/organism="Homo sapiens"
/nol_type="genomic DNA"
/db_xref="texon;9606"
/chromosome="6"

    .255
/organism="Homo sapiens"
/mol_type="genomic DNA"

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Human major histoccmpatibility complex class II (HLA-DPB21) gene,
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1 (bases 1 to 260)
Begovich, A.B., Moonsamey, P., Suraj, V., Bugawan, T.L., Stoneking, M., Roudier, J. and Hills, A.V. S.
Genetic diversity within the HLA class II region: ten new DPB1 alleles and their population distribution
Immunogenetics 40, 153-157 (1992)
Original source text: Homo sapiens (individual_isolate Indonesian 57) DNA.
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ch 0.6%; Score 21; DB 1; Length 255; 1 Similarity 49.5%; Pred. No. 1.2e+02; 54; Conservative 0; Mismatches 55; Indels
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Human MHC class II HLA-DP-betal (HLA-DPB1) gene, allele 2.
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paralabrax maculatofasciatus (spotted sand bass)

Paralabrax maculatofasciatus

Paralabrax maculatofasciatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Achinopterygii; Neoperygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

Percoidei; Serranidae; Paralabrax.
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1 (Dases 1 to 285)
Easteal, S. and Croft, L.
Easteal, S. and Croft, L.
Unpublished (1992)
Original source text: Homo sapiens blood DNA.
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Properties of polyamines producers yeast as potential probiotics for the spotted sand bass Paralabrax maculatofasciatus larvae Unpublished
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Direct Submission
Submitted (29-AUG-2001) Dariel T.R., Unite mixte INRA-IFREMER de
Nutrition, Ifremer, BP 70., Plouzane, 29280, FRANCE
1. 535
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196 AGCGGGCAGTGCCGGACAGGATGTGCAGACACAACTACGAGCTGGTCGG 244
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Paralabrax maculatofasciatus partial mRNA for trypsin.
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llarity 49.5%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 55;
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20. .283
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Petromyzon marinus trypsinogen b2 (TRYPB2) mRNA, partial cds.
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Petromyzon marinus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Submitted (01-JUL-1997) Molecular Biotechnology, University
Washington, Seattle, WA 98155, USA
Location/Qualifiers
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2 (bases 1 to 836)
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llarity 51.6%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 45; Indels
organism="Paralabrax maculatofasciatus"
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/product="trypsin"
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/gene="TRYPB2"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0.6%; Score 21; DB 1;
Best Local Similarity 62.3%; Pred. No. 1.6e+02;
Matches 33; Conservative 0; Mismatches 20
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Patent: WO 0194629-A 3775 13-DEC-2001;
Avalon Pharmaceuticals (US)

Location/Qualifiers

1. 850
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Seguence 3775 from Patent WO0194629,
AX333266
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Homo sapiens (human)
Homo sapiens
                                                            42. .737
/gene="TRYPB2"
/product="trypsin b2"
/evidence=not_experimental
/gene="TRYPB2"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
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Wiegand, U.
                                                                                                                                                                                                                                                                         51; Conservative
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AX333266/c
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Direct Submission
Submitted (06-APR-1993) U. Wiegand, Institut fuer Genetik der Univ
zu Koeln, Weyertal 121, 5000 Koeln 41, FRG
Location/Qualifiers
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                                                                                                    1. .850
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/db_xref=teaxon:9606"
/tissue type="brain"
join(<1. .79,80. .236,237. .490,491. .627,628. .>850)
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/codon_start=1
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/db_xref="GOA:P35030"
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0.6%; Score 21; DB 1; Length 933

Best Local Similarity 54.5%; Pred; No. 1.6e+02.

Matches 42; Conservative 0; Mismatches 35; Indels
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Unclassified.

1 (bases 1 to 933)
Antalis T.M. and Hooper, J.D.
DNA molecules encoding human HELA2 or the patent: US 6479274-A 29 12-NOV-2002;
to 1. 933
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Sequence 29 from patent US 6479274.
AR255972.1 GI:27302467
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Gaps

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10664775-2.rge

RESULT 117 AF465269/c LOCUS

DEFINITION

ACCESSION

VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL

FEATURES

JOURNAL

TITLE

gene

CDS

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'fe. .1356--
'fene="KVII"
'note="initiation of extrinsic pathway of blood
coagulation; serine protease"
'codon start=1
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'LEBLWPGSLERECRESSORSEGGSFEBARIFKSPRRYCPWIYYSDGDQCASNPCQNVGTC
ODHLKSYVCFCLLDFEGRNCEKSKNEQLICANENDEDCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1850 bp mRNA linear ROD 23-MAY-1996
Mus musculus coagulation factor VII (fVII) mRNA, complete cds.
U44795.1 GI:1184738
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Submitted (05-JAN-1996) Elliot D. Rosen, Chemistry, Univ. of Notre
Dame, Notre Dame, IN 46556, USA
Location/Qualifiers
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

I (bases 1 to 1850)

Idusogie, E., Rosen, E., Geng, J.P., Carmeliet, P., Collen, D. and

Castellino, P.U.
                                                               Homo sapiens
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Characterization of a cDNA encoding murine coagulation factor VII Thromb. Haemost. 75 (3), 481-487 (1996) 96276538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1450 GAGACCATCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGGCC 1506
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                                                                                                                                                    Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J. Variants of alternative splicing Patent: Wo 0186632-A 59 25-MAY-2001; Compugen Ltd. (IL) Location/Qualifiers
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2 (Dases 1 to 1850)
2 (Dases 1 to 1850)
Castellino, F.J.
                                                                                                                                                                                                                                                                                                                                                                                 th 0.6%; Score 21; DB 1; Length 1551; Similarity 48.7%; Pred. No. 1.7e+02; 57; Conservative 0; Mismatches 60; Indels
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/tissue type="liver"
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
  GI:14346662
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                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                           1351. .1
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LEBLIPGNLERECTEEKCSFEEAREVFENTBKTWEFWKIYIJGDQCNSNPCKNGAVCK
GOYGSYEKCMCPEGYGGRNCEIDSTCATKNGGCEHFCRHDTPQKAVCSCASGYKLHEDG
KSCKRAYYPCGRITAPERMGKYTRTENTIERWNITAHDEGDAHDBALDITEPEPPPT
TSAAPAKIVPITKNDTRVVGGYDSVKGQLPWQVHLVDSRGLGFCGGSIINEKWVTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCLEBGDNVTAVAGEYNTKEDDHTEGRROVVKILPYPTYNRTRNKHHNDIALLELDOP
LIFBNSYVPETCIGSRDFTNNLLSNGPGTVSGRGSMLYRGRSALVLQVLVPFVDRVTC
LKSTSTTILHSNAFGXTAGROTCGGDSGGPYTNSIGETWFLTGVTSWGEEGARPGX
YGIYTKCAKYVKWIRETTRLT"
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                                                                      VRT 02-FEB-2003 mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EC number="3.4.21.22"
/function="converts factor X to its active form in the presence of Ca++ ions, phospholipids, and factor VIIa"
/note="vitamin K dependent serine protease; christmas factor; contains 2 EGF-like domains; member of peptidase family $1/trypsin family"
                                                                                                                                                                                                                                    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRC Clinical Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished

(bases 1 to 1416)

(comput.)

(control of the faculty of Medicine, Imperial College, Hammersmith Campus, Du Campus, Du Cane Road, London W12 ONN, UK
                                                                                                                                                                                                                                                                                                                         l (bases 1 to 1416)
Davidson,C.J., Hirt,R.P., Lal,K., Snell,P., Elgar,G.,
Tuddenham,E.G.D. and McVey,J.H.
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes
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yroduc=-coagulation factor IX precursor"
protein_id="AAO33364_1"
db_xref="GI:28194010"
                                                                      AF465269 mRNA linear Gallus gallus coagulation factor IX precursor (F9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1269 ATTCAGACTTAAATTGA 1285
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                                                                                                                                                                  GI:28194009
                                                                                                                                                                                                              Gallus gallus (chicken)
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Best Local Similarity 54.5%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="F9"
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                                                                                                                                                                AF465269.1
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LOCUS DEFINITION ACCESSION RESULT 118 AX147505

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RESULT 121
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Altschul, S.E., Feingold, E.A., Grouse, D.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schamen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schamen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McTwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butferdield, Y.S., Krzywinski, M.I., Schlska, U., Snailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC061149
Mus musculus coagulation factor VII, mRNA (cDNA clone MGC:74281
MAGE:30305571), complete cds.
                                                         RGKINHDIALLRLHRPVTFTDYVVPLCLPEKSFSENTLARIRFSRVSGWGQLLDRGAT
ALELMSIEVPRLMTQDCLEHAKHSSNTPKITENMFCAGYMDGTKDACKGDSGGPHATH
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                                                                                                                                                                                                                                                                                                                                                                                             1390 GACAGAGTACCTAATGAACTATGGACAGGGTTCATGACATTGTACAGGAGACAGGGATC 1449
LQPDEVSCKPKVEYPCGRIPVVEKRNSSSRQGRIVGGNVCPKGECPWQAVLKINGLLL
                         CGAVILDARWIVTAAHCFDNIRYWGNITVVMGEHDFSEKDGDEQVRRVTQVIMPDKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1869)
                                                                                                                  YHGTWYLTGVVSWGEGCAAIGHIGVYTRVSQYIDWLVRHMDSKLQVGVFRLPLL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1450 GAGACCATCCCCATGGAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGGCC 1506
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 TGGCCCGGCTCTCTGGAGAGAGAGTGCAATGAGAACAGTGCTCCTTTGAGGAGGCC 219
                                                                                                                                                                                                                                                                                                                                Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                    Length 1850;
                                                                                                                                                                                                                                                                    0.6%; Score 21; DB 1; Length 185(
48.7%; Pred. No. 1.7e+02;
tive 0; Mismatches 60; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                           /gene="fVII"
/note="54 A nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC061149.1 GI:38511701
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Best Local Similarity 48.7%
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Direct Submission
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KEYWORDS
SOURCE
ORGANISM
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BC061149
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AUTHORS
TITLE
JOURNAL
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TITLE

COMMENT

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/ note: "SGC CA, Region: Calcium-binding EGF-like domain, present in a large number of membrane-bound and extracellular (mostly animal) proteins. Many of these proteins require calcium for their biological function and calcium-binding sites have been found to be located at the N-terminus of particular EGF-like domains."

/ db. xref="CDD:cd00054"
/ db. xref="CDD:cd00054"
/ db. xref="CDD:cd00190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="coagulation factor VII"
/protein id="AAH61149.1"
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LQPDEVSCKPKVEYPCGRIPVVEKRNSSRQCRIVGGNVCPKGECPWQAVLKINGLLL
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                                                           94305
                                                                                                                                                                                                                                                                                                                                                                                           found
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KRINHIDILALHRPWTFTDYVVPLCLDEKSESBNTLARIPSEKSRWGLLDRGAT
ALELMSIEVPRLMTODCLEHAKHSSNTPKITENMFCAGYMDGTKDAGKGDSGGPHATH
YHGTWYLTGVVSWGEGCAAIGHIGVYTRVSQYIDWLVRHMDSKLQVGVPRLPLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1390 GACAGAGTACCTAATGAACTATGGACAGAGGTTCATGACATTGTACAGGAGACAGGGATC 1449
                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRL Plate: 53 Row: n Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center, Stanford University School of Medicine, Stanford, CA 943 Web site:
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1450 GAGACCATCCCCATGGAAAAGAAATGCAAAAAGCAAAATGGCTGTCTGGGGAGGCC 1506
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/note="GLA; Region: Domain containing Gla
/damma-carboxyglutamate) residues"
/db xref="CDD:smart00069"
268. .378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/lab host="mH06"
/note="Wector: pDNR-LIB"
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Pred. No. 1.7e+02;
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Best Local Similarity 48.7%; Pred. No. 1.7e+
Best Acthes 57; Conservative 0; Mismatches
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E 3 (bases 1 to 2078)
S Hu,Z. and Garen,A.

Location,A.

Direct Submission

AL Submitted (25-MAY-2000) Molecular Biophysics and Biochemistry, Yale
University, 266 Whitney Ave, New Haven, CT 06520, USA

Location/Qualifiers

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Best Local Similarity 48.7%; Pred. No. 1.7e+02;
Matches 57; Conservative 0; Mismatches 60; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2078)

Hu, Z. and Garen, A.

Intratumoral injection of adenoviral vectors encoding tumor-targeted immunoconjugates for cancer immunotherapy Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9221-9225 (2000) 20381364
immunoconjugate mRNA, complete cds. AF272773
AF272773.1 GI:9837149
                                                                                                                                            synthetic construct
synthetic construct
artificial sequences.
I (bases 1 to 2078)
Hu,Z., Sun,Y. and Garen,A.
                                    ACCESSION
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UnClassified.
1 (bases 1 to 2422)
Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and Bregengaard.
Modified factor VII
Patent: US 5817788-A 1 06-OCT-1998;
Location/Qualifiers
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Berkner, K.L., Petersen, L. Christian., Hart, C.E., Hedner, U. and Bregengaard, C.
Modified factor VII
Patent: US 5833982-A 1 10-NOV-1998;
Location/Qualifiers
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0.6%; Score 21; DB 1; Length 2422;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
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0.6%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      linear
Unclassified.
Unclassified.
1 (bases 1 to 2422)
1 (bases 1 to Petersen, L. Christian. and Hart, C. E. Modified Factor VII
Patent: US 5861374-A 1 19-JAN-1999;
Location/Qualifiers
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Sequence 1 from patent US 5833982.
AR052946
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Sequence 1 from patent US 5817788.
AR045090
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PAT 29-SEP-1999

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AR030786 2422 bp Sequence 1 from patent US 5861374. AR030786 AR030786.1 GI:5944000

RESULT 122
AR030786/c
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Furederitsuku, E.H., Maaku, J.M., Shiyaaron, J.B., Kiyasuriin, E.B., Maagarestsuto, W.I., Richiyaado, J.U. and Chiyaaruzu, E.G. DNA ENCODING FACTOR VII
Parent: JP 1997000283.A 2 06-JAN-1987;
HEMOJIENETEITSUKUSU INC NIPPON SODA CO LTD, NISSAN CHEM IND LTD,
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Conservative 0; Mismatches 0;
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Sequence 3 from Patent BP 0200421.
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/db_xref="taxon:32644"
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| Berkhar,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and Bregengaard,C.
| Modified factor VII | Patent: US 6168789-A 1 02-JAN-2001; | Patent: US 10cation/Qualifiers | 1.2422
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Unclassified.
1 (bases 1 to 2422)
Hart,C.E., Petersen,L.C., Hedner,U. and Rasmussen,M.E. Modified factor VII
Patent: US 6183743-A 1 06-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Score 21; DB 1; Length 2422; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 21; Conservative 0; Mismatches 0; Indels
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/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 1 from patent US 6168789.
AR122899 GI:14107865
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Sequence 1 from patent US 6183743.
AR127821 GI:14115483
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JP 1987000283-A/2.
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1 (bases 1 to 2483)
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PAT 02-DEC-1994

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Hagen, F.S., Murray, M.J., Busby, S.J., Berkner, K.L., Insley, M.Y., Woodbury, R.G. and Gray, C.L.
Expression of factor VII and IX activities in mammalian cells
Patent: EP 0200421-A2 3 10-DEC-1986;
Location/Qualifiers
1. .2483 Gaps . ch 0.6%; Score 21; DB 1; Length 2483; 1 Similarity 100.0%; Pred. No. 1.7e+02; 21; Conservative 0; Mismatches 0; Indels 51

10664775-2.rge

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/product="protein C"
/protein id="AAB25410.1"
/db_xref="G1:26566#"
/translation="VSWVRAVGSFTTTAFTPKSAATSTGSMGTSETTKKPPRRAGHLSD
PPCRAGLLHGNGWDIKGTCNKHTGLLFCPSIPLLGSSGGK"
                                       S55227 293 DNA linear PRI 08-MAY-1993 protein C {exon IX} [human, peripheral blood, Genomic Mutant, 290
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Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
S' EST of secretory protein expressed in prostate
Patent: JP 2001512013-A 35 21-AUG-2001;
GENSET
                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (2020)
Tokinaga,F., Wakabayashi,S., Sato,H., Arakawa,M., Tawaraya,H. and
                                                                                                                                                                                                                                                                                                                                                                                             GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 125544] from the original journal article. This sequence comes from Fig. 3. deletion of a G in codon for Gly381. Location/Qualifiers
                                                                                                                                                                                                                                                                                Identification of one base deletion in exon IX of the protein gene that causes a type I deficiency Thromb. Res. 68 (4-5), 417-423 (1992)
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/note="This sequence comes from Fig. 3"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
1. 255
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JP 2001512013-A/35
21-AUG-2001
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JP 2001512013-A/35.
Homo sapiens (human)
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SS5227.1 GI:265667
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM Unknown.
Unclassified.
CE 1 (bases 1 to 252)
RS Deretic, V. and Martin, D.W.
RS Deretic, V. and Martin, D.W.
Infecting cystic fibrosis patients involving the algu gene infecting cystic fibrosis patients involving the algu gene NAL Patent: US 5573910-A 26 12-NOV-1996;
Location/Qualifiers
Location/Qualifiers
1. 252
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                       Bracco,L., Brinkman,B. and Coignard,F.
Variants of human kallikrein-2 and kallikrein-3 and uses thereof
Patent: WO 03076610-A 23 18-SEP-2003;
Exonhit Therapeutics S.A. (FR)
Location/Qualifiers
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Pred. No. 1.4e+02;
0; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Sequence 26 from patent US 5573910.
                                                            394 bp
23 from Patent WO03076610.
                                                                                                                   AX839180.1 GI:39922629
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Best Local Similarity 55.6%;
Matches 40; Conservative (
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                                                                                                                                                          Homo sapiens (human)
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Best Local Similarity
Matches 77; Conserva
                                                          AX839180
Sequence 2
AX839180
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3189 GCTCTTTAATTCATTATTCTTTGATAACAGCTTCAGTTCTATGGCTTTAATAAAGTTTT 3248
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1 (bases 1 to 823)

2 Sarkar, G., Koeberl, D.D. and Sommer, S.S.

Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species

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Sudduth-Xinger, J., Reinhard, C., He, Z., Randazzo, F., Kennedy, G.C.,
Boc, D., Kassam, A., Lamson, C., Dramanac, R., Crkvenjakov, R.,
Dickson, M., Drmanac, S., Labat, I., Leshkowitz, D., Kita, D.,
Garcia, V., Jones, L.W. and Stache-Crain, B.
Patent: W. 0.172781-A 230 04-OCT-2001;
Chiron Corporation (US); Hyseq Inc. (US)
139 CATCTGGCAGGGTTCTTATATGTTGTAAAACAGTGAGCAGCACTCACAAGCCATGTGGCA 80
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 230 from Patent WO0172781.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sheep factor IX mRNA, partial cds.
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M26233.1 GI:165878
factor IX.
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Ovis aries
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                                                                                                               79 Traarraaggrr
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AX262150/c
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Sudduth-Klinger, J., Reinhard, C., He.Z., Randazzo, F., Kennedy, G.C.,
Sudduth-Klinger, J., Reinhard, C., He.Z., Randazzo, F., Kennedy, G.C.,
Dickson, M., Lamson, G., Drmanac, R., Labat, I., Leshkovitz, D., Kita, D.,
Garcia, V., Jones, L.W. and Stache-Crain, B.
Patent: Wo 0.172781-A 234 04-0CT-2001;
Chiron Corporation (US); Hyseq Inc. (US)
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                                                                                             C12N15/09, C07K14/47, C12P21/02, C12Q1/02, C12Q1/68, C12N15/00 CC
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    31-JUL-1998 JP 2000505291
01-AUG-1997 US 08/905144
JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO
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Pred. No. 1.5e+02;
0; Mismatches 107; Indels
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Sequence 234 from Patent WO0172781.
AX262154
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 44.3%;
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    PF 31-JUL-1998 JP PR 01-AUG-1997 US PR 01-AUG-1997 US PC C12N15/09,C07K7 VON Heljne matrix CC score 10. CC score 10. CC score 10. CC n=a, g, c or t FH Key sig_peptide FT sig_peptide
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Best Local Similarity
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HUMPRC7/c
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YHFCGGSLINSQWYVSAAHCYQTASRISVR.GEHNIFVNEGTEQQIQASKAIQHPQYN
SWTIDNDIMLIKLSSPATLNQYAQAIALPSSCVNTGVMCTISGWGETQTSIGSPDVLM
RUZOAPVLSDTSCRNSYPGDITNNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWG
RGCALPNYPGVYTKVCNYNAMIAQTIAAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHNTEKPEPTEQKRÅVIRÅIPYHGYNASINKYSHDIALLELDEPLELNSYYPPICIAD
REYTNIFLKFGYGYVSGWGRVFNRGRSASILQYLKVPLVDRATCLRSTKFTIYNHMFC
AGYHEGGKDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="RASVLHTSKKLTRAETIFSNMYENSSEAEIIWDNVTQSNQSFD
DFNRVVGGEDAARGQFPWQVLLHGBIAAFCGGSIVNEKWVVTAAHCIKPGVKITVVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 CAAAGACTAATAGAGTTTTGCCAAGAAATGCACTGGTCATAGCAAACACCCTCTTCCAA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRT 09-SEP-1997
Original source text: Sheep liver, cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly provided by G.Sarkar, 18-JUL.18-St.18-St.18-JUL.18-St.18-St.18-JUL.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.18-St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petromyzon marinus
Bukarycota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       860 bp mRNA linear VRT 09-SEI AF011898 GI:2367494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-JUL-1997) Molecular Biotechnology, University Washington, Seattle, WA 98195, USA
Location/Qualifiers
1.860
/organisme"Petromyzon marinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 20.8; DB 1; Length 823; larity 57.8%; Pred. No. 1.7e+02; Conservative 0; Mismatches 27; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-mixto-m
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protein_id="AAB69654.1"
db_xref="GI:2367495"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA31520.1"
/db_xref="GI:552419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petromyzon marinus (sea lamprey)
                                                                                                                                                                                                                     /organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                    <1. . . > 823
/note="factor IX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
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les 37; Conserv
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                                                                                                                                                                                             source
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ACCESSION
VERSION
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 136
AF011898/c
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Matches
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AUTHORS
TITLE
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REFERENCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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         COMMENT
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/map="2q13-q21"
join(M12682.1:198. .300,M12683.1:1. .430,M12684.1:1. .710,
M12685.1:1. .733,M12686.1:1. .411,M12687.1:1. .1190,1. .797)
/gene="PROC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2646
                                                                                                                                                                                                                                                                              2706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MWQLTSLLLFVATWGISGTPAPLDSVFSSSERAHQVLRIRKRAN
                                                                                                                                                  ô
                                                                                                                                                                                                                                     520 CAGGAGGTGTCGCTCAGCACGGCCCCTGGACGCACATGAGGACGTCGGGACTGCCGATG 461
                                                                                                                                                                                                                                                                                                                        460 CTGGTCTGGGTCTCGCCCCAGCCGGAGATGGTGCACATGACTCCGGTGTTGACGCAGGAG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1259)
Bulutky, J., Hoskins, J.A., Long, G.L. and Crabtree, G.R.
Brolution and organization of the human protein C gene
Proc. Natl. Acad. Sci. U.S.A. 83 (3), 546-550 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jóin (M12683.1:106. 175, M12684.1:354. ;520, M12685.1:58. M12685.1:174. 311, M12685.1:414. .548, M12686.1:45. .187, M12687.1:397. .514, 205. .797)
                                                                                                                                                                                            2587 CTGGAAAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGGAGAAAGGGGACGACAGAGG
                                                                                                                                                                                                                                                                              2647 ATGAGATGGCTGGATGCCATCACTGACTCGACGCACGTGAGTCTGGGTGAACTCCTGGAG
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Human liver, DNA clones lambda-pc4, lambda-pc14 and lambda-pc17.
                                                                                                                                                     .
                                                                                                       Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein; protease; protein C; serine protease. 7 of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                Indels
                                                                                                     0.6%; Score 20.8; DB 1;
llarity 47.1%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ο,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/protein_id="AAA60165.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                             /product="trypsin a2'
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/note="ProC mRNA"
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                      51. .746
/gene="TRYPA2"
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                                                                                                                              Similarity
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/mol_type="mRNA"
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                                                                                                                                                                                                                 Location/Qualifiers
AX211661.1 GI:15523893
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K02059
                                                                synthetic construct artificial sequences.
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/gene="PROC"
                                            synthetic construct
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GSKDSGCKGDSGGFHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMR
SEPRRGVLLRAPFP"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                             Query Match
0.6%; Score 20.8; DB 1; Length 1259;
Best Local Similarity 57.8%; Pred. No. 1.8e+02;
Matches 37; Conservative 0; Mismatches 27; Indels 0
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Factor vii or viia-like molecules
Patent: WO 0158935-A 2 16-AUG-2001;
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                        205. .>797
/gene="PROC"
/note="Protein C; G00-120-317"
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-115. .1335
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Sequence 4 from Patent WO0158935.
AX211661
    'note="ProC intron H"
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                                                                                         /number=9
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FEATURES

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REFERENCE AUTHORS

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TITLE

RESULT 139 AX211661 LOCUS DEFINITION ACCESSION

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 138 AX211659 LOCUS

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organial source text: Human liver, cDNA (library of Woo) to mRNA, clones lambda-HC1026 and lambda-HC1375.

clones lambda-HC1026 and lambda-HC1375.

clones lambda-HC1026 and lambda-HC1375.

protein C is a precursor to a serine protease called 'activated protein C that has a strong anticoagulant activity. The amino acid sequence as determined from the cDNA indicates that protein C is synthesized as a single-chain polypeptide containing the light chain and the heavy chain connected by a dipeptide of Lys-Arg. This precursor peptide is then connected to the light and heavy chains by cleavage of two or more internal peptide bonds. The amino acid sequence of thuman protein C shows a high homology with that of the bovine molecule. Two clones were sequenced in [1] and shown to code for human protein C. Clone lambda-HC1026 covers by 146-1140, and clone lambda-HC1375 covers by 1-1366. The two cDNA clones had a poly-A tail at different positions; both poly-A sites were location (Jualifiers)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="synthetic construct".
/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="Expression cassette for expression of FVII in mammalian cells"
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Foster, D. and Davie, E.W.
Characterization of a cDNA coding for human protein C
Proc. Natl. Acad. Sci. U.S.A. 81 (15), 4766-4770 (1984)
84272714
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glycoprotein; protease; protein C; serine protease.
Homo sapiens (human)
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Best Local Similarity 57.8%; Pred. No. 1.9e+02;
Matches 37; Conservative 0; Mismatches 27; Indels
Andersen, K.V., Pedersen, A.H. and born S,C.
Factor vii or viia-like molecules
Patent: WO 158935-A 4 16-AUG-2001;
Maxygen Aps (DK)
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Homo sapiens (human)
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Best Local Similarity
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  513 TGGT 516
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AX886683/c
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I05477/c
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GLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVHNECSEVMSNMV
SENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVS
                                                                                                                                                                                                                                                                                                                                                                                         YCLEEVGWRRCSCAPCYKLGDDLLQCHPAVKFPCGRPWKRMEKKRSHLKRDTEDQEDQ
VDPRLIDGKYTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRL
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                                                                                                                                                                                                                                                                               | protein id="AAA60164.1"
| Ab_xref="G1:190323"
| db_xref="G1:600-123"
| translation="QGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFINCSLDNGGCTH
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Patent: US 522537-A 1 06-UUL-1993;
Location/Qualifiers
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gene="Rpooter"
product="protein C activated heavy chain"
/note="G00-120-317"
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note="G00-120-317"
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'note="G00-120-317"
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57.8%; Pred. No. 1.9e+02;
iive 0; Mismatches 27;
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Sequence 1 from patent US 5225537.
AR363767.1 GI:34425772
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product="protein C"
:1. .1366
'gene="PROC"
'note="G00-120-317"
                                                                                                             gene="PROC"
note="G00-120-317"
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'gene="PROC"
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Unclassified.
1 (bases 1 to 1755)
Foster, D.C.
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Best Local Similarity 57.8
Matches 37; Conservative
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Matches 37; Conservative
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      PAT 02-DEC-1994
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 57.8%; Pred. No. 1.9e+02;
Matches 37; Conservative 0; Mismatches 27;
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                                                                                                                                                                          1 (bases 1 to 1756)
Foster, D.C., Murray, W.J. and Berkner, K.L.
Expression of protein C
Patent: BP 0266190-A2 12 04-MAY-1988;
Location/Qualifiers
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Sequence 2546 from Patent EP1033401.
AX886683
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Sequence 12 from Patent EP 0266190.
105477
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Eumalacostraca, Eucarida, Decapoda, Dendrobranchiata, Penaecidea,
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Molecular cloning and sequencing of trypsin cDNAs from Penaeus
vannamie (Crustacea, Decapoda): use in assessing gene expression
during the moult cycle
Int. J. Biochem. Cell Biol. 28 (5), 551-563 (1996)
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Submitted (18-APR-1995) A.E. Van Wormhoudt, College de France /
CNRS, Laboratoire de Biologie Marine, BP 225, 29182 Concarneau,
                                                                                                                                                                                                                                                                                                                                                              1654 CCTCTGTATCATGGAAAAAGCAAGAGGTTCCAGAAAAACATCTATTTCTGCTTTATTGA
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                                                                                                                                                                                                               Query Match
0.6%; Score 20.6; DB 1; Length 3:
Best Local Similarity 54.7%; Pred. No. 1.6e+02;
Matches 41; Conservative 0; Mismatches 34; Indels
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Litopenaeus vannamei
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    .312
    /organism="Zea mays"
    /mol_type="unassigned DNA"
    /db_xref="taxon:4577"

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X86369
Location/Qualifiers
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Van Wormhoudt, A.E.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, FACCAD
clade, Panicoideae, Andropogoneae, Zea.
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1 (Dases 1 to 228)

Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein
Patent: JP 2001269182-A 2539 02-0CT-2001;
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JP 2001269182-A/2539
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44. .226.
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Sequence tag and encoded human protein.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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JP 2001269182-A/2539.
Homo sapiens (human)
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2 Cariman, Dr. S., Coller, M. B. and Kim, H.
Direct Submission
Submitted (01-0CT-1999) Research/S.S.F., Shriners Hospital, 12502
North Pine Drive, Tampa, FL 33612, USA
1. of 1514
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/organism="Sus scrofa"
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Kurachi, K. and Kurachi, S.
Nuclectide sequences for gene regulat
Patent: US 6610906-A 49 26-AUG-2003;
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Sequence 49 from patent US 6610906.
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WSWQVSLQDQTGFHFCGGSLINENWVVTAAHCNVKNYHRVVLGEHDRSSNSEGVQVMT
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LTRYNAADTPALLQQAALPLLTNEQCKKFWGNKISDLMICAGAAGASSCMGDSGGPLV
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                                                                                                                                                                      VRT 23-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 867)
Gudmundsdottir,A.
Direct Submission
Submitted (24-MAR-1994) A. Gudmundsdottir, Science Institute, University of Iceland, Dunhagi 3, IS-107 Reykjavik, ICELAND Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guthmundsdottir, A., Oskarsson, S., Eakin, A.E., Craik, C.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bjarnason, J.B.
Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen Biochim. Biophys. Acta 1219 (1), 211-214 (1994)
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Pred. No. 1.9e+02;
0; Mismatches 64; Indels (
                   819 ATGTTAAACAACTTGATTAAACAGCATTGGCCTTAATCCAATC 777
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="texon:8049"
/dbsucetype="pyloric caeca"
/clone_lib="lambda UNI-ZAP XR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/protain_id="CAS55242.1"
/db_xref="GI:46A751"
/db_xref="GOA:P47796"
/db_xref="SWISS-PROT:P47796"
                                                                                                                                                         867 bp mRNA Gor prechymotrypsinogen. X78490
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/EC_number="3.4.21.1"
/note="prechymetrypsinogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="chymotrypsin"
/note="prechymetrypsinogen"
/EC_number="3.4.21.1"
                                                                                                                                                                                                                                                                                         chymotrypsin; prechymotrypsinogen.
Gadus morhua (Atlantic cod)
Gadus morhua
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Best Local Similarity 48.0
Matches 59; Conservative
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595. .1531
'note="heavy chain (aa 57-419)"
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    121
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    /db_xref="taxon:9606"

                                                                                                                                    197. .223
/note="propeptide (aa -9
                                                                                                                                                                                                                                                                                                                                                                                                                 .759. .1764
/note="polyA signal"
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Best Local Similarity
Matches 33; Conserv
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VERSION
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AUTHORS
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AX265022/c
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SFLEELRHSSLERRGIEEICDFREAKBIFQNVDDTLAFWSKHVDGDQCLVLPLEHPCA
                                                                                                                      PAT 14-JUN-2002
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                                1806
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(bases 1 to 1843)

Beckmann, R.J., Schmidt, R.J., Santerre, R.F., Plutzky, J.,

Ectabtree, G.R. and Long, G.L.

The structure and evolution of a 461 amino acid human protein C precursor and its messenger RNA, based upon the DNA sequence of Cloned human liver cDNAs

Nucleic Acids Res. 13 (14), 5233-5247 (1985)
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                       TTACAAATAGCTGTGAAAAGAAGAGAGAAAGCAAAGGAAAAAAGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="unnamed protein product; protein C precursor"
                                                                                                                                                                                                                                                                                       Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. Gene expression profiles in liver cancer wo 0229103-A 3673 11-APR-2002; GENE LOGIC INC (US).
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                                                                                                                                                                                                                                                                                                                                                                             1. .1843 |
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db xref="taxon:9606"
/noTe="EMBL/GenBank Accession No. X02750"
                                                                                                                      linear
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Location/Qualifiers
1. .1843
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59.3%; Pred. No. 2.1e+02;
vative 0; Mismatches 24;
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                                                                                                             1843 bp Di
Sequence 3673 from Patent W00229103.
AX411026
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/db_xref="taxon:9606"
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Human liver mRNA for protein
X02750
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protein C; signal peptide.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                       Homo sapiens (human)
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Best Local Similarity 59.3%
Matches 35; Conservative
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1507
                                                                               RESULT 150
AX411026
LOCUS
DEFINITION
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SOURCE
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AUTHORS
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HSPROTC
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JOURNAL
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SLCCGHGTCIDGIGSFSCDCRSGWBGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRC
SRCAPOYKLGDDLLQCHPAVEPCGRPWKNEKKEKSHKKDPEDGDPQVDPDFLIDGKMT
SRCADSPWQYVLLDSKKKLACGAVI THPSWVLTAAHCMDESKKLLVRLGEYDLRSWBKW
BLDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPBSGLAERELNQAG
ORTLVTGWGYFHSRREKBAKRNTFVLNFIKIPVVPHNBCSEVMSNNYSENMLCAGILG
DRODACEGDSGGPWVASFHGTWFLVGLVSWGEGGGLLHNYGVYTKVSRYLDWIHGHIR
DKEAPQKSWAP"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2412 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653. .730
/note="activation peptide region (aa 144-169)"
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                                                                                                                                                                                                                                                                                                                                                       (aa 1-45)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="serine protease region (aa 170-419)"
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0.6%; Score 20.6; DB 1; Length 1
Best Local Similarity 59.3%; Pred. No. 2.1e+02;
Matches 35; Conservative 0; Mismatches 24; Indels
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                                                                                                                                                                               98. .196
/note="signal peptide (aa -42 to -10)"
                                                                                                                                                                                                                                                                             197. .634
/note="EGF-domain II (aa 92-137)"
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TITLE Targeted chromosomal genomic alterations with modified single stranded oligonuclectides  JOURNAL Patent: WO 0173002-A 2425 04-0CT-2001;  UNIVERSITY OF DELAWARE (US)  FEATURES  1. 121  Cocation/Qualifiers  1. 121  Anol type="unassigned DNA"  Ab_xref="taxon:9606"  Ab_xref="taxon:9606"  Ab xref="taxon:9606"  Atches 33; Conservative 0; Mismatches 21; Indels '0; Gaps 0;  Matches 33; Conservative 0; Mismatches 21; Indels '0; Gaps 0;  Db 59 GAAGTTTTGAAAACGACAAAAGAACAAGAACAATTTCCACATAATACCCTTCA 6	121 bp DNA linear Patent WO0173002. 1836	e itc	RESULT 157 AX265038/C LOCUS LOCUS Sequence 2429 from Patent W00173002. AZCESSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265038 VERSION AZ265001 AZ265001 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ26501 AZ2650
ACCESSION AX265022 VERNORDS SOURCE ORGANISM Home sapiens (human) ORGANISM Home sapiens CRGANISM Home sapiens CRGANISM Home sapiens CRGANISM Home sapiens CRGANISM Home sapiens CRGANISM Home sapiens AUTHORS TATILE AUTHORS TATILE STRANGE OHIGOMUCHOCOTION OUTHOUS TATILE STRANGE OHIGOMUCHOCOTION TATILE STRANGE OHIGOMUCHOCOTION TOTAL PATENTY OF DELAWARE (US) LOCATION/QUALIFIERS  1.121 SOURCE // Organism="Home sapiens" // AD_XTREF="LAXON:9606"	Query Match  0.6%; Score 20.4; DB 1; Length 121;  Best Local Similarity 61.1%; Pred. No. 1.48+02;  Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  785 GCAGTCTCAAAACGACAGAATGATCTTCTTTCTAAGGAAACCATCA 838  Oy 785 GCAGTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCAAGACAAACATCA 1  Db 54 GAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCA 1	RESULT 154  AX265033  AX265033  AX265033  AX265033  AX265033  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX265033.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26503.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX26500.1  AX2	Ouery Match  Best Local Similarity 61.1%; Pred. No. 1.4e+02;  Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  Qy 785 GCAGTCTCAAAACGACAGAATGATCTCTTTCTAAGCAACCATTCA 838  Db 63 GAAGTTTTTGAAAACACTGAAACACTGAATTTCCACATAATACCCTTCA 116  RESULT 155  AX265034/c  AX265034 AX265034  AX265034 AX265034  DEFINITION AX265034  WENGENOW AX265034  WENGENOW AX265034  WENGENOW AX265034  Homo sapiens (human)  ORGANISM Homo sapiens (human)  ORGANISM Homo sapiens (human)  CORGANISM Homo sapiens (human)  AX265034. AX265034. GI:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034. Gi:16513833  WENGENOW AX265034  AX265034. AX265034  AX265034. AX265034  AX265034. AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265034  AX265

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                          Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 2436 04-0CT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
Patent: WO 0173002.A 2437 04-0CT-2001,
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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61.1%; Pred. No. 1.46+02;
iive 0; Mismatches 21; Indels
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O.6%; Score 20.4; DB 1;
Best Local Similarity 61.1%; Pred. No. 1.4e+02;
Matches 33; Conservative 0; Mismatches 21;
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Seguence 2437 from Patent WO0173002.
AX265046
                                           AX265045 121 bp D Sequence 2436 from Patent WO0173002.
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Sequence 2440 from Patent WO0173002.
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     RESULT 160
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1. 121
/organism="Homo sapiens"
//mol_type="unassigned DNA"
//db_xref="taxon:9606"
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Targeted chromosomal genomic alterations with modified single
stranded oligomucleotides
Patent: WO 0173002.A 2432 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
                                           Gaps
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Seguence 2432 from Patent WO0173002.
AX265041
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Sequence 2433 from Patent W00173002.
AX265042

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AX265041
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                                                                                                                                                                                                                                                                                     gene="PRSS1"
                                                                                                                                                                                                                                                                                                                          <1. .>160
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                                                                                                                                                                                                                                                                                                                                                                                                    gene="PRSS1"
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                                                                                                                                                                                                                                               /map="7q34"
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AY307359/c
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Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Chen, J.M., Le Marechal, C., Lucas, D., Raquenes, O. and Ferec, C.
Loss of function; mutations in the cationic trypsinogen gene
(PRSS1) may act as a procective factor against pancreatitis
Mol. Genet. Metab. 79 (1), 67-70 (2003)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single
stranded chigonuclectides
Patent: WO 0173002-A 2441 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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                                                                              Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonuclectides
Fatent: WO 0173002-A 2001;
UNIVERSITY OF DELAMARE (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                    785 GCAGTCTCAAAAAGGACAGAATGATCTCTGTTTGTTTCCAAGGCAAACCATTCA
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                                                                                                                                                                                                                                                                                         0.6%; Score 20.4; DB 1;
ilarity 61.1%; Pred. No. 1.46+02;
Conservative 0; Mismatches 21;
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 33; Conserv
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RESULT 163 AX265050/c LOCUS

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ACCESSION VERSION

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

RESULT 164 AY254094/c LOCUS DEFINITION

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

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Ar3U/359
Homo sapiens cationic trypsinogen (PRSSI) gene, PRSSI-K23R allele, exon 2 and partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PRSS1"
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protein results from a mutation that creates a premature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoffa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Butheria, Primates; Catarrhini, Hominidae; Homo.

[ (bases 1 to 160)
Ferec,C., Raguenes,C., Salomon,R., Roche;C., Bernard,J.P., Guillot,M., Quere,I., Faure,C., Mercier,B., Audrezet,M.P., Guillausseau,P.J., Dupont,C., Munnich,A., Bignon,J.D. and Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen,J.M., Piepoli Bis,A., Le Bodic,L., Ruszniewski,P.,
Robaszkiewicz,M., Deprez,P.H., Raguenes,O., Quere,I., Andriulli,A.
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Chen, J.-M., Le Marechal, C., Raguenes, O. and Ferec, C.
Chen, J.-M., Le Marechal, C., Raguenes, O. and Ferec, C.
Direct Submission
Submitted (11-MAR-2003) INSERM 0115, Universite de Bretagne
Occidentale, 46 rue Felix Le Dantec, Brest 29275, France
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="truncated trypsin 1"
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/trānslation="AAPFDDDDKIVGGYNCEENSVRYQVSLNSGYHFCGGSLINEQWV
VSAGHCYKS"
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.

    (bases 1 to 162)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-MAR-2003) INSERM 0115, Universite de Bretagne
Occidentale, 46 rue Felix Le Dantec, Brest 29275, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921 CCTTTTAGAACTAACACCCAAAAAGATGTCCTTCTCATTATAGGGGACTGGAA
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/note="serine protease 1; cationic trypsinogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 160;
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Chen, J.-M., Le Marechal, C., Raguenes, O. and Perec, C.
Direct Submission
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O.6%; Score 20.4; DB 1;
Best Local Similarity 61.1%; Pred. No. 1.5e+02;
Matches 33; Conservative 0; Mismatches 21;
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/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                      codon_start=3
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                                              /map="7q34"
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Homo sapiens
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KEYWORDS
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AUTHORS
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Homo sapiens cationic trypsinogen (PRSSI) gene, PRSSI-P36R allele,
Avon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="AAPFDDDDRIVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWV
VSAGHCYKS".
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                                      Jacases 1 to 160)
Chen, J.M., Raguenes, O. and Ferec, C.
Direct Submission
Submitted (127-MAY-2003) INSERM 0115, BFS-Bretagne, Universite de
Bretagne Occidentale, 46 rue Felix Le Dantec, Brest 29220, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160)
Chen,J.M., Piepoli Bis,A., Le Bodic,L., Ruszniewski,P.,
Robaszkiewicz,M., Deprez,P.H., Raguenes,O., Quere,I., Andriulli,A. and Ferec,C.
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Direct Submission
Submitted (27-MAY-2003) INSERM 0115, BFS-Bretagne, Universite de
Bretagne Occidentale, 46 rue Felix Le Dantec, Brest 29220, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutational screening of the cationic trypsinogen gene in a large cohort of subjects with idiopathic chronic pancreatitis Clin. Genet. 59 (3), 189-193 (2001)
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/branelarion="VFLDHENANKILNQPKRYNSGKLEEFVQGNLERECMEEKCSFEE
ARBYFENTERT"
                                                                                   S68634 CRM+ factor IX Strasbourg 2-cross reacting material positive factor IX Strasbourg 2 {exon 2} [human, hemophilia B patient J-C L, blood, Genomic Mutant, 199 nt].
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1 (bases 1 to 199)

de la Salle, C., Charmantier, J.L., Ravanat, C., Ohlmann, P., Barland, A. et al.

Enthann, M.L., Schuhler, S., Bischoff, R., Ebel, C., Roecklin, D., Balland, A. et al.

The Arg-4 mutant factor IX Strasbourg 2 shows a delayed activation by factor XIa

Nouv. Rev. Fr. Hematol. 35 (5), 473-480 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cross reacting material positive factor IX
Strasbourg 2; Arg-4 to Gln transition; Method: conceptual
translation with partial peptide sequencing"
/codon_start=1
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 143652] from the original journal article.
G6365 to A transition.
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0.6%; Score 20.4; DB 1; Length 199;
Best Local Similarity 61.1%; Pred. No. 1.6e+02;
Matches 33; Conservative 0; Mismatches 21; Indels
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/mol_type="genomic DNA"
/isolate="hemophilia B patient J-C I
/db_xref="taxon:9606"
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Curagen Corporation (US)
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Sequence 33 from Patent WO0063435.
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Homo sapiens
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TITLE
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                                                                                                                                                                                          /gene="PRSS1"
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Submitted (21-APR-1999) Stein U., Oncology and Surgical Oncology,
Max Delbrueck Center for Molecular Medicine, Robert-Roessle-Str.
10, Berlin 13092, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                      Query Match 0.6%; Score 20.4; DB 1; Length 162; Best Local Similarity 61.1%; Pred. No. 1.5e+02; Matches 33; Conservative 0; Mismatches 21; Indels
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0.6%; Score 20.4; DB 1; 3
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 26;
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Homo sapiens MVP gene, partial, exon 3
AJ238514
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major vault protein; MVP gene.
Homo sapiens (human)
Homo sapiens
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/gene="PRSS1"
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 171 BD071430/c

source

FEATURES

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This sequence codes for amino acids 9-146 of mature porcine factor IX. Amino acids 1-8 were previously identified by amino acid sequencing as YNSGKLEE, where the glutamic acid residues are gamma carboxy glutamic acids in the mature molecule (Lollar, P. et al. Biochemistry 26, 7627-7636, 1987). Amino acids 1-146 constitute the gla domain, the two epidermal growth factor-like domains and the linker peptide region, which collectively make up the light chain of activated factor ix. The remainder of porcine factor ix consists of the activation peptide (residues 147-181) and the catalytic domain (residues 182-146). The cDNA-derived sequence of the activation peptide and catalytic domain has been previously reported (Sarkar, G. et al. Genomics 6, 133-143, 1990 and Sarkar, G. et al. PCR Meth. Appl. 2, 318-322, 1993) with corrections as noted in Brandstetter, H. et al. Proc. Natl. Acad. Sci. U.S.A. 100cation/Qualifiers
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Submitted (12-MAR-1996) Pete Lollar, Medicine, Emory University,
Room 1008, Woodruff Mem. Bldg, 1639 Pierce Drive, Atlanta, GA
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Brandstetter,H., Bauer,M., Huber,R., Lollar,P. and Bode,W.

X-ray structure of clotting factor IXa: active site and module structure related to Xase activity and hemophilia B

Proc. Natl. Acad. Sci. U.S.A. 92 (21), 9796-9800 (1995)
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<1. >414
/ove="Christmas factor; when activated to factor IXa
/coverts factor X to factor Xa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa mature porcine factor IX mRNA, partial cds. U51135.1 GI:1256427
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/protein_id="AAA96318.1"
    Bougueleret, L., Niknejad, A. and Saudrais, C.
                        Gene encoding serine proteases
Patent: WO 9304641-A 56 07-AUG-2003;
Geneprot, Inc. (CH)
Location/Qualifiers
                                                                                                                  1. 394
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. 394
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/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol type="mRNA"
|db_xref="taxon:9823"
|chromosome="X"
                                                                                                                                                                                                                                     /note="exon 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 414)
Lollar, P.
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                                                                                                                                                                                                               misc_feature
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 173
SSU51135/c
LOCUS
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JOURNAL
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VERSION
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TITLE
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REFERENCE
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JP 2001519667-A/240
23--CCT-2001
10-APR-1998 JP 1998543069
10-APR-1997 US 08/838821
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                         Gaps
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Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
Secreted expressed sequence tags (SESTS)
Patent: JP 2001519567-A 240 23-OCT-2001;
GENETICS INSTITUTE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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                                                                                                                                      Length 315;
                                                                                                                                    Score 20.4; DB 1; Length 3 Pred. No. 1.8e+02; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                linear
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Secreted expressed sequence tags (SESTs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Unidentified'
                                                                                                                                                                                                                                                                             272 GCATCACAAGCTGGGGTGAAGGCTGCGGCCAGAAGAG 235
                                                                                                                                                                                                                                                                                                                                                                                           BD071430 334 bp DNA
Secreted expressed sequence tags (sESTs)..
BD071430
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AX814618
AX814618.1 GI:39103831
                                       /organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD071430.1 GI:22617033
JP 2001519667-A/240.
unidentified
                                                                                                                                    Query Match 0.6%;
Best Local Similarity 71.1%;
Matches 27; Conservative
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Homo sapiens
                        .315
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Best Local Similarity
Matches 33; Conserva
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CC To;
CC Sec
FH Ke;
FT so
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source

FEATURES

DEFINITION ACCESSION VERSION

AX814618/c LOCUS

RESULT 172

δ g KEYWORDS SOURCE ORGANISM

REFERENCE

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DVDGLSCKAKESVACGMVLGAGFEHNQLNPRAR I VGGNECPKGECPWQVLLVYKGKGF
CGGVIYKPTWILTASHCMADIDVQFLKVVAGEHNTEYDEGFEQIIOVSEIIMIEKYVP
RTADNDIALLHLAVDITYTTYAIPVCLPTRPLAERELMAVSLHTVGGWGRRSENGPTS
HILRQVKVPRIRTQCGESGGVYTQVMFCAGYMGGRQDSCKGDSGGFLVTKKKTVF
LLGIVSWGKGCARPGNYGIYTRVANYLEWIHNRTATVNQPTNNTENFT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRLRVFFTLVFTFTHCRAASVFLDADKAHDVLVFTRRYNSGWLE
BLOKGDLKRECLEBICSYEBAREVFEHTKTTDEFWKIYNRPNSCKSNPCLNGGSCSAE
GSSYTCFCLPEFSGVDCELBYQTVPDTCLLENGGCEHFCHENSAGORGNCSCADGYDL
                                                                                                                 AF465273 1326 bp mRNA linear VRI 02-FEB-2003
Takifugu rubripes coagulation factor VII precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                 Takifugu rubripes
Takifugu rubripes
Butaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Meoterygii, Acanthomorpha, Tetradontiformes;
Teradontoidea, Tetraodontidae, Takifugu.

[bases 1 to 1326]
Davidson, C.J., Hirt, R.P., Lal, K., Snell, P., Elgar, G.,
Comparative sequence analysis and molecular evolution of blood coagulation genes from Gallus gallus and Fugu rubripes

[https://www.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited.new.bited
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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McVey,J.H., Davidson,C.J., Lal,K., Snell,P. and Elgar,G.
Direct Submission

Submitted (04-JAN-2002) Haemostasis Group, MRC Clinical Sciences
Centre, The Faculty of Medicine, Imperial College, Hammersmith
Campus, Du Cane Road, London W12 ONN, UK
Location/Qualifiers
1. 1326

/organism="Takifugu rubripes"
//mol_type="mRNA"
//db trace="taxon:31033"
1. 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /EC_number="3.4.21.21"
/function="serum prothrombinconversion accelerator"
/function="serum prothrombinconversion accelerator"
/fnote="witamin K dependent serine protease; contains 2
EGF-like domains; member of peptidase family $1/trypsin family; found in plasma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2592 AAAGACCCTGATGCTGGGAGGGATTGGGGGCAGGAGAAGGGGACGACAGAG 2645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="coagulation factor VII precursor"
(protein id="AAO33368.1"
/db_xref="GI:28194018"
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AX427734
                                                                                                                                                                                                                                                                                                          Takifugu rubripes (Fugu rubripes)
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                                                                                                                                                                                                                                             GI:28194017
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AF465273.1
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AX427734/c
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                                                          RESULT 175
AF465273/c
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ORGANISM
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YHFCGGSLINSQWVVSAAHCYQTASRISVRIGEHNIFVNEGTEQQIQASKAIQHPQYN
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CVQAPVLSDTSCRNSYPGDITNNMICLGYLEGGKDSCQGDSGGPVVCNGELQGIVSWG
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CTTGYRLAPDQKSCKPAVPFPCGRVSVSHSPTTLTR"
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                                                                                                                                                                                                                                                                             2919 TACTTATTTAATTTTGGGATTTTAACTATTTCTAATGACTTGTATTTCTAATATTTAC 2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF011899 855 bp mRNA linear VRT 09-SEP-1997 Petromyzon marinus trypsinogen a3 (TRYPA3) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                        107 recirceaaaircarragirircreagigrrireaaaacircreggerrereaaa 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Perromyzontiformes; Petromyzontidae; Petromyzon.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-JUL-1997) Molecular Biotechnology, University of Washington, Seattle, WA 98195, USA
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                                                                                                                                                     0.6%; Score 20.4; DB 1; Length 414; 52.3%; Pred. No. 1.90+02; ive 0; Mismatches 41; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 855;
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/db_xref="taxon:7757"
/db_xref="taxon:7757"
/de-stage="ammocoete"
/tissue_lib="anterior intestine"
1. 855_lib="anterior intestine"
/gene="TRYPA3"
/gene="TRYPA3"
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71.1%; Pred. No. 2.2e
:ive 0; Mismatches
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/product="trypsin a3"
/evidence=not_experimental
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'protein_id="AAB69655.1"
'db_xref="GI:2367497"
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Best Local Similarity 71.1
Matches 27; Conservative
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nes 45; Conserv
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Matches 45
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PAT 20-JUN-2002

linear

PAT 17-JUL-2003

10664775-2.rge

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 1386)

Gerlitz, B. E. and Jones, B. E.

Protein C derivatives

L. Patent: JP 200242832-A 2 17-DEC-2002;

ELI LILLY AND CO

OS Homo sapiens (human)

PN 17-DEC-2002

PP 13-APR-2000 JP 2000615776

PR 30-APR-1999 US 60/131801

PI BRUCE EDWARD GERLITZ, BRYAN EDWARD JONES

PC CINIS/09, A61K38/48, A61P7/02, A61P9/10, A61P11/00, PC
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                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 1386)

Bang,N.U., Ehrlich,H.J., Grinnell,B.W. and Yan,S.-C.B.
Vectors and compounds for expression of zymogen forms of human protein C
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pc CI2N5/10,C12N9/64,C12N15/00,C12N5/00,A61K37/547 CC
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Location/Qualifiers
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Sequence 1 from Patent EP 0323149.
106643.
106643.1 GI:590170
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    .1386
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

                                                                                                                      1386 bp
                                                                                                                                                                                                          BD246883.1 GI:33056653
                                                                                                                                     Protein C derivatives.
BD246883
                                                                                                                                                                                                                                  JP 2002542832-A/2.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                      /proteIn_id="CAD35979.1"
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/translation="MWCLTSLLLFVATWGISGTPAPLDSVFSSSERAHQVLRIRKRAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKHVDGDQCIVLPLEHPCA
SLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFLNCSLDNGGCTHYCLEEVGWRRC
SCAPOYXLGDDLLQCHPAVKPPCGRPWKRMEKKRSHLKRDDGDGDQVDDRLIOGKMT
RROSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEDYDDRHST
BLDLDIKEVFYHPWYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAEREINQAG
OETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILG
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DKEAPQKSWAP"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 013645-4 14 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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Andersen, K.V., Freskgaard, P.O. and Pedersen, A.H. Protein C or activated protein C-like molecules Patent: WO 0232461-A 1 25-APR-2002;
MAXYGEN APS (DK); MAXYGEN HOLDINGS LTD (US)
Location/Qualifiers
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ilarity 55.7%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 31;
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/note="unnamed protein product"
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                                                                                                                                           1. .1383
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/product="unnamed"
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PAT 02-DEC-1994

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DEFINITION ACCESSION VERSION XEYWORDS

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2651 GATGGCTGGATGGCATCACTGGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGG
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| Gerlitz, B.E., Grimmell, B.W. and Jones, B.E.
| Protein C derivatives
| Patent: US 6630138-A 12 07-0CT-2003;
| Location/Qualifiers
| 1 . 1386
| /organism="unknown"
| mol_type="genomic DNA"
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Gerlitz,B.E., Grinnell,B.W. and Jones,B.E.
Protein C derivatives
Patent: US 6630138-A 11 07-OCT-2003;
Location/Qualiflers
1.1386
/organism="unknown"
/mol_type="genomic DNA"
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Sequence 12 from patent US 6630138.
AR404696.1 GI:40153408
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Sequence 11 from patent US 6630138.
AR404695.1 GI:40153407
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Sequence 7 from Patent WO0066754.
AX044042
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AR404695/c
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Unclassified.

I (bases 1 to 1386)

S Bang, N. U., Ehrlich, H. J., Grinnell, B.W. and Jaskunas, S.R.J.

Vectors and compounds for direct expression of activated human protein C protein C Location/Qualifiers

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Best Local Similarity 55.7%; Pred. No. 2.3e+02;
Matches 39; Conservative 0; Mismatches 31; Indels
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1 (Bases I to 1386)
2 (Barlitz, B.E., Grinnell, B.W. and Jones, B.E. Protein C derivatives
AL Patent: US 6530138-A 8 07-0CT-2003;
Location/Qualifiers
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0.6%; Score 20.4; DB 1;
Best Local Similarity 55.7%; Pred. No. 2.38+02;
Matches 39; Conservative 0; Mismatches 31;
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Sequence 8 from patent US 6630138.
AR404692 GI:40153404
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Sequence 1 from Patent EP 0319312.
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/wol_type="genomic DNA"
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IO8112.1 GI:589175
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2.38+02;
0; Mismatches 31; Indels 0;
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Patent: WO 013645-4 10 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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                                                                                                                                                                                         Gerlitz, B.E. and Jones, B.E.
Protein c derivatives
Patent: WO 0066754-A 7 09-NOV-2000;
ELI LILLY AND COMPANY (US)
LOCATION/Qualifiers
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AX149641
AX149641.1 GI:14348040
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Sequence 10 from Patent WO0136462.
AX149640
  GI:11342921
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1 Similarity 55.7%;
39; Conservative (
                                                        Homo sapiens (human)
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                                                                                      Homo sapiens
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                          Gerlitz,B.E., Grinnell,B.W., Huang, L. and Jones,B.E. Protein c derivatives
Patent: WO 0136462-A 11 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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55.7%; Pred. No. 2.3e+02;
:ive 0; Mismatches 31;
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Patent: WO 0136462-A 13 25-MAY-2001;
ELI LILLY AND COMPANY (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .1386
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
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Sequence 16 from Patent WO0136462.
AX149646
AX149646.1 GI:14348045
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Sequence 13 from Patent WO0136462.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.6%; Score 20.4; DB 1; Length 1386;
Best Local Similarity 55.7%; Pred. No. 2.3e+02;
Matches 39; Conservative 0; Mismatches 31; Indels 0.
                                                                                                                                                                           Score 20.4; DB 1; Length 1386; Pred. No. 2.3e+02; 0; Mismatches 31; Indels 0
            derlitz, B.E., Grinnell, B.W., Huang, L. and Jones, B.E.
Protein c derivatives
Patent: WO 0136462-4 16 25-MAY-2001;
ELI LILX AND COMPANY (US)
Location/Qualifiers
1.1386
//organism="Homo sapiens"
//mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Gerlitz,B.E., Grinnell,B.W. and Jones,B.E.
Protein c derivatives
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Protein c derivatives
Protein: wo 0157193-A 8 09-AUG-2001;
Ell LillY AND COMPANY (US)
Location/Qualifiers
1. 1386
| norganism="Homo sapiens" |
| mol_type="unassigned DNA" |
| db_xref="taxon:9606"
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Sequence 7 from Patent WO0159084.
AX212331
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Best Local Similarity 55.7%;
Matches 39; Conservative
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Homo sapiens
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AX212331/c
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Unclassified.

1 (bases 1 to 1386)

1 (bases 1 to 1386)

Garner, I., Cottingham, I.R., Temperley, S.M., Foster, D.C., Sprecher, C.A. and Prunkard, D.B.
Protein C production in non-human transgenic mammals Patent: US 5905185-A 3 18-WAY-1999;

Location/Qualifiers

1. 1386
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Patent: WO 0159084-A 7 16-AUG-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
                                        1. .1386
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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JP 2002542832-A/3.
Homo sapiens (human)
Homo sapiens
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BD246884
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AR070468/c
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Gerlitz, B.E., Grinnell, B.W., Huang, L. and Jones, B.E.
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AX149645/c
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                                                                     A61P17/02, A61P31/00, A61P31/12, A61P37/06, C12N1/15, C12N1/19, PC
13-APR-2000 JP 2000615776
30-APR-1999 US 60/131801
BRUCE EDWARD GERLEZ BRYAN EDWARD JONES
C12N15/09,A61X38/48,A61P7/02,A61P7/06,A61P9/10,A61P11/00, PC
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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C12N5/10,C12N9/64,C12N15/00,C12N5/00,A61K37/547 CC
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Gerlitz, B.E., Grimmell, B.W. and Jones, B.E.
Protein C derivatives
Patent: US 6630139-A 9 07-OCT-2003;
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Pred. No. 2.3e+02;
0; Mismatches 31;
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Sequence 9 from patent US 6630138.
AR404693
                                                                                                                                                                                       1. .1386
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Sequence 8 from Patent WO0066754.
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Best Local Similarity 55.7'
Matches 39; Conservative
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                                                                                   C12N1/21,
PC C12N5/10
derivatives
FH Key
FT source
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PF 13-APF
PR 30-APF
PI BRUCE
PC C12N1E
A61P13/00,
PC A61P17
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AR404693/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Patent: WO 013645-7-A 12 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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                                          Gerlitz, B.E. and Jones, B.E.
Protein c derivatives
Patent: WO 0066754-A 8 09-NOV-2000;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
                                                                                                                                                                1. .1386 // Organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 12 from Patent WO0136462.
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Sequence 15 from Patent WO0136462.
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AXI49642.1 GI:14348041
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BD246885.1 GI:33056655
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Homo sapiens
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Matches 39; Conserv
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Protein c derivatives
Patent: WO 0136462-A 15 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
1. .1386
//organism="Homo sapiens"
//mol_type="unassigned DNA"
//db_xref="taxon:9606"
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Protein c derivatives
Patent: WO 0157193-A 11 09-AUG-2001;
ELI LILLY AND COMPANY (US)
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Protein c derivatives
Patent: WO 0157193-A 9 09-AUG-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 11 from Patent WO0157193.
AX207787
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Sequence 9 from Patent W00157193.
AX207785
AX207785.1 GI:15422461
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Best Local Similarity 55.7%;
Matches 39; Conservative
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AX207787/c
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AX207785/c
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1 (bases 1 to 1386)
Gerlitz, B.E. and Jones, B.E.
Gerlitz, B.E. and Jones, B.E.
Protein C derivatives
Patent: JP 200242832-A 4 17-DEC-2002,
Ell LILLY AND CO
S Homo sapiens (human)
Py 2002542832-A/4
Py 17-DEC-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.6%; Score 20.4; DB 1; Length 1386;
Best Local Similarity 55.7%; Pred. No. 2.38+02;
Matches 39; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                      Length 1386;
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Protein c derivatives
Patent: WO 0159084-A 8 16-AUG-2001;
ELI LILLY AND COMPANY (US)
1. 1386
1. 1386
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larity 55.7%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 31;
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1. .1386
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/mol_type="unassigned DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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30-APR-1999 US 60/131801
BRUCE EDWARD GERLITZ, BRYAN EDWARD JONES
CI2N15/09,A61K38/48,A61P7/02,A61P7/06,A61P9/10,A61P11/00, PC
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A61P13/00,
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O.6%; Score 20.4; DB 1; Length 1386;
Best Local Similarity 55.7%; Pred. No. 2.3e+02;
Matches 39; Conservative 0; Mismatches 31; Indels 0;
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Location/Qualifiers
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Sequence 10 from patent US 6630138.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Protein c derivatives
Patent: WO 0157193-A 10 09-AUG-2001;
BLI LILLY AND COMPANY (US)
LOCATION/Qualifiers
Gerlitz, B.E. and Jones, B.E.
Protein c derivatives
Patent: WO 0066754-A 9 09-NOV-2000;
ELI LILLY AND COMPANY (US)
LOCATION/Qualifiers

    .1386
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/mol_type="unassigned DNA"
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Sequence 10 from Patent WO0157193.
AX207786
AX207786.1 GI:15422462
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Sequence 12 from Patent W00157193.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Catarrhini, Hominidae, Homo.
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                                                                                                                                           Query Match 0.6%; Score 20.4; DB 1; Length 1386; Best Local Similarity 55.7%; Pred. No. 2.38+02; Matches 39; Conservative 0; Mismatches 31; Indels 0
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Patent: WO 0159084-A 9 16-AUG-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
1. 1386
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Noted 10 13305656

DECAGORD 13305656

DECAGORD 13305656

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Gukaryota, Metazoa, Chordata, Craniata, Mammalia, Eutheryota, Metazoa, Chordata, Craniata, Mercayota, Butharia, Primates, Catarrhini, (hases 1 to 1386)

Gerlitz, B.E. and Jones, B.E.

Protein C derivatives

Patent: JP 2002542832-A 5 17-DEC-2002,

ELI LILLY AND CO
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 Protein c derivatives
Patent: WO 0157193-A 12 09-AUG-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
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AX212333/c
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OS Homo sapiens (human)
PN JP 202542832-A/5
PP 17-202542832-A/5
PP 13-APR-2000 JP 2000615776
PF 13-APR-2000 JP 2000615776
PP 30-APR-1999 US 60/131801
PC C12N15/09, A61K38/48, A61P7/02, A61P7/06, A61P9/10, A61P11/00, PC A61P1/02, A61P31/12, A61P3/06, C12N1/15, C12N1/19, PC C12N1/12,
PC C12N1/21,
PC C12N5/10,C12N9/64,C12N15/00,C12N5/00,A61K37/547 CC Protein C
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 55.7%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 31;
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Protein c derivatives
Patent: WO 0066754-A 10 09-NOV-2000;
BLI LILLY AND COMPANY (US)
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Sequence 10 from Patent WO0066754.
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AX044045.1 GI:11342924
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FH Key
FT source
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Matches 39; Conserv
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1387)
Gerlitz, B.E. and Grinnell, B.W.
Vectors and compounds for expression of zymogen forms of human protein C
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                                                                                                                   Gerlitz, B.E., Grinnell, B.W. and Jones, B.E. Protein c derivatives
Patent: WO 0159084-A 10 16-AUG-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Patent: US 5270178-A 1 14-DEC-1993;
Location/Qualiflers
1. .1387
/mcl_type="genomic DNA"
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Sequence 1 from patent US 5861374.
AR030786
 AX212334.1 GI:15524090
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                                            Homo sapiens (human)
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AR364387/c
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1 (bases 1 to 2422)

Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and Bregengaard,C.
Modified factor VII
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Berkner, K.L., Petersen, L. Christian., Hart, C.E., Hedner, U. and Bregengaard.C.
Modified factor VII
Patent: US 5833982-A 1 10-NOV-1998;
1. .2422
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                                                                                                                                                                              Length 2422;
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                                                                                                                                                                                                                   41; Indels
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           1 (bases 1 to 2422)
Berkner, K.L., Petersen, L. Christian. and Hart, C.E. Modified Pactor VII
Patent: US 5861374-A 1 19-JAN-1999;
Location/Qualifiers
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0.6%; Score 20.4; DB 1;
Best Local Similarity 52.3%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 41;
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                                                                                                                        /organism="unknown"
/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 1 from patent US 5817788.
AR045090
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Sequence 1 from patent US 5833982.
AR052946.1 GI:5977808
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AR052946
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                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
Unclassified.
1 (Cases I to 2422)
1 Eases I to 2422)
Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and Bregengaard,C.
Modified factor.
Patent: US 6168789-A 1 02-JAN-2001;
Patent: Us 6168789-A 1 02-JAN-2001;
1 . . 2422
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Unclassified.
1 (bases 1 to 2422)
Hart,C.E., Petersen,L.C., Hedner,U. and Rasmussen,M.E. Modified factor VII
Patent: US 6183743-A 1 06-FEB-2001;
                                                 Ouery Match 0.6%; Score 20.4; DB 1; Length 2422; Best Local Similarity 52.3%; Pred. No. 2.3e+02; Matches 45; Conservative 0; Mismatches 41; Indels 0
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    2422
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Sequence 1 from patent US 6183743.
AR127821.1 GI:14115483
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ARQUENCE 1 from patent US 6168789.
AR122899 GI:14107865
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1 (bases 1 to 2462)

Thorpe,P.E. and Edgington,T.S.

Methods and compositions for the specific coagulation of
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S Thorpe, P.E. and Edgington, T.S.
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Matches 45; Conservative 0; Mismatches 41; Indels
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Horrigan, S., Soppet, D.R. and Weaver, 2.
Cancer gene determination and therapeutic screening using signature
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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אוסייי 2462 bp mRNA linear PRI 13-FEB-1996
Human factor VII serine protease precursor mRNA, complete cds,
clone lambda-HVII2463.
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INHDIALLRLHQPVVLIDHVVPLCLPERTFSERTLAPVRFSLVSGWGQLLDRGATALE
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join(36. .99, &66. .215)
/note="factor VIIb signal peptide"
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Draft entry and sequence in computer-readable form for [1] kindly provided by F.S.Hagen.

[1] sequenced two alternatively spliced mRNAs that produced shortened signal peptides. One is presented as factor VIIb below. Location/Qualifiers
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factor VII; serine protease; serum glycoprotein.
Homo sapiens (human)
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'note="preprofactor VIIb"

PAT 02-DEC-1994

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240 bp DNA linear PRI 22-OCT-1995
H.sapiens CpG island DNA genomic Msel fragment, clone 88al2,
reverse read cpg88al2.rtla.
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Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hagen,F.S., Murray,M.J., Busby,S.J., Berkner,K.L., Insley,M.Y., Woodbury,R.G. and Gray,C.L.
Expression of factor VII and IX activities in mammalian cells Patent: EP 0200421-A2 3 10-DEC-1986;
Location/Qualifiers
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CpG island; genomic Msel fragment.
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Furederitsuku, E.H., Maaku, J.M., Shiyaaron, J.B., Kiyasuriin, E.B.,
Maggaretsuto, W.I., Richiyaado, J.U. and Chiyaaruzu, E.G.
DNA ENCODING FACTOR VII
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                                                                                                                                                                                   Score 20.4; DB 1; Length 2462;
Pred. No. 2.3e+02;
0; Mismatches 41; Indels 0;
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                                   100. .165
/note="alternate exon; putative"
1166. .2462
/note="factor VIIb"
/number=2
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CDNA sequence of Factor VII fragment.
E01076

    .2483
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:3264"

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Matches 45; Conservative
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H.sapiens CpG island DNA genomic Msel fragment, clone 88a12,
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MACACA fascicularis (individual isolate 2368) MHC-DRB5 class II
(Mafa-DRB5*09a) gene, partial cds.
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Purification of CpG islands using a methylated DNA binding column
Mat. Genet. 6 (3), 236-244 (1994)
94282070
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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cell surface glycoprotein; class II gene; integral membrane protein; major histocompatibility complex.
Macaca fascicularis (crab-eating macaque)
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MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.
Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambr
CBIO 1RQ, England. E-mail contact: humquery@sanger.ac.uk
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CpG island; genomic Msel fragment.
Homo sapiens (human)
Homo sapiens
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/dev_stage="adult"
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/clone_lib="CGI-1"
/dev_stage="adult"
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/clone="88a12"
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Conserved sequence motifs create a pattern of MHC genetic diversification within primate DRB lineages Unpublished (1994) original source text: Macaca fascicularis (individual_isolate 2368) original source text: Macaca fascicularis (individual_isolate 2368) adult PBL DNA.
Derived from DRB (PCR) amplification, exon 2, (codons 7 to 87) Sequence ID Mafa-DRB5*09a.
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TELGRPDAEYWNGQKDILERRRAEVDTVCRHNYGVFE"
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Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrinin; Cercopithecidae;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                             Gaur, L.K., Nepom, G.T., Snyder, K.E., Anderson, J., Pandarpurkar, M.
and Heise, E.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 CAGAGACATCTACAACCAAGAGGAGGACTTGCGCTTCGACAGCGACGTGGGGGAGTACCG
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                                                                                          Cercopithecinae; Macaca.
1 (bases 1 to 243)
Gaur, L.K. and Nepom, G.T.
Ancestral MHC-DRB genes beget conserved patterns of localized
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                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. (1996) In press 2 (bases 1 to 243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Macaca fascicularis"
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79

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151

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148...>582
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A novel mutation nt10788 A-5G(315,Thr->Ala) located in exon IX of A novel mutation nt10788 A-5G(315,Thr->Ala) located in exon IX of the budan protein C gene in a family presenting with hereditary thrombophilia
Unpublished
2 (bases 1 to 582)
Liu,J., Wang,X., Wei,W., Li,F. and Sun,H.
Direct Submission
Submitted (33-JUL_2003) Biology, Northeast Normal University, Renming Street N0138, Changchun, Jilin 130024, China
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 582)
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Pred. No. 2.3e+02;
0; Mismatches 38; Indels
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Homo sapiens protein C gene, exon 9 and partial cds.
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/number=9
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Best Local Similarity 53.1;
Matches 43; Conservative
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A novel mutation nt10788 A->G(315,Thr->Ala) located in exon IX of
A novel mutation nt10788 A->G(315,Thr->Ala) located in exon IX of
the human protein C gene in a family presenting with hereditary
thrombophila
Unpublished
J. (bases 1 to 582)
Liu,J., Wang,X., Wei,W., Li,F. and Sun,H.
Direct Submission
Submitted (23-JUL-203) Biology, Northeast Normal University,
Renming Street NO138, Changchun, Jilin 130024, China
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Komatsu,N., Takata,M., Otsuki,N., Toyama,T., Ohka,R., Takehara,K.
and Saijoh,K.
         and Saijoh, K.
Expression and localization of tissue kallikrein mRNAs in human epidermis and appendages
2 (bases I to 378)
                                                                                                                                                                        2 (bases 1 to 378)
Saijoh,K. and Komatsu,N.
Direct Submission
Submitted (18-APR-2003) Kiyofumi Saijoh, Kanazawa Univ Sch Med,
Dept Hygiene, 13-1 Takara-machi, Kanazawa 920-8640, Japan
(E-mail:saijohk@med.kanazawa-u.ac.jp, Tel:81-76-265-2213,
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llarity 50.5%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 48; Indels
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/organism="Homo sapiens"
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Ono,M., Dongchon,K. and Hamasaki, I.
Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
Patients. Genetic Background of Thrombophilia in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-APR-2002) Naotaka Hamasaki, Kyushu University Nappital. Department of clinical Chemietry and laboratory medicine, 3-1-1 maidashi, Higashi-ku Fukuokasi, Fukuoka 812-8583, Japan (E-mail:hamasaki@cclm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
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GLLHNYGVYTSQPLPRLDPWAHQRQGSPPEELGTLATLPAGLGFCMAMDGT"
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/replace="aa"
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Oro,M., Dongchon,K. and Hamasaki,N.
Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
Patients. Genetic Background of Thrombophilia in Japan
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/mol type="genomic DNA"
/isolate="Patient:PC11"
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GLLHNYGVYTKVSRYLDWIHGHIRDKBAPQKSWAP"
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Homo sapiens PROC gene for Protein C, partial cds, isolate:patient:
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Gene Analysis of Atticosqulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan Unpublished
2 (bases 1 to 696)
                                                                     Kinoshita,S., Iida,H., Inoue,S., Watanabe,K., Kurihara,M., Wada,Y., Ono,M., Dongchon,K. and Hamasaki,N. Gene Analysis of Anticoagulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (14-APR-2002) Nactaka Hamasaki, Kyushu University
Hospital, Department of clinical chemistry and laboratory medicine;
3-1-1 maidashi, Higashi-ku Fukuokasi, Fukuoka 812-8582, Japan (E-mail:hamasaki@cclm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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llarity 53.1%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 38;
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/product="Protein_C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subblitted (14-APR-2002) Naotaka Hamasaki, Kyushu University Hospital, Department of clinical chemistry and laboratory medicine; 3-1-1 maidashi, Higashi-ku Fukuokasi, Pukuoka 812-8582, Japan (E-mail:hamasaki@cclm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
                                                                                                                                                                                                                                                                                                                                                                                             Kinoshita,S., Iida,H., Inoue,S., Watanabe,K., Kurihara,M., Wada,Y., Ono,M., Dongchon,K. and Hamasaki,N. Gene Analysis of Anticoagulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan
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               Direct Submission
Submitted (14-APR-2002) Naotaka Hamasaki, Kyushu University
Hospital, Department of clinical chemistry and laboratory medicine,
3-1-1 maidashi, Higashi-ku Fukuokasi, Fukuoka 812-8582, Japan
(E-mail:hamasaki@cclm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAC21168.1"
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Submitted (14-APR-2002) Naotaka Hamasaki, Kyushu University
10-partment of clinical chemistry and laboratory medicine;
3-1-1 maidshi, Higashi-ku Fukuokasi, Fukuoka 812-8582, Japan
(E-mail:hamasaki@clm.med.kyushu-u.ac.jp, Tel:81-92-642-5770,
Pax:81-92-642-5772)
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eene Analysis of Anticoagulation Factors in Japanese Thrombotic Patients. Genetic Background of Thrombophilia in Japan
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/organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="patient: PC 2"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 747)
Liu,J. and Sun,H.
Direct Submission
Submisted (30-OCT-2003) School of Life Sciences, Northeast Normal Submitted (30-OCT-2004) School of Life Sciences, Northeast Normal University, Renming Street No138, Changchun, Jilin 130024, China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703 TACTACTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAGA
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Homo sapiens protein C gene, exon 9 and partial cds.
AY454079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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Pred..No. 2.3e+02;
0; Mismatches 38;
                                                                                                                                                                                                                                              <61. .651
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477</pre>
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706. .711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .747
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/product="protein C"
70. .>726
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                                                                                                                                                                                               'product="Protein
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PAT 24-OCT-2002

linear

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                            Seldon, R. F., Miller, A.M. and Treco, D.S.
Optimized messenger rna
Patent: WO 02064799-A 105 22-AUG-2002;
TRANSKARVIIC THERAPIES, INC. (US)
Location/Qualifiers
1. 1505
// organism="Homo sapiens"
//mol type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 20.2; DB 1;
ilarity 54.8%; Pred. No. 2.5e+02;
Conservative 0; Mismatches 33;
     1505 bp DNA
Sequence 105 from Patent WO02064799.
                                                                    AX523898.1 GI:24412662
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                                                                                                            Homo sapiens (human)
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Best Local Similarity
Matches 40; Conserv
                                                                                                                               Homo sapiens
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AR095304/c
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AX523898/c
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ALGILWYTRACTYGVNSWGGGCFHATH
YHGTWYLTGVVSWGGCGAAIGHIGVYTRVSQYIDWLVKYMDSKLRVGISRVSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy, K. and Ramaker, M.

Murphy, K. and Ramaker, M.

Unpublished

2 (fases 1 to 134)

Murphy, K. and Ramaker, M.

Direct Submission

2 (134.7UL-2012) Biotechnology, Bristol-Myers Squibb, P.O.

Box 80336, Wilmingtion, DE 19880-0336, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               967 TGACCCTCGAGAAGCGGATGCTGGCTAGGGTGTTCTCGGAGAAGGCCCGTTCAGGCAGAC 908
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                                                                                            762
                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                  14 TGCCACTGGGGAGAGGCTCCCGCAGCTCTGACTGTGCCCTCTGCCCTGCAGAGA
                                                                                            703 TACTACTGCGGGCAGGAATCCCTCAGAAGAAATGGAGTAGCCATCATGGTCAACAAAAGA
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                 Length 747;
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                   Score 20.2; DB 1;
Pred. No. 2.4e+02;
0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1341
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1. .1341
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1 Similarity 53.1%;
43; Conservative
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Best Local Similarity
Matches 67; Conserv
                         Query Match
Best Local Similarity
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AF532184/c
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PAT 08-SEP-2000
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                                                                                                                       Unclassified.

1 (bases 1 to 2462)

Thorpe, P.E. and Edgington, T.S.
Methods for the specific coagulation of vasculature Patent: US 6004555-A 25_21-DEC-1999;
                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                 53;
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49.5%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR103988
Sequence 25 from patent US 6093399.
AR103988
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   AR095304 ~2462 bp
Sequence 25 from patent US 6004555.
AR095304 1 GI:10023060
                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 49.5
Matches 52; Conservative
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                                                                                       Unknown.
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236

RESULT

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="coagulation factor VII"
protein_id="AAA88040.1"
db_xref="G1:182801"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 2462
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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:1. .2462
                                                                                                     Location/Qualifiers
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M13222.1 GI:182799
factor VII; serine pro
Homo sapiens (human)
Homo sapiens
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Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                           1 (Desertion 1 to 2462)
Thorpe, P.E. and Edgington, T.S.
Methods and compositions for the specific coagulation of
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O.6%; Score 20.2; DB 1; Length 2462;
Best Local Similarity 49.5%; Pred. No. 2.5e+02;
Matches 52; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2462;
                                                                                                                                                                                                                                                                                                                                          2631 AAGGGACGACAGAGGATGAGTGGCTGGATGGCATCACTGACTC 2675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2631 AAGGGGACGACAGAGGATGAGATGGCTGGATGGCATCACTGACTC 2675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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0.6%; Score 20.2; DB 1;
Best Local Similarity 49.5%; Pred. No. 2.5e+02;
Matches 52; Conservative 0; Mismatches 53
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Sequence 5592 from Patent WO0194629.
AX335083.1 GI:18125802
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                                                                                                              Patent: US 6093399-A 25 25-JUL-2000;
Location/Qualifiers
1. .2462
                                                                                                                                                                             /mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                              /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                Unclassified.
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   Unknown.
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AX335083/c
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AX409604/c
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HUMFVII 2462 bp mRNA linear PRI 13-FEB-1996
Human factor VII serine protease precursor mRNA, complete cds,
clone lambda-HVII2463.
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FVTOBEAHGYLHRRRRANAFLEELRFOSLERECKEBGCSFEBAREIFKDAENLEVNE
FVTOBEAHGYLHRRRRANAFLEELRFOSLERECKEBGCSFEBAREIFKDADULICVNENGGEG
YSSDHOGCASS PROGNGGSCKDQLOSY ICTCLDAFFEGRNCETHKDDQLICVNENGGEG
YCSDHYGTKRSCRCHEGYSLLADGVSCTPYTVSYPCGKI PILEKRNASKPGGRYVGKY
DGDEGRRWAVQVIIDSTYVPYGTYNHDIALLAHQPVULTDHVVPLCLDFRTFSERTLA
FVRFSLVSGWQQLLDFRGATALLELMVLNVPRLATQDCLQGSRKVGDSPNITEYMFCAGY
SDGSKDSCKGDSGGPHATHYRGTWYLTGIVSMGGGGATVGHFGVYTRVSQYIEWLQKI
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Draft entry and sequence in computer-readable form for [1] kindly provided by F.S.Hagen.

[1] sequenced two alternatively spliced mRNAs that produced shortened signal peptides. One is presented as factor VIIb below.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (Bases I to 2462)
Hagen, F.S., Gray, C.L., O'Hara, P.J., Grant, F.J., Saari, G.C.,
Woodbury, R.G., Hart, C.E., Insley, M., Kisiel, W., Kurachi, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. Gene expression profiles in liver cancer Patent: WO 0229103-A 2251 11-APR-2002; GENE LOGIC INC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%; Score 20.2; DB 1; Length 2462; Best Local Similarity 49.5%; Pred. No. 2.5e+02; Matches 52; Conservative 0; Mismatches 53; Indels 0
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Characterization of a cDNA coding for human factor VII
Proc. Natl. Acad. Sci. U.S.A. 83 (8), 2412-2416 (1986)
86205965
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                                                                                                                                                                                         1. 2462
Coganism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. M13232"
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AF005089

276 bp mRNA linear PLN 18-FEB-2000
Triticum aestivum phenylalanine ammonia lyase (War7.2) mRNA,
partial cds.
AF005089.1 GI:6996627
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codon Start==2
/product="adenylyl cyclase 7"
/product="adenylyl cyclase 7"
/protein id="AAN34659 1"
/bx xxef="d1:23477359 1"
/translation="LLLKPRESCYEKIKTIGSTYMAAAGLSVPSGHENQDLERKHVHI
GYLVBFSMALMSKLDGINRHSFNSFRLRVGINHGPVIAGVI"
                                                                                                                                                                                                                                                                                                      AF542508 256 bp mRNA linear ROD 03-OCT-2002 Rattus norvegicus adenylyl cyclase 7 mRNA, partial cds. AF542508
                                                                                       2665 ATCACTGACTCGATGGACGTGAGTCTGGGTGAACTCCTGGAGTTGGTGATGGACAGGGAG 2724
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
1 (bases 1 to 276)
          2605 CTGGGAGGGATTGGGGGGCAGGAGAAGGGGACGACAAGAAGGATGAGATGGCTGGATGGC 2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I (bases 1 to 256)
Haunso, A. and Antoni, F.
Direct Submission
Submitsed (02-889-2002) Department of Neuroscience, University of Edinburgh, 1 George Square, Edinburgh EH8 9JZ, UK
Location/Qualifiers
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
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<1. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
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ilarity 51.1%; Pred. No. 2.2e+02;
Conservative 0; Mismatches 45
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Rattus norvegicus
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47; Conserv
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AF005089
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AF542508
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                                                                                               /codon_start=1
/brotein_id=MAAR88041.1"
/brotein_id=MAAR88041.1"
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LOSYICFCLPAFEGGRNCETHUDDOLICTWNENGGCEQVCSDHTGTKRSCRCHEGYSLLA
DGVSCTPTVEYPCRTFILEKNASKFQGRTVGGKCPEGCPWQVLLLVNGAQLCGG
TLINTINVSAAHCPRITKONASKPQETYFSRRTLAFVRFSLVGGWQDLLDKGATALE
TWHIDIALLAELHQPVVLTPHVVPLCLPERTFSRRTLAFVRFSLVGGWQDLLDKGATALE
TWYLTGITSWGGGCATVGHFQVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP"
join (36. . 99, 166. . 215)
/note="factor" VIIb signal peptide"
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Patent: WO 0300898-A 5040 03-JAN-2003;
Syngenta Participations AG (CH)
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                     36. .215
/note="factor_VIIa signal peptide"
                                                                                                                                                                                                                                                                                                                                                                     216. .671
/product="coagulation factor VII"
/note="light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="coagulation factor VII"
/note="heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="alternate exon; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX655170 199 bp DNA
Sequence 5040 from Patent WO03000898.
AX655170
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                                                        join(36. .99,166. .1436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <36. .99 
/note="preprofactor VIIb"</pre>
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/note="factor VIIb"
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                   sig_peptide
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AX655170/c
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PAT 18-SEP-2002

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168 GCTGCTCTGCCACCTSGACGCCACCCTGGCCATGGAGCAGCAGCTGGTGGTTCCTAA 109
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1 (Dases 1 to 300)

Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.

Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.

Par and encoded human protein

Parent: JP 2002010789-A 12438 15-JAN-2002;
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C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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    .300
    /organism='Homo sapiens (human)'.

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48.9%; Pred. No. 2.2e+02;
tive 3; Mismatches 43; Indels'
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                                                              71 TGGAGCAGCCGTAAAGAGATACCCCACGCC 100
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                                                                                           108 TCGTGCAACCATSSAAACCAGCCSCCSGC 79
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2012010789-A/12438
15-JAN-2002
07-AUG-2000 US 60/147499
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BD120361.1 GI:23215271
JP 2002010789-A/12438.
Homo sapiens (human)
Homo sapiens
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Matches 44; Conserve
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BD120361/c
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Hamel, F., Breton, C. and Houde, M.
Isolation and characterization of wheat aluminum-regulated genes:
possible involvement of aluminum as a pathogenesis response
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                                                                                                                                                                            Thamel.F., Breton, C. and Houde, M.

Direct Submission.

Submitted (22-MAY-1997) Departement des Sciences Biologiques,
Universite du Quebec a Montreal, C.P. 8888, Succ. Centre-ville,
Montreal, Quebec H3C 3P8, Canada

Location/Qualifiers
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1 (bases 1 to 300)
Edwards,J.-B.D.M. Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639065-A 16305 28-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="root tips"
/dev_stage="5 days old seedlings"
/note="hexaploid"
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Pred. No. 2.2e+02;
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4565"
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                                                                                 elicitor
Planta 205 (4), 531-538 (1998)
98348982
                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="Atlas-66"
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/gene="War7.2"
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Matches 44; Conservative
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MAM 05-FEB-1999
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Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
Dog gene for coagulation factor VII, partial cds. D21213.
D21213.1 GI:415264
Canis familiaris (dog)
Bukarvore. VII.
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/protein_id="Bra07812.1"
/db_xref="G1:1304147"
/rdanslation="photein CESTIVHPNYTRGSSDNDIALLRLAQPATLSKTIVP
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ICLPNNGLAQOELPOAGGETVVTGMGYQSDRIKDGRRNRTFILTFIRIPLVARNECVE
VMXNVVSENMLCAGIIGNTRDACDGDSGGPMVVFFRGTWFLVGLVSWGEGGGHTNNYG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0.6%; Score 20; DB 1; Length 483;
Best Local Similarity 47.6%; Pred. No. 2.5e+02;
Matches 59; Conservative 0; Mismatches 65; Indels
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72.2%; Pred. No. 2.5e+02;
tive 0; Mismatches 10;
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Patent: US 6331427-A 109 18-DEC-2001;
Location/Qualifiers
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Seguence 221 from Patent WO0140466.
                                                       organism="Mus musculus"
                                                                                                                                                                                                                                   /note="catalytic region'
/codon_start=1
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                                                                               /mol type="genomic DNA"
/strain="Balb/c"
/db_xref="taxon:10090"
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/organism="unknown"
Location/Qualifiers
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AR263931.1 GI:28075935
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Robison, K.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="coagulation factor VII"
/protein_id="BAA04754.1"
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/db_xref="cd1:455390"
/tanslation="EDDGDEGERHVARVIVPDKYIPLKTNHDIALLHLRTPVAYTDHV
VPLCLPERTFSERTLAFIRFSTVSGWGGLLDRGATALQLMAIDVPRVMTQDCQEQSRR
RSGSPAITENNFCAGYLDGSKDACQGDSGGPHATKFQGTWYLTGVVSWGEGCAAEGH"
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Br. J. Haematol. 86 (3), 590-600 (1994)
94318474
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 483)
Murakawa,M., Okamura,T., Kamura,T., Kuroiwa,M., Harada,M. and
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Submitted (06-DEC-1994) Masahiro Murakawa, Harasanshin General
Hospital, Division of Hematology; 1-8 Taihaku-machi, Hakata-Ku,
Fukuoka, Pukuoka 812, Japan (Tel:092-291-3434, Fax:092-291-3266)
                                                                                                                                                                                                 Submitted (18-0CT-1993) Masahiro Murakawa, Harasanshin General Hospital, Division of Hematology; 1-8 Taihaku-machi, Hakata-ku, Fukuoka, Fukuoka 812, Japan (Tel:092-291-3434, Fax:092-291-3266) Submitted (18-0ct-1993) to DDBJ by:
Masahiro Murakawa
Division of Hemotology
Harasanshin General Hospiral
1-8 Taihaku-machi, Hakata-ku
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D43755.1 G1:601897
Drotein C; serine protease zymogen; vitamin K-dependent serine
protease; blood coagulation-related.
Mus musculus (house mouse)
Mus musculus
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0.6%; Score 20; DB 1; Length 478;
Best Local Similarity 55.9%; Pred. No. 2.5e+02;
Matches 38; Conservative 0; Mismatches 30; Indels
                                    Haematol. 52 (3), 162-168 (1994)
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/organism="Canis familiaris"
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/db_xref="taxon:9615"
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Fax : 092-291-3266.
Location/Qualifiers
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/codon_start=2
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Murakawa, M.
                                                                                                                                 (bases 1 to 478)
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            factors VII and
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                                                                                                                                                            durakawa, M.
                                              Eur. J. Ha
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MUSBALB6
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Gaps

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddadd, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 221 07-JUN-2001;
Genentech Inc. (US)
FEATURES

1. 1129
Cocation/Qualifiers
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Creation date: 08-26-2004

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